

GenCore version 5.1.6
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OM protein - protein search, using bw model

Run on: January 18, 2006, 20:50:17 : Search time 129 Seconds
(without alignments)
34.060 Million cell updates/sec

Title: US-09-930-125-3
Perfect score: 10
Sequence: 1 ERYLVPQGR 10

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 243163 seqs, 439378781 residues

Word size : 0

Total number of hits satisfying chosen parameters: 556551

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Listing first 200 summaries

Database :

A_Geneseq_21: *
1: geneseqp19808: *
2: geneseqp20008: *
3: geneseqp20018: *
4: geneseqp20028: *
5: geneseqp20038: *
6: geneseqp20048: *
7: geneseqp20058: *
8: geneseqp20068: *
9: geneseqp20078: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	100.0	100.0	10	AAE20480	Naturally
2	100.0	100.0	10	AAU77115	Human Her
3	100.0	100.0	10	ADN64634	HLA bindi
4	100.0	100.0	10	ADP80240	Human HLA
5	90.0	90.0	9	ADM12634	MHC class
6	90.0	90.0	9	ADN64592	HLA bindi
7	90.0	90.0	9	ADN64592	HLA bindi
8	90.0	90.0	9	ADN64592	HLA bindi
9	90.0	90.0	9	ADN64592	HLA bindi
10	90.0	90.0	9	ADN64592	HLA bindi
11	90.0	90.0	9	ADN64592	HLA bindi
12	90.0	90.0	9	ADN64592	HLA bindi
13	90.0	90.0	9	ADN64592	HLA bindi
14	90.0	90.0	9	ADN64592	HLA bindi
15	90.0	90.0	9	ADN64592	HLA bindi
16	90.0	90.0	9	ADN64592	HLA bindi
17	90.0	90.0	9	ADN64592	HLA bindi
18	90.0	90.0	9	ADN64592	HLA bindi
19	90.0	90.0	9	ADN64592	HLA bindi
20	90.0	90.0	9	ADN64592	HLA bindi
21	90.0	90.0	9	ADN64592	HLA bindi
22	90.0	90.0	9	ADN64592	HLA bindi
23	90.0	90.0	9	ADN64592	HLA bindi
24	90.0	90.0	9	ADN64592	HLA bindi

25	40.0	6	AAU80407	Positive
26	40.0	7	AAE20480	Cyclic hi
27	40.0	7	AAE20480	Cyclic hi
28	40.0	7	AAE20480	Cyclic hi
29	40.0	7	AAE20480	Cyclic hi
30	40.0	7	AAE20480	Cyclic hi
31	40.0	7	AAE20480	Cyclic hi
32	40.0	7	AAE20480	Cyclic hi
33	40.0	7	AAE20480	Cyclic hi
34	40.0	7	AAE20480	Cyclic hi
35	40.0	7	AAE20480	Cyclic hi
36	40.0	7	AAE20480	Cyclic hi
37	40.0	7	AAE20480	Cyclic hi
38	40.0	7	AAE20480	Cyclic hi
39	40.0	7	AAE20480	Cyclic hi
40	40.0	7	AAE20480	Cyclic hi
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42	40.0	7	AAE20480	Cyclic hi
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44	40.0	7	AAE20480	Cyclic hi
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49	40.0	7	AAE20480	Cyclic hi
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62	40.0	7	AAE20480	Cyclic hi
63	40.0	7	AAE20480	Cyclic hi
64	40.0	7	AAE20480	Cyclic hi
65	40.0	7	AAE20480	Cyclic hi
66	40.0	7	AAE20480	Cyclic hi
67	40.0	7	AAE20480	Cyclic hi
68	40.0	7	AAE20480	Cyclic hi
69	40.0	7	AAE20480	Cyclic hi
70	40.0	7	AAE20480	Cyclic hi
71	40.0	7	AAE20480	Cyclic hi
72	40.0	7	AAE20480	Cyclic hi
73	40.0	7	AAE20480	Cyclic hi
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77	40.0	7	AAE20480	Cyclic hi
78	40.0	7	AAE20480	Cyclic hi
79	40.0	7	AAE20480	Cyclic hi
80	40.0	7	AAE20480	Cyclic hi
81	40.0	7	AAE20480	Cyclic hi
82	40.0	7	AAE20480	Cyclic hi
83	40.0	7	AAE20480	Cyclic hi
84	40.0	7	AAE20480	Cyclic hi
85	40.0	7	AAE20480	Cyclic hi
86	40.0	7	AAE20480	Cyclic hi
87	40.0	7	AAE20480	Cyclic hi
88	40.0	7	AAE20480	Cyclic hi
89	40.0	7	AAE20480	Cyclic hi
90	40.0	7	AAE20480	Cyclic hi
91	40.0	7	AAE20480	Cyclic hi
92	40.0	7	AAE20480	Cyclic hi
93	40.0	7	AAE20480	Cyclic hi
94	40.0	7	AAE20480	Cyclic hi
95	40.0	7	AAE20480	Cyclic hi
96	40.0	7	AAE20480	Cyclic hi
97	40.0	7	AAE20480	Cyclic hi

98	4	40.0	9	7	ABW00532	Abw00532 Human cyt	171	4	40.0	10	2	AAV46515	AAV46515 Immunogen
99	4	40.0	9	7	ABW00531	Abw00531 Human cyt	172	4	40.0	10	3	AAW49127	AAW49127 Hepatitis
100	4	40.0	9	7	ABW00564	Abw00564 Human cyt	173	4	40.0	10	3	AAV53096	AAV53096 Anticoagu
101	4	40.0	9	7	ABW00555	Abw00555 Human cyt	174	4	40.0	10	3	AAV53084	AAV53084 Anticoagu
102	4	40.0	9	7	ABW00566	Abw00566 Human cyt	175	4	40.0	10	3	AAV53066	AAV53066 Anticoagu
103	4	40.0	9	7	ABW00553	Abw00553 Human cyt	176	4	40.0	10	3	AAV53100	AAV53100 Anticoagu
104	4	40.0	9	7	ABW00556	Abw00556 Human cyt	177	4	40.0	10	3	AAV53069	AAV53069 Anticoagu
105	4	40.0	9	7	ABW00563	Abw00563 Human cyt	178	4	40.0	10	3	AAV53105	AAV53105 Anticoagu
106	4	40.0	9	7	ABW32935	Abw32935 HLA bindi	179	4	40.0	10	3	AAV73049	AAV73049 Hepatitis
107	4	40.0	9	8	ADP37700	Adp37700 Immunogen	180	4	40.0	10	3	AAW14923	AAW14923 Random 27
108	4	40.0	9	8	ADP37666	Adp37666 Immunogen	181	4	40.0	10	4	AAE06547	AAE06547 Forythia
109	4	40.0	9	8	ADK38445	Adk38445 Hepatitis	182	4	40.0	10	4	AAU24412	AAU24412 Human MHC
110	4	40.0	9	8	ADK37830	Adk37830 Hepatitis	183	4	40.0	10	4	AAU24276	AAU24276 Human MHC
111	4	40.0	9	8	ADK39150	Adk39150 Hepatitis	184	4	40.0	10	4	AAU23979	AAU23979 Human MHC
112	4	40.0	9	8	ADK02485	Adk02485 Hepatitis	185	4	40.0	10	4	AAU24282	AAU24282 Human MHC
113	4	40.0	9	8	ADK04911	Adk04911 Hepatitis	186	4	40.0	10	4	AAU24404	AAU24404 Human MHC
114	4	40.0	9	8	ADM78176	Adm78176 Hepatitis	187	4	40.0	10	4	AAU24404	AAU24404 Human MHC
115	4	40.0	9	8	ADO17559	Ado17559 Different	188	4	40.0	10	4	AAU24288	AAU24288 Human MHC
116	4	40.0	9	8	ADO17225	Ado17225 Different	189	4	40.0	10	5	AAE28763	AAE28763 Human CNS
117	4	40.0	9	8	ADO17510	Ado17510 Different	190	4	40.0	10	5	ABJ09870	ABJ09870 Hepatitis
118	4	40.0	9	8	ADO17530	Ado17530 Different	191	4	40.0	10	5	ABJ10131	ABJ10131 Hepatitis
119	4	40.0	9	8	ADO24039	Ado24039 HBV epito	192	4	40.0	10	5	ABJ10038	ABJ10038 Hepatitis
120	4	40.0	9	8	ADO23899	Ado23899 HBV HLA-A	193	4	40.0	10	5	ABJ10038	ABJ10038 Hepatitis
121	4	40.0	9	8	ADO01421	Ado01421 Human cyt	194	4	40.0	10	5	ABJ10081	ABJ10081 Hepatitis
122	4	40.0	9	8	ADO01432	Ado01432 Human cyt	195	4	40.0	10	5	ABJ09598	ABJ09598 Hepatitis
123	4	40.0	9	8	ADO01425	Ado01425 Human cyt	196	4	40.0	10	5	ABJ07090	ABJ07090 Hepatitis
124	4	40.0	9	8	ADO01399	Ado01399 Human cyt	197	4	40.0	10	5	ABJ08626	ABJ08626 Hepatitis
125	4	40.0	9	8	ADO01400	Ado01400 Human cyt	198	4	40.0	10	5	ABJ06551	ABJ06551 Hepatitis
126	4	40.0	9	8	ADO01433	Ado01433 Human cyt	199	4	40.0	10	6	ABR21075	ABR21075 Human can
127	4	40.0	9	8	ADO01434	Ado01434 Human cyt	200	4	40.0	10	6	ABR22655	ABR22655 Human can

ALIGNMENTS

130	4	40.0	9	8	ADO01431	Ado01431 Human cyt	130	4	40.0	10	5	AAE20480	AAE20480 standard; peptide; 10 AA.
131	4	40.0	9	8	ADO01432	Ado01432 Human cyt	131	4	40.0	10	5	AAE20480	AAE20480 standard; peptide; 10 AA.
132	4	40.0	9	8	ADO01426	Ado01426 Human cyt	132	4	40.0	10	5	AAE20480	AAE20480 standard; peptide; 10 AA.
133	4	40.0	9	8	ADO12318	Ado12318 Hepatitis	133	4	40.0	10	5	AAE20480	AAE20480 standard; peptide; 10 AA.
134	4	40.0	9	8	ADO12314	Ado12314 Hepatitis	134	4	40.0	10	5	AAE20480	AAE20480 standard; peptide; 10 AA.
135	4	40.0	9	8	ADO12317	Ado12317 Hepatitis	135	4	40.0	10	5	AAE20480	AAE20480 standard; peptide; 10 AA.
136	4	40.0	9	8	ADO12316	Ado12316 Hepatitis	136	4	40.0	10	5	AAE20480	AAE20480 standard; peptide; 10 AA.
137	4	40.0	9	8	ADO12313	Ado12313 Hepatitis	137	4	40.0	10	5	AAE20480	AAE20480 standard; peptide; 10 AA.
138	4	40.0	9	8	ADO12315	Ado12315 Hepatitis	138	4	40.0	10	5	AAE20480	AAE20480 standard; peptide; 10 AA.
139	4	40.0	9	8	ADR23509	Adr23509 Human thr	139	4	40.0	10	5	AAE20480	AAE20480 standard; peptide; 10 AA.
140	4	40.0	9	8	ADR23510	Adr23510 Human thr	140	4	40.0	10	5	AAE20480	AAE20480 standard; peptide; 10 AA.
141	4	40.0	9	8	ADR23479	Adr23479 Human thr	141	4	40.0	10	5	AAE20480	AAE20480 standard; peptide; 10 AA.
142	4	40.0	9	8	ADR23508	Adr23508 Human thr	142	4	40.0	10	5	AAE20480	AAE20480 standard; peptide; 10 AA.
143	4	40.0	9	8	ADV98702	Adv98702 TY6 assoc	143	4	40.0	10	5	AAE20480	AAE20480 standard; peptide; 10 AA.
144	4	40.0	9	8	ABY01304	AbY01304 SARS coro	144	4	40.0	10	5	AAE20480	AAE20480 standard; peptide; 10 AA.
145	4	40.0	9	9	ADW22953	Adw22953 SARS coro	145	4	40.0	10	5	AAE20480	AAE20480 standard; peptide; 10 AA.
146	4	40.0	9	9	ADV57828	Adv57828 G protein	146	4	40.0	10	5	AAE20480	AAE20480 standard; peptide; 10 AA.
147	4	40.0	9	9	ADW71145	Adw71145 Mouse tum	147	4	40.0	10	5	AAE20480	AAE20480 standard; peptide; 10 AA.
148	4	40.0	9	9	ADZ05835	Adz05835 Hepatitis	148	4	40.0	10	5	AAE20480	AAE20480 standard; peptide; 10 AA.
149	4	40.0	9	9	ADZ05220	Adz05220 Hepatitis	149	4	40.0	10	5	AAE20480	AAE20480 standard; peptide; 10 AA.
150	4	40.0	9	9	ADZ06540	Adz06540 Hepatitis	150	4	40.0	10	5	AAE20480	AAE20480 standard; peptide; 10 AA.
151	4	40.0	9	9	ADZ40426	Adz40426 HBV vacci	151	4	40.0	10	5	AAE20480	AAE20480 standard; peptide; 10 AA.
152	4	40.0	9	9	ADZ40448	Adz40448 HBV vacci	152	4	40.0	10	5	AAE20480	AAE20480 standard; peptide; 10 AA.
153	4	40.0	9	9	ADZ40859	Adz40859 HBV Epige	153	4	40.0	10	5	AAE20480	AAE20480 standard; peptide; 10 AA.
154	4	40.0	9	9	ADZ40524	Adz40524 HBV vacci	154	4	40.0	10	5	AAE20480	AAE20480 standard; peptide; 10 AA.
155	4	40.0	9	9	ADZ40441	Adz40441 HBV vacci	155	4	40.0	10	5	AAE20480	AAE20480 standard; peptide; 10 AA.
156	4	40.0	9	9	ADZ50139	Adz50139 Y. pestis	156	4	40.0	10	5	AAE20480	AAE20480 standard; peptide; 10 AA.
157	4	40.0	9	9	ADZ56790	Adz56790 Cytochrome	157	4	40.0	10	5	AAE20480	AAE20480 standard; peptide; 10 AA.
158	4	40.0	10	1	AAFP5092	Aapf5092 Cholecyat	158	4	40.0	10	5	AAE20480	AAE20480 standard; peptide; 10 AA.
159	4	40.0	10	1	AAFP5093	Aapf5093 Cholecyat	159	4	40.0	10	5	AAE20480	AAE20480 standard; peptide; 10 AA.
160	4	40.0	10	2	AAAR3532	Aar3532 Hirtudin-d	160	4	40.0	10	5	AAE20480	AAE20480 standard; peptide; 10 AA.
161	4	40.0	10	2	AAAR3569	Aar3569 Cyclic hl	161	4	40.0	10	5	AAE20480	AAE20480 standard; peptide; 10 AA.
162	4	40.0	10	2	AAAR3674	Aar3674 Hirtudin d	162	4	40.0	10	5	AAE20480	AAE20480 standard; peptide; 10 AA.
163	4	40.0	10	2	AAAR3928	Aar3928 N-termina	163	4	40.0	10	5	AAE20480	AAE20480 standard; peptide; 10 AA.
164	4	40.0	10	2	AAAR3926	Aar3926 N-termina	164	4	40.0	10	5	AAE20480	AAE20480 standard; peptide; 10 AA.
165	4	40.0	10	2	AAAY18020	Aay18020 Hirtudin C	165	4	40.0	10	5	AAE20480	AAE20480 standard; peptide; 10 AA.
166	4	40.0	10	2	AAAR61560	Aar61560 Peptid f	166	4	40.0	10	5	AAE20480	AAE20480 standard; peptide; 10 AA.
167	4	40.0	10	2	AAAR92928	Aar92928 Hirtudin p	167	4	40.0	10	5	AAE20480	AAE20480 standard; peptide; 10 AA.
168	4	40.0	10	2	AAAW5034	Aaw5034 Forythia	168	4	40.0	10	5	AAE20480	AAE20480 standard; peptide; 10 AA.
169	4	40.0	10	2	AAAY46031	Aay46031 Immunogen	169	4	40.0	10	5	AAE20480	AAE20480 standard; peptide; 10 AA.
170	4	40.0	10	2	AAAY46440	Aay46440 Immunogen	170	4	40.0	10	5	AAE20480	AAE20480 standard; peptide; 10 AA.

RESULT 1
 ID AAE20480 standard; peptide; 10 AA.
 AC AAE20480;
 XX
 DT 01-JUL-2002 (first entry)
 XX
 DE Naturally processed HLA-B*44-restricted epitope of human Her-2/neu.
 XX
 KW Human; Her-2/Neu protein; immune response; gene therapy; breast cancer;
 human leukocyte antigen; HLA; vaccine; malignancy; cytostatic.
 OS Homo sapiens.
 PN WO200214503-A2.
 PD 21-FEB-2002.
 XX
 PF 14-AUG-2001; 2001WO-US041733.
 XX
 PR 14-AUG-2000; 2000US-0225152P.
 PR 28-SEP-2000; 2000US-0234628P.
 PR 21-FEB-2001; 2001US-0270520P.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Hand-Zimmermann S, Cheever MA, Foy TM, Lodes MJ, Kalos MD;
 PI McNeill PD, Veddyck TS;
 XX
 DR WPI, 2002-280758/32.
 XX
 PT Novel isolated Her-2/Neu polypeptide composition useful for therapy,
 PT prevention and diagnosis of cancer, preferably breast cancer.
 XX
 PS Claim 2; Page 87; 12pp; English.
 XX
 CC The invention relates to an isolated Her-2/Neu polypeptide composition

CC effective for eliciting an immune response. The invention is useful for
CC eliciting an immune response in a patient, where the patient is human
CC leukocyte antigen (HLA)-B44 positive or is affected with breast cancer.
CC The composition is useful for the therapy and diagnosis of cancer,
CC preferably breast cancer, in pharmaceutical compositions, e.g., vaccine
CC and other compositions for the diagnosis, prevention and treatment of
CC human malignancies, for stimulating and/or expanding T cells specific for
CC Her-2/Neu polypeptide and for inhibiting the development of cancer in a
CC patient. The invention is useful for stimulating a T cell response in a
CC human patient, as probe or primer for nucleic acid hybridisation, to
CC selectively form duplex molecules with complementary stretches of the
CC entire Her-2/Neu gene or gene fragments of interest, to isolate a full
CC length gene from a suitable library, and to direct expression of a
CC polypeptide in appropriate host cells. The composition is useful in
CC prophylactic or therapeutic applications and for the treatment of cancer,
CC preferably for the immunotherapy of breast cancer and other Her-2/Neu-
CC associated malignancies. The invention is useful in gene therapy. The
CC present sequence is naturally processed HLA-B44-restricted epitope of
CC human Her-2/neu protein

CC XX Sequence 10 AA;

Query Match 100.0%; Score 10; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0006;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYLVPOQGF 10
| | | | | | | |
Db 1 EBYLVPOQGF 10

RESULT 2
AAU77115
ID AAU77115 standard; peptide; 10 AA.

XX AAU77115;

XX 05-JUN-2002 (first entry)

XX Human Her-2/neu immunogenic epitope.

XX Human; Her-2/neu; cytostatic; haematological malignancy; CML;

XX acute myelogenous leukaemia; AML; chronic myelogenous leukaemia; CLL;

XX chronic lymphocytic leukaemia; myeloma; non-Hodgkin's lymphoma; MDS;

XX Hodgkin's lymphoma; T cell therapy.

XX Homo sapiens.

XX WO200213847-A2.

XX 21-FEB-2002.

XX 13-AUG-2001; 2001WO-US025408.

XX 14-AUG-2000; 2000US-00638280.

XX 28-SEP-2000; 2000US-00675904.

XX (CORI-) CORIXA CORP.

XX Gaiger A, Cheever MA, Hand-Zimmermann S;

XX WPI, 2002-280741/32.

XX Inhibiting hematological malignancy development by administering

XX polypeptide comprising immunogenic portion of Her-2/neu, polynucleotide

XX encoding the polypeptide, or antigen presenting cells expressing the

XX polypeptide.

XX Claim 2; Page 49; 74pp; English.

XX The invention relates to a method for inhibiting development of

XX haematological malignancy in a patient by administering a polypeptide

XX comprising an immunogenic portion of Her-2/neu or a polynucleotide

CC encoding the polypeptide. Antigen presenting cells that express the
CC protein can also be administered. The sequences are used for inhibiting
CC development of hematological malignancy such as acute myelogenous
CC leukaemia (AML), chronic myelogenous leukaemia (CML), chronic lymphocytic
CC leukaemia (CLL), MDS, myelomas, Hodgkin's lymphoma and non-Hodgkin's
CC lymphoma. This sequence represents a human Her-2/neu immunogenic epitope

CC XX Sequence 10 AA;

Query Match 100.0%; Score 10; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0006;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYLVPOQGF 10
| | | | | | | |
Db 1 EBYLVPOQGF 10

RESULT 3
ADN64634
ID ADN64634 standard; peptide; 10 AA.

XX ADN64634;

XX 01-JUL-2004 (first entry)

XX HLA binding peptide #1234.

XX cytostatic; hepatotropic; virucide; antiinflammatory; anti-HIV;

XX gene therapy; vaccine; HLA binding peptide; HTL epitope; liposome;

XX prostate specific antigen; prostate specific membrane antigen;

XX hepatitis B virus antigen; hepatitis C virus antigen;

XX malignant melanoma antigen; MAGE; Epstein Barr virus; cancer;

XX prostate cancer; AIDS; renal carcinoma; cervical carcinoma; lymphoma;

XX chondyoma acuminatum.

XX Unidentified.

XX WO2004031211-A2.

XX 15-APR-2004.

XX 03-OCT-2003; 2003WO-US031308.

XX 03-OCT-2002; 2002US-0416207P.

XX 08-OCT-2002; 2002US-0417269P.

XX (EPIM-) EPIMUNE INC.

XX Sidney J, Southwood S, Sette A;

XX WPI, 2004-347953/32.

XX New composition of peptides and nucleic acids capable of binding Major

XX Histocompatibility Complex molecules, useful for diagnosing, preventing

XX or treating viral infections or cancer, such as prostate cancer,

XX hepatitis B or AIDS.

XX Claim 1; SEQ ID NO 1234; 186pp; English.

XX The invention relates to a novel composition comprising one or more

XX peptides or nucleic acids encoding an HLA binding peptide. The

XX composition further comprises an HTL epitope. It also comprises a spacer

XX molecule, a carrier, an MHC targeting sequence or a lipid. The peptides

XX are incorporated as part of a liposome. The peptide is from an antigen

XX selected from prostate specific antigen (PSA), prostate specific membrane

XX antigen (PSM), hepatitis B virus (HBV) antigen, hepatitis C virus (HCV)

XX antigen, malignant melanoma antigen (MAGE), Epstein Barr virus, human

XX immunodeficiency type-1 (HIV-1), human immunodeficiency type-2 (HIV-2),

XX Papilloma virus, Laesa virus, Mycobacterium tuberculosis (MT), p53,

XX murine p53 (mp53), CEA, HER2/neu, and tyrosine kinase related protein

XX (TKP). The composition is useful for preventing or treating viral

XX infections or cancer, such as prostate cancer, hepatitis B, hepatitis C,

CC AIDS, renal carcinoma, cervical carcinoma, lymphoma, CMV or chondyoma
 CC acuminatum. The composition is also be used for diagnosing such diseases.
 CC This sequence represents a peptide of the invention.

XX Sequence 10 AA;

Query Match 100.0%; Score 10; DB 8; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0006;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYLVPQGGF 10
 |||||
 DB 1 EYLVPQGGF 10

RESULT 4

ID ADP80240 standard; peptide; 10 AA.

XX AC ADP80240;

XX DT 18-NOV-2004 (first entry)

DE Human HLA-B44 epitope vaccine peptide SegID496.

XX epitope; HLA-A1; HLA-A2; HLA-A3; HLA-A24; HLA-B7; HLA-B44;

KW tumour associated antigen peptide; cytostatic; vaccine; human.

XX Homo sapiens.

XX WO2004052917-A2.

XX PD 24-JUN-2004.

XX PF 10-DEC-2003; 2003WO-US038949.

XX PR 10-DEC-2002; 2002US-0432017P.

XX PA (EPIM-) EPIMMUNE INC.

XX PI Keogh EA, Southwood S, Fikes JD, Sette A;

XX DR WPI; 2004-468809/44.

XX New HLA-A1, A2, A3, A24, B7 or B44 tumor associated antigen peptides,
 PT useful in preparing a composition for diagnosing or treating tumor
 PT associated antigen-related disease.

XX Claim 1; SEQ ID NO 496; 244pp; English.

XX This invention relates to a novel isolated peptide which comprises at
 CC least 1, 2, 3, 4, 5, 6 or 7 epitopes or analogues of the epitopes given
 CC in the specification. The peptide comprises HLA-A1, A2, A3, A24, B7 or
 CC B44 tumour associated antigen peptide. The invention may be useful for
 CC the production of compounds with a cytostatic activity or for the
 CC production of a vaccine. The peptide is useful in preparing a composition
 CC diagnosing or treating tumour associated antigen-related disease. The
 CC present sequence is that of an epitope peptide for use in the peptide of
 CC the invention.

XX Sequence 10 AA;

Query Match 100.0%; Score 10; DB 8; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0006;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYLVPQGGF 10
 |||||
 DB 1 EYLVPQGGF 10

RESULT 5

ADM12634

ID ADM12634 standard; peptide; 9 AA.

XX AC ADM12634;

XX DT 20-MAY-2004 (first entry)

DE MHC class I epitope of human Her-2/neu, 16-5-6.

XX antigen presentation enhancing hybrid polypeptide; mammalian II-Key;
 KW MHC class II; antibacterial; virucide; fungicide; antirheumatic;
 KW antiarthritic; neuroprotective; dermatological; immunosuppressive;
 KW antiinflammatory; antidiabetic; antihypoid; immune;
 KW rheumatoid arthritis; multiple sclerosis; lupus erythematosus;
 KW diabetes mellitus; myasthenia gravis; autoimmune thyroiditis;
 KW scleroderma; dermatomyositis; pemphigus.

XX Homo sapiens.

XX US2003235594-A1.

XX PD 25-DEC-2003.

XX PF 17-SEP-2002; 2002US-00245871.

XX PR 14-SEP-1999; 99US-00396813.

XX PR 17-JUL-2002; 2002US-00197000.

XX PA (ANTI-) ANTIGEN EXPRESS INC.

XX PI Humphreys R, Xu M;

XX DR WPI; 2004-070554/07.

XX Novel II-Key/antigen presentation enhancing hybrid polypeptide, useful
 PT for treating infections, rheumatoid arthritis, multiple sclerosis, lupus
 PT erythematosus and diabetes mellitus.

XX Example 16; Page 54; 87pp; English.

XX The invention relates to a novel antigen presentation enhancing hybrid
 CC polypeptide. The novel polypeptide has an N-terminal element consisting
 CC of 4-16 residues of a mammalian II-Key peptide and its non-N-terminal
 CC deletion modifications, a chemical structure covalently linking the N-
 CC terminal element to an MHC class II-presented epitope of a C-terminal
 CC element. The C-terminal element comprises an antigenic epitope, which
 CC binds to an antigenic peptide binding site of an MHC class II molecule.
 CC The antigen presentation enhancing hybrid polypeptide has the following
 CC activities: antibacterial, virucide, fungicide, antirheumatic,
 CC antiarthritic, neuroprotective, dermatological, immunosuppressive,
 CC antiinflammatory, antidiabetic, and antihypoid. The antigen presentation
 CC enhancing hybrid polypeptide is useful for modulating the immune response
 CC in an individual and for treating infections (such as bacteria, virus,
 CC parasite and fungus), rheumatoid arthritis, multiple sclerosis, lupus
 CC erythematosus, diabetes mellitus, myasthenia gravis, autoimmune
 CC thyroiditis, scleroderma, dermatomyositis and pemphigus. This sequence
 CC represents a mammalian II key related peptide epitope of the invention.

XX Sequence 9 AA;

Query Match 90.0%; Score 9; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EYLVPQGGF 10
 |||||
 DB 1 EYLVPQGGF 9

RESULT 6

ADN64592

ADN64592

AC ADN64592;

XX 01-JUL-2004 (first entry)
 XX HLA binding peptide #1192.
 XX cytostatic; hepatotropic; virucide; antiinflammatory; anti-HIV;
 XX gene therapy; vaccine; HLA binding peptide; HTL epitope; liposome;
 XX prostate specific antigen; prostate specific membrane antigen;
 XX hepatitis B virus antigen; hepatitis C virus antigen;
 XX malignant melanoma antigen; MAGE; Epstein Barr virus; cancer;
 XX prostate cancer; AIDS; renal carcinoma; cervical carcinoma; lymphoma;
 XX chondyroma acuminatum.
 XX Unidentified.
 XX WO2004031211-A2.
 XX 15-APR-2004.
 XX 03-OCT-2003; 2003WO-US031308.
 XX 03-OCT-2002; 2002US-0416207P.
 XX 08-OCT-2002; 2002US-0417269P.
 XX (EPTM-) EPTMUNE INC.
 XX Sidney J, Southwood S, Sette A;
 XX MPI; 2004-347953/32.
 XX New composition of peptides and nucleic acids capable of binding Major
 XX Histocompatibility Complex molecules, useful for diagnosing, preventing
 XX or treating viral infections or cancer, such as prostate cancer,
 XX hepatitis B or AIDS.
 XX Claim 1; SEQ ID NO 1192; 186bp; English.
 XX
 XX The invention relates to a novel composition comprising one or more
 XX peptides or nucleic acids encoding an HLA binding peptide. The
 XX composition further comprises an HTL epitope. It also comprises a spacer
 XX molecule, a carrier, an MHC targeting sequence or a lipid. The peptides
 XX are incorporated as part of a liposome. The peptide is from an antigen
 XX selected from prostate specific antigen (PSA), prostate specific membrane
 XX antigen (PSM), hepatitis B virus (HBV) antigen, hepatitis C virus (HCV)
 XX antigen, malignant melanoma antigen (MAGE), Epstein Barr virus, human
 XX immunodeficiency type-1 (HIV-1), human immunodeficiency type-2 (HIV-2),
 XX Papilloma virus, Lassa virus, Mycobacterium tuberculosis (MT), p53,
 XX murine p53 (mp53), CEA, HER2/neu, and tyrosine kinase related protein
 XX (TKP). The composition is useful for preventing or treating viral
 XX infections or cancer, such as prostate cancer, hepatitis B, hepatitis C,
 XX AIDS, renal carcinoma, cervical carcinoma, lymphoma, CMV or chondyroma
 XX acuminatum. The composition is also be used for diagnosing such diseases.
 XX This sequence represents a peptide of the invention.
 XX
 XX Sequence 9 AA;
 XX
 XX Query Match 90.0%; Score 9; DB 8; Length 9;
 XX Best Local Similarity 100.0%; Pred. No. 2e+06;
 XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 EBYLVPOQG 9
 XX | | | | | | | | | |
 XX Db 1 EBYLVPOQG 9
 XX
 XX RESULT 7
 XX ADO38867
 XX ID ADO38867 standard; peptide; 9 AA.
 XX AC ADO38867;
 XX XX
 XX DT 15-JUL-2004 (first entry)

DE Human Her-2/neu MHC class II-presented epitope #54.
 XX
 XX Antibacterial; Virucide; Fungicide; Antiparasitic; Antiarthritic;
 XX Antitumematic; Neuroprotective; Antiinflammatory; Dermatological;
 XX Immunosuppressive; Antidiabetic; Antichyroid; Antistematic;
 XX Antiallergic; Cytostatic; Antiposrotatic; Gene therapy; Vaccine;
 XX MHC Class II; II-key motif; immune response; anthrax; EBOLA; HIV;
 XX influenza; vaccinia virus; infection; bacterium; virus; parasite; fungus;
 XX rickettsia; rheumatoid arthritis; multiple sclerosis;
 XX lupus erythematosus; diabetes mellitus; myasthenia gravis;
 XX autoimmune thyroiditis; scleroderma; dermatomyositis; pemphigus; aschma;
 XX allergic rhinitis; topical dermatitis; colitis; cancer; psoriasis;
 XX adenoma.
 XX
 XX Homo sapiens.
 XX US2004058881-A1.
 XX 25-MAR-2004.
 XX 24-SEP-2002; 2002US-00253286.
 XX 24-SEP-2002; 2002US-00253286.
 XX (ANTI-) ANTIGEN EXPRESS INC.
 XX Humphreys RE, Xu M;
 XX MPI; 2004-294259/27.
 XX New non-naturally occurring protein or polypeptide modified by
 XX recombinant DNA techniques, useful for treating multiple sclerosis,
 XX diabetes mellitus, myasthenia gravis, scleroderma, allergic rhinitis,
 XX colitis, cancer or psoriasis.
 XX
 XX Example 16; Page 57; 90bp; English.
 XX
 XX The invention relates to a non-naturally occurring protein or polypeptide
 XX (I) modified by recombinant DNA techniques comprising: a C-terminal
 XX element comprising an MHC Class II-presented epitope; an N-terminal
 XX element comprising an II-key motif; and an intervening element comprising
 XX a sequence of 4-11 amino acid residues where the modification by
 XX recombinant DNA techniques taking place within elements (b) and (c). Also
 XX described are methods for: suppressing or enhancing an immune response
 XX directed toward an MHC (major histocompatibility complex) Class II-
 XX presented epitope of interest. Suppressing an immune response directed
 XX toward an MHC Class II-presented epitope of interest comprises: providing
 XX a nucleic acid sequence encoding the MHC Class II-presented epitope of
 XX interest, the nucleic acid sequence encoding an II-key motif located 4-11
 XX amino acids upstream from the N-terminal residue of the MHC Class II-
 XX presented epitope of interest; and modifying the II-key motif to decrease
 XX its conformance to the archetypal II-key regulatory motif. Enhancing an
 XX immune response directed toward a nucleic acid sequence encoding the MHC
 XX Class II-presented epitope of interest, the nucleic acid sequence lacking
 XX an II-key motif located 4-11 amino acids upstream from the N-terminal
 XX residue of the MHC Class II-presented epitope of interest; and modifying
 XX the nucleic acid sequence to introduce an II-key motif appropriately
 XX spaced from the MHC Class II-presented epitope. The protein or
 XX polypeptide of interest corresponds to a protein or polypeptide encoded
 XX by an infectious pathogen selected from anthrax, EBOLA, HIV or influenza,
 XX preferably vaccinia virus. The non-naturally occurring protein or
 XX polypeptide (II) modified by recombinant DNA techniques is useful for
 XX treating infectious diseases caused or associated with infection by a
 XX bacterium, virus, parasite, fungus, rickettsia or other infectious
 XX agents. It is also useful for treating rheumatoid arthritis, multiple
 XX sclerosis, lupus erythematosus, diabetes mellitus, myasthenia gravis,
 XX autoimmune thyroiditis, scleroderma, dermatomyositis, pemphigus, asthma,
 XX allergic rhinitis, topical dermatitis, colitis, cancer, psoriasis or
 XX adenomas. The present sequence represents the amino acid sequence of an
 XX MHC class II-presented epitope used in the invention.
 XX
 XX Sequence 9 AA;
 XX

Query Match 90.0%; Score 9; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 EYLVPQGGF 10
 |||||
 Db 1 EYLVPQGGF 9

RESULT 8

ID ADP80239 standard; peptide; 9 AA.
 XX
 AC ADP80239;

DT 18-NOV-2004 (first entry)
 XX
 DE Human HLA-B44 epitope vaccine peptide SeqID495.

XX epitope; HLA-A1; HLA-A2; HLA-A3; HLA-A24; HLA-B7; HLA-B44;
 KW tumour associated antigen peptide; cytostatic; vaccine; human.

XX Homo sapiens.

OS WO2004052917-A2.

PN 24-JUN-2004.

PD 10-DEC-2003; 2003WO-US038949.

PR 10-DEC-2002; 2002US-0432017P.

XX (EPIM-) EPIMMUNE INC.

PA Keogh EA, Southwood S, Fikes JD, Sette A;

PI WPI; 2004-468809/44.

DR New HLA-A1, A2, A3, A24, B7 or B44 tumor associated antigen peptides,
 PT useful in preparing a composition for diagnosing or treating tumor
 associated antigen-related disease.

XX Claim 1; SEQ ID NO 495; 244bp; English.

PS This invention relates to a novel isolated peptide which comprises at
 XX least 1, 2, 3, 4, 5, 6 or 7 epitopes or analogues of the epitopes given
 CC in the specification. The peptide comprises HLA-A1, A2, A3, A24, B7 or
 CC B44 tumour associated antigen peptide. The invention may be useful for
 CC the production of compounds with a cytostatic activity or for the
 CC production of a vaccine. The peptide is useful in preparing a composition
 CC diagnosing or treating tumour associated antigen-related disease. The
 CC present sequence is that of an epitope peptide for use in the peptide of
 CC the invention.

XX Sequence 9 AA;

Query Match 90.0%; Score 9; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYLVPQGGF 9
 |||||
 Db 1 EYLVPQGGF 9

RESULT 9

ID AAY46040 standard; peptide; 10 AA.

XX AAY46040;

DT 01-DEC-1999 (first entry)

XX Immunogenic peptide having a human leukocyte antigen binding motif #651.
 DE Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
 KW immune response; T cell activation; major histocompatibility complex;
 KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
 KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
 KW vaccine; immunisation.

XX Synthetic.

OS Homo sapiens.

PN WO9945954-A1.

PD 16-SEP-1999.

PR 13-MAR-1998; 98WO-US005039.

XX 13-MAR-1998; 98WO-US005039.

PA (EPIM-) EPIMMUNE INC.

PI Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;

DR WPI; 1999-551214/46.

PT New immunogenic peptides with HLA binding motif, useful in treatment and
 diagnosis of cancers and viral diseases.

XX Claim 1; Page 53; 150bp; English.

PS AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
 CC having a human major histocompatibility complex (MHC) Class I (also known
 CC as human leukocyte antigen (HLA)) binding motif. The immunogenic peptides
 CC can bind to a specific HLA allele (i.e. HLA-A subtype HLA-A2.1, A1, A3.2
 CC or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against
 CC the antigen from which the peptide is derived. Cytotoxic T lymphocytes
 CC (CTLs) which destroy antigen-bearing cells are normally induced by an
 CC antigen in the form of a peptide fragment bound to a HLA molecule, rather
 CC than the intact foreign antigen itself, and are particularly important in
 CC tumour rejection and in fighting viral infections. The peptides are
 CC therefore useful therapeutically to treat or prevent viral infections and
 CC cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B
 CC and C, AIDS, and renal carcinoma. They can be administered as vaccines to
 CC elicit an immune response in individuals susceptible or otherwise at risk
 CC of viral infection or cancer, or used to treat chronic or acute
 CC conditions. They are also useful diagnostically, and can be used to
 CC induce a cytotoxic T cell response, by contacting a cytotoxic T cell with
 CC the peptide e.g. to produce CTLs ex vivo for infusion back into a
 CC patient. The polynucleotides encoding the immunogenic peptides are also
 CC useful therapeutically and for immunisation as above

XX Sequence 10 AA;

Query Match 90.0%; Score 9; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0069; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EYLVPQGGF 10
 |||||
 Db 1 EYLVPQGGF 9

RESULT 10

ID AAY46513 standard; peptide; 10 AA.

XX AAY46513;

DT 01-DEC-1999 (first entry)

XX Immunogenic peptide having a human leukocyte antigen binding motif #1124.

KW Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
 KW immune response; T cell activation; major histocompatibility complex;
 KW cytotoxic T lymphocytes; CTL; tumour rejection; viral infection; cancer;
 KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
 KW vaccine; immunisation.
 OS Synthetic.
 OS Homo sapiens.
 XX WO9945954-A1.
 XX 16-SEP-1999.
 PD 13-MAR-1998; 98WO-US005039.
 XX 13-MAR-1998; 98WO-US005039.
 PR 13-MAR-1998; 98WO-US005039.
 XX (EPIM-) EPIMUNE INC.
 PA Sette A, Kubo RT, Sidney J, Cells E, Grey HM, Southwood S;
 PI WPI, 1999-551214/46.
 DR New immunogenic peptides with HLA binding motif, useful in treatment and
 XX diagnosis of cancers and viral diseases.
 PT Claim 1; Page 75; 150pp; English.
 PS AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
 XX having a human major histocompatibility complex (MHC) Class I (also known
 XX as human leukocyte antigen (HLA)) binding motif. The immunogenic peptides
 CC can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, A1, A3.2
 CC or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against
 CC the antigen from which the peptide is derived. Cytotoxic T lymphocytes
 CC (CTLs) which destroy antigen-bearing cells are normally induced by an
 CC antigen in the form of a peptide fragment bound to a HLA molecule, rather
 CC than the intact foreign antigen itself, and are particularly important in
 CC tumour rejection and in fighting viral infections. The peptides are
 CC therefore useful therapeutically to treat or prevent viral infections and
 CC cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B
 CC and C, AIDS, and renal carcinoma. They can be administered as vaccines to
 CC elicit an immune response in individuals susceptible or otherwise at risk
 CC of viral infection or cancer, or used to treat chronic or acute
 CC conditions. They are also useful diagnostically, and can be used to
 CC induce a cytotoxic T cell response, by contacting a cytotoxic T cell with
 CC the peptide e.g. to produce CTLs ex vivo for infusion back into a
 CC patient. The polynucleotides encoding the immunogenic peptides are also
 CC useful therapeutically and for immunisation as above
 XX Sequence 10 AA;
 SQ

Query Match 90.0%; Score 9; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0069;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EYLVPQGGF 10
 |||||
 Db 1 EYLVPQGGF 9

RESULT 11
 AAY46437
 ID AAY46437 standard; peptide; 10 AA.
 XX AAY46437;
 AC
 XX 01-DEC-1999 (first entry)
 DT
 XX Immunogenic peptide having a human leukocyte antigen binding motif #1048.
 DE
 XX Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
 KW immune response; T cell activation; major histocompatibility complex;
 KW cytotoxic T lymphocytes; CTL; tumour rejection; viral infection; cancer;

KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
 KW vaccine; immunisation.
 OS Synthetic.
 OS Homo sapiens.
 XX WO9945954-A1.
 XX 16-SEP-1999.
 PD 13-MAR-1998; 98WO-US005039.
 XX 13-MAR-1998; 98WO-US005039.
 PR 13-MAR-1998; 98WO-US005039.
 XX (EPIM-) EPIMUNE INC.
 PA Sette A, Kubo RT, Sidney J, Cells E, Grey HM, Southwood S;
 PI WPI, 1999-551214/46.
 DR New immunogenic peptides with HLA binding motif, useful in treatment and
 XX diagnosis of cancers and viral diseases.
 PT Claim 1; Page 71; 150pp; English.
 PS AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
 XX having a human major histocompatibility complex (MHC) Class I (also known
 XX as human leukocyte antigen (HLA)) binding motif. The immunogenic peptides
 CC can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, A1, A3.2
 CC or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against
 CC the antigen from which the peptide is derived. Cytotoxic T lymphocytes
 CC (CTLs) which destroy antigen-bearing cells are normally induced by an
 CC antigen in the form of a peptide fragment bound to a HLA molecule, rather
 CC than the intact foreign antigen itself, and are particularly important in
 CC tumour rejection and in fighting viral infections. The peptides are
 CC therefore useful therapeutically to treat or prevent viral infections and
 CC cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B
 CC and C, AIDS, and renal carcinoma. They can be administered as vaccines to
 CC elicit an immune response in individuals susceptible or otherwise at risk
 CC of viral infection or cancer, or used to treat chronic or acute
 CC conditions. They are also useful diagnostically, and can be used to
 CC induce a cytotoxic T cell response, by contacting a cytotoxic T cell with
 CC the peptide e.g. to produce CTLs ex vivo for infusion back into a
 CC patient. The polynucleotides encoding the immunogenic peptides are also
 CC useful therapeutically and for immunisation as above
 XX Sequence 10 AA;
 SQ

Query Match 90.0%; Score 9; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0069;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EYLVPQGGF 10
 |||||
 Db 1 EYLVPQGGF 9

RESULT 12
 ADN64633
 ID ADN64633 standard; peptide; 10 AA.
 XX ADN64633;
 AC
 XX 01-JUL-2004 (first entry)
 DT
 XX HLA binding peptide #1233.
 DE
 XX cytotoxic; hepatotropic; virucide; anti-inflammatory; anti-HIV;
 KW gene therapy; vaccine; HLA binding peptide; HTL epitope; liposome;
 KW prostate specific antigen; prostate specific membrane antigen;
 KW hepatitis B virus antigen; hepatitis C virus antigen;
 KW malignant melanoma antigen; MAGE; Epstein Barr virus; cancer;
 KW prostate cancer; AIDS; renal carcinoma; cervical carcinoma; lymphoma;

KW	chondy/loma acuminatum.
XX	
OS	Unidentified.
XX	
PN	WO2004031211-A2.
PD	
XX	15-APR-2004.
PP	
XX	03-OCT-2003; 2003WO-US031308.
FK	
XX	03-OCT-2002; 2002US-0416207P.
PR	
XX	08-OCT-2002; 2002US-0417269P.
XX	
PA	(EPIM-) EPIMMUNE INC.
XX	
PI	Sidney J, Southwood S, Sette A;
DR	
XX	WPI; 2004-347953/32.
XX	
PT	New composition of peptides and nucleic acids capable of binding Major
PT	Histocompatibility Complex molecules, useful for diagnosing, preventing
PT	or treating viral infections or cancer, such as prostate cancer,
PT	hepatitis B or AIDS.
XX	
PS	Claim 1; SEQ ID NO 1233; 186bp; English.
XX	
CC	The invention relates to a novel composition comprising one or more
CC	peptides or nucleic acids encoding an HTL epitope. It also comprises a spacer
CC	composition further comprising an HTL epitope. It also comprises a spacer
CC	molecule, a carrier, an MHC targeting sequence or a lipid. The peptides
CC	are incorporated as part of a liposome. The peptide is from an antigen
CC	selected from prostate specific antigen (PSA), prostate specific membrane
CC	antigen (PSM), hepatitis B virus (HBV) antigen, hepatitis C virus (HCV)
CC	antigen, malignant melanoma antigen (MAGE), Epstein Barr virus, human
CC	immunodeficiency type-1 (HIV-1), human immunodeficiency type-2 (HIV-2),
CC	Papilloma virus, Laaga virus, Mycobacterium tuberculosis (MT), p53,
CC	murine p53 (mp53), CBA, HER2/neu, and tyrosine kinase related protein
CC	(TRP). The composition is useful for preventing or treating viral
CC	infections or cancer, such as prostate cancer, hepatitis B, hepatitis C,
CC	AIDS, renal carcinoma, cervical carcinoma, lymphoma, CMV or chondy/loma
CC	acuminatum. The composition is also be used for diagnosing such diseases.
CC	This sequence represents a peptide of the invention.
XX	
SQ	Sequence 10 AA;
Query Match	90.0%; Score 9; DB 8; Length 10;
Best Local Similarity	100.0%; Pred. No. 0.0069;
Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 EBYLVPOQG 9
DB	2 EBYLVPOQG 10
RESUR.T 13	
ID	ADP80281 standard; peptide; 10 AA.
XX	
AC	ADP80281;
XX	
DT	18-NOV-2004 (first entry)
XX	
DE	Human HLA-B*44 epitope vaccine peptide SeqID537.
XX	
KW	epitope; HLA-A1; HLA-A2; HLA-A3; HLA-A24; HLA-B7; HLA-B44;
KW	tumour associated antigen peptide; cytostatic; vaccine; human.
XX	
OS	Homo sapiens.
XX	
FN	WO2004052917-A2.
PD	
XX	24-JUN-2004.
XX	

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PF 10-DEC-2003; 2003MO-US038949.
XX
XX 10-DEC-2002; 2002US-0432017P.
XX
XX (EPIM-) EPIMMUNE INC.
XX
PI Keogh EA, Southwood S, Fikes JD, Sette A;
XX
XX WPI; 2004-468809/44.
XX
XX New HLA-A1, A2, A3, A24, B7 or B44 tumor associated antigen peptides,
XX
XX useful in preparing a composition for diagnosing or treating tumor
XX
XX associated antigen-related disease.
XX
XX Claim 1; SEQ ID NO 537; 244pp; English.
XX
XX This invention relates to a novel isolated peptide which comprises at
XX
XX least 1, 2, 3, 4, 5, 6 or 7 epitopes or analogues of the epitopes given
XX
XX in the specification. The peptide comprises HLA-A1, A2, A3, A24, B7 or
XX
XX B44 tumour associated antigen peptide. The invention may be useful for
XX
XX the production of compounds with a cytostatic activity or for the
XX
XX production of a vaccine. The peptide is useful in preparing a composition
XX
XX diagnosing or treating tumour associated antigen-related disease. The
XX
XX present sequence is that of an epitope peptide for use in the peptide of
XX
XX the invention.
XX
XX Sequence 10 AA;
XX
XX Query Match 90.0%; Score 9; DB 8; Length 10;
XX
XX Best Local Similarity 100.0%; Pred. No. 0.0069;
XX
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 EEYLVPQOG 9
XX
XX |||||
XX
XX DB 2 EEYLVPQOG 10
XX
XX RESULT 14
XX
XX AAM64460
XX
XX ID AAM64460 standard; protein; 9 AA.
XX
XX AC AAM64460;
XX
XX DT 16-OCT-1998 (first entry)
XX
XX DE Human ErbB-2 cytoplasmic domain tyrosine phosphorylated peptide p5.
XX
XX KW Breast; cancer; mark; CSK homologous kinase; CHK; detection; diagnosis;
XX
XX cytoplasmic protein; tyrosine kinase; ErbB-2; negative regulator;
XX
XX mitogenic signalling; ErbB-2.
XX
XX OS Synthetic.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX
XX FT Modified-site 4 /note= "phosphorylated tyrosine"
XX
XX FT
XX
XX PN WO9830704-A1.
XX
XX PD 16-JUL-1998.
XX
XX PF 07-JAN-1998; 98WO-US000420.
XX
XX PR 08-JAN-1997; 97US-0035228P.
XX
XX PR 16-JUN-1997; 97US-00876882.
XX
XX PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
XX
XX PI Avraham H, Groopman JE;
XX
XX WPI; 1998-399149/34.
XX
XX

```

PT Detecting breast cancer by detecting Csk homologous kinase expression -
PT especially in humans and use of Csk homologous kinase in treatment or
PT prophylaxis of breast cancer and for producing medicaments.

XX Example 7; Page 33; 54pp; English.

PS AAW64457-W64460 are tyrosine phosphorylated peptides derived from the
CC cytoplasmic domain of the human ErbB-2/neu receptor. These peptides are
CC used in a novel method to detect breast cancer using a Csk homologous
CC kinase (CHK) fragment which is used in a method of detecting cancer in
CC breast tissue. The method allows diagnosis of breast cancer in mammals,
CC especially humans. It is based on the discovery that a cytoplasmic
CC protein tyrosine kinase, CHK, is expressed in human breast tissue, but
CC not in adjacent tissue. This protein can be used to raise antibodies
CC which can be included in compositions and diagnostic kits for diagnosis
CC of breast cancer. The presence of CHK in breast tissue can also be
CC determined using other standard methods (e.g. Northern blotting) or by
CC detecting nucleic acid sequences encoding all/a portion of the protein
CC (e.g. using hybridisation probes). Over-expression of the receptor
CC tyrosine kinase ErbB-2 has previously been associated with the
CC development of breast cancer, and CHK specifically interacts with
CC activated ErbB-2, and may function as a negative regulator of ErbB-2
CC mediated mitogenic signalling. The compositions may also be used to
CC design drugs (e.g. which incorporate CHK analogues with greater
CC biological activity than CHK) and to identify CHK antagonists and
CC agonists for therapeutic use

XX Sequence 9 AA;

SQ Query Match 60.0%; Score 6; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2e+06; Mismatches 0; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EBYLVP 6
|||||
DB 2 EBYLVP 7

RESULT 15

AAAG88685
ID AAG88685 standard; peptide; 9 AA.

XX AAG88685;

AC 11-SEP-2001 (first entry)

DE HER2/NEU DR 3a motif binding peptide core sequence #11.

XX Human, HER2/neu; epitope; human leukocyte antigen; HLA; T cell;

XX immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;

XX tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.

OS Homo sapiens.

XX Synthetic.

XX WO200141787-A1.

XX 14-JUN-2001.

XX 11-DEC-2000; 2000WO-US033591.

XX 10-DEC-1999; 99US-00458299.

XX (EPRM-) EPRIMUNE INC.

XX Pike J, Sette A, Sidney J, Southwood S, Chesnut R, Celis B;

XX Keogh B;

XX WPI, 2001-374995/39.

An isolated prepared HER2/neu epitope useful in a vaccine for inducing cellular immune responses for the prevention and treatment of cancer.

PS Disclosure; Page 174; 199pp; English.

XX The present invention describes isolated prepared HER2/neu epitopes (I).
CC Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is
CC culture in vitro and binds to a complex of an epitope (I), bound to a
CC human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)
CC and a second epitope and the peptide is less than 50 contiguous amino
CC acids that have 100% identity with a native peptide sequence of HER2/neu;
CC (3) a vaccine composition (III) comprising (II) and a pharmaceutical
CC excipient; (4) an isolated nucleic acid encoding a peptide comprising (I)
CC ; and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and
CC immunostimulant activities, and can be used in vaccines. (I), (II) and
CC (III) are useful for inducing cellular immune responses for the
CC prevention and treatment of cancer. (I) and (II) are useful for
CC monitoring or evaluating an immune response to a tumour-associated
CC antigen when incubated with a T lymphocyte sample from a patient and
CC detecting the presence of bound T lymphocyte to (I) or (II). Epitope
CC based vaccines mean that immunosuppressive epitopes that may be present
CC in whole antigens may be avoided. Selected epitopes may be combined to
CC enhance immunogenicity. The possible pathological side effects caused by
CC infectious agents or whole protein antigen is eliminated. The vaccine
CC provides the ability to direct and focus an immune response to multiple
CC selected antigens from the same pathogen. Epitope-based anti-tumour
CC vaccines provides the opportunity to combine epitopes derived from
CC multiple tumour-associated molecules addressing the problem of tumour-
CC tumour variability and reducing the likelihood of tumour escape due to
CC antigen loss. AAG88266 to AAG89121 represent amino acid sequences used in
CC the exemplification of the present invention

XX Sequence 9 AA;

SQ Query Match 60.0%; Score 6; DB 4; Length 9;

Best Local Similarity 100.0%; Pred. No. 2e+06; Mismatches 0; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EBYLVP 6
|||||
DB 4 EBYLVP 9

RESULT 16

AAAR41654
ID AAR41654 standard; peptide; 6 AA.

XX AAR41654;

AC 25-MAR-2003 (revised)

DT 10-MAR-1994 (first entry)

XX Internalisation signal #19.

XX Internalisation signal; core; modulation; receptor; transport; ligand;

XX cytoplasmic tail; endocytosis.

OS Synthetic.

XX WO9318185-A1.

XX 16-SEP-1993.

XX 01-MAR-1993; 93WO-US001669.

XX 03-MAR-1992; 92US-00844852.

XX (SALK) SALK INST BIOLOGICAL STUDIES.

XX (SCRI) SCRIPPS RES INST.

XX Trowbridge IS, Collawn JF, Tainer JA, Kuhn LA;

XX WPI, 1993-303496/38.

Modulating receptor mediated transport of ligand into cell - by introducing heterologous internalisation signal into cell.

XX Claim 19; Page 50; 60pp; English.

PS The sequences given in AA31636-57 represent the cores of internalisation

CC signals which were used in the method of the invention for modulating

CC receptor mediated transport of a ligand into a cell. These sequences are

CC derived from the cytoplasmic tails of surface receptors. These amino acid

CC internalisation signals have a tight turn structure. The introduction of

CC one of these sequences into a receptor within a cell, modulates the

CC transport of ligand into a cell having a surface receptor reactive with

CC that ligand. This modulation can cause an increase or a decrease in

CC endocytosis, depending on the choice of internalisation signal. (Updated

CC on 25-MAR-2003 to correct PN field.)

XX

XX Sequence 6 AA:

Query Match 50.0%; Score 5; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 6 PQQGF 10

Db 1 PQQGF 5

RESULT 17

AAE31156

ID AAE31156 standard; peptide; 9 AA.

XX

XX AAE31156;

XX

XX 24-FEB-2003 (first entry)

XX

XX Human erb2 peptide #41.

XX

XX Human; T-lymphocyte; vaccine; viral infection; gene therapy; cancer.

XX

XX Homo sapiens.

XX

XX WO200272627-A2.

XX

XX 19-SEP-2002.

XX

XX 11-MAR-2002; 2002MO-BP002666.

XX

XX 09-MAR-2001; 2001US-0274250P.

XX

XX 14-MAY-2001; 2001US-0290353P.

XX

XX 18-MAY-2001; 2001US-0291610P.

XX

XX (CALL-) CALLISTOGEN AG.

XX

XX Wrede P, Walden P, Eichler-Wertens M, Filter M;

XX

XX WPI; 2002-759836/82.

XX

XX Providing, identifying or optimizing peptides for inducing cytotoxic T-

XX lymphocytes and for treating cancer, comprises selecting conserved

XX PT regions in antigenic proteins and identifying CD8+ T-cell epitopes in the

XX PT protein.

XX

XX Disclosure; Page 8; 32pp; English.

XX

XX The invention relates to a method for providing, identifying or/and

XX CC optimizing peptides which induce cytotoxic T-lymphocytes and to the uses

XX CC of the obtained peptides for vaccination. The method is useful for

XX CC providing, identifying and/or optimizing peptides that are useful in

XX CC manufacturing a pharmaceutical composition for the induction of cytotoxic

XX CC T-lymphocytes, and for the prevention, treatment or diagnosis of cancer

XX CC or viral infections. The invention is also used in gene therapy. The

XX CC present sequence is human erb2 peptide used to illustrate the method of

XX CC the invention

XX

XX Sequence 9 AA;

Query Match 50.0%; Score 5; DB 5; Length 9;

Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 EBYLV 5

Db 5 EBYLV 9

RESULT 18

ADZ50235

ID ADZ50235 standard; peptide; 9 AA.

XX

XX ADZ50235;

XX

XX 14-JUL-2005 (first entry)

XX

XX Y. pestis cytotoxic T-cell epitope SEQ ID 303.

XX

XX Yersinia pestis infection; antibacterial; infection; epitope; T-cell;

XX

XX vaccine; biological warfare.

XX

XX Yersinia pestis.

XX

XX WO2005037855-A2.

XX

XX 28-APR-2005.

XX

XX 15-OCT-2004; 2004WO-US033883.

XX

XX 17-OCT-2003; 2003US-0511653P.

XX

XX (PECO-) PECOS LABS INC.

XX

XX Lund O, Lundegaard C, Nielsen M, Worming P, Deans RJ, Buus S;

XX

XX Brunak S;

XX

XX WPI; 2005-315677/32.

XX

XX Claim 1; SEQ ID NO 303; 235pp; English.

XX

XX The invention relates to a cytotoxic Yersinia pestis T-cell epitope,

XX CC selected from any of the 1000 sequences of 9 amino acids appearing as

XX CC AD249933-AD250932. Also included are predicting peptides that are

XX CC epitopes or can be used as diagnostic tools (comprising predicting which

XX CC peptides bind to a HMC molecule (not defined) with high affinity using a

XX CC neural network with at least one of the following features: some or all

XX CC of the inputs to the neural networks are generated using a hidden Markov

XX CC model; or some or all of the inputs are encoded by an amino acid

XX CC substitution matrix; different from an identity matrix) and a vaccine or

XX CC diagnostic tool using a limited number such as at least 1, 2, 3, 4, 5, 8,

XX CC 16, 32, 64, 128, 256, 512 of the peptides of AD249933-AD250932. In

XX CC predicting peptides, the prediction of the neural network is combined

XX CC with prediction or measurement of one of the following: proteasomal

XX CC cleavage sites; MHC binding; presence of sequence or related sequence(s)

XX CC in patent databases; YAP binding; gene or protein expression level;

XX CC function of the protein; localization of the protein; and similarity to

XX CC self proteins. The epitope is useful as a vaccine or diagnostic tool, and

XX CC for inducing immune response in a subject (said immunity to Yersinia

XX CC pestis infection, the causative agent of plague). The present sequence is

XX CC a cytotoxic Yersinia pestis T-cell epitope of the invention.

XX

XX Sequence 9 AA;

Query Match 50.0%; Score 5; DB 9; Length 9;

Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLVPO 7
 XX |||||
 DB 1 YLVPO 5

RESULT 19
 ID AAR61601 standard; peptide; 10 AA.

AC AAR61601;

DT 25-MAR-2003 (revised)
 DT 12-MAY-1995 (first entry)

DE Peptide fragment (1.0757) of c-ERB2 binds HLA-A2.1.

XX antigen; epitope; immunogenic target protein; PSA; HBVC; HBVs; EBV; HIV1;
 KW plasma specific antigen; hepatitis B virus; Epstein Barr;
 KW human immunodeficiency virus; human papilloma virus; p53; c-ERB2; MAGE-1;
 KW melanoma antigen-1; core antigen; surface antigen;
 KW pharmaceutical composition; in vivo; ex vivo; therapeutic; diagnostic;
 KW MHC class I molecule; major histocompatibility complex; HLA-A2.1; 9mer;
 KW 10mer; anchor; human leukocyte antigen.

XX Homo sapiens.

XX MO9420127-A1.

PD 15-SEP-1994.

PF 04-MAR-1994; 94MO-US002353.

PR 05-MAR-1993; 93US-00027146.

PR 04-JUN-1993; 93US-00073205.

PR 29-NOV-1993; 93US-00159184.

PA (CYTE-) CYTEL CORP.

PI Grey HM, Sette A, Sidney J, Kast W;

DR WPI; 1994-302678/37.

XX Immunogenic peptide(s) having an HLA-A2.1 binding motif - used for

PT treatment or prophylaxis of cancer, virus infection or autoimmune

PT diseases.

XX Example 5; Page 11; 138pp; English.

CC AAR59496-R61666 are immunogenic 10mer peptides that contain a HLA-A2.1
 CC binding motif. These peptides bind HLA-A2.1 and have a binding affinity
 CC of at least 1% as compared to a reference peptide (AAR71293). AAR61601
 CC has an IC50 of 0.0002 and the sequence occurs at position 1016 in the
 CC human c-ERB2 gene product. Peptides of the invention can induce cytotoxic
 CC T lymphocytes which can react with target cells. They can be used for the
 CC treatment or prophylaxis of cancer, eg prostate cancer or lymphoma, etc.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 CC
 XX SQ Sequence 10 AA;

QY Query Match 50.0%; Score 5; DB 2; Length 10;
 DB Best Local Similarity 100.0%; Pred. No. 1.2e+02; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 BEYLV 5
 XX |||||
 DB 6 BEYLV 10

RESULT 20
 ID AAB14919 standard; peptide; 10 AA.

XX AAB14919;
 AC AAB14919;

XX 11-JAN-2001 (first entry)
 DT
 XX
 DE Random 27-mer library peptide R6-52.

XX RNA-protein fusion; protein library; protein isolation; gene cloning;
 KW myc epitope tag.

XX Synthetic.

XX WO200047775-A1.

XX 17-AUG-2000.

PF 01-FEB-2000; 2000MO-US002589.

PR 09-FEB-1999; 99US-00247190.

PA (GENO) GEN HOSPITAL CORP.

PI Szostak JM, Roberts RM, Liu R;

DR WPI; 2000-533022/48.

XX Producing protein or DNA libraries which are useful for improving
 PT existing proteins, by in vitro translating protein coding sequences to
 PT produce RNA-protein fusions and incubating these protein fusions under
 PT high salt conditions.

XX Disclosure; Fig 22; 121pp; English.

XX The present sequence was isolated from an RNA-protein fusion library
 CC following selection for peptides that bound to a c-myc monoclonal
 CC antibody. RNA-protein fusions comprise a protein covalently linked to the
 CC 3' end of its own mRNA. The fusions are made by synthesis and in vitro or
 CC in situ translation of an mRNA molecule with a peptide acceptor attached
 CC to its 3' end. The RNA-protein fusions are incubated under high salt
 CC conditions to produce a protein library. This method is useful for
 CC improving or altering existing proteins, as well as for isolating new
 CC proteins and nucleic acid or small molecule targets. It may also be used
 CC to improve human or humanised single-chain antibodies for the treatment
 CC of a number of diseases. The method is useful for the isolation of
 CC proteins with specific binding properties, for screening cDNA libraries
 CC and cloning new genes on the basis of protein-protein interactions.
 CC CC Unlike prior art, the new method does not rely on maintaining the
 CC integrity of an mRNA:ribosome:nascent chain ternary complex, which is
 CC very fragile and is therefore of limited use. The method does not rely on
 CC topological links between the protein and the nucleic acid so that the
 CC information of the protein is retained and can be recovered in readable,
 CC nucleic acid form
 CC
 XX SQ Sequence 10 AA;

QY Query Match 50.0%; Score 5; DB 3; Length 10;
 DB Best Local Similarity 100.0%; Pred. No. 1.2e+02; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 BEYLV 5
 XX |||||
 DB 1 BEYLV 5

RESULT 21
 ID ADE97832 standard; peptide; 10 AA.

XX ADE97832;
 AC ADE97832;

DT 12-FEB-2004 (first entry)

XX Immunogenic HLA-A2.1 binding peptide #314.

XX cytostatic; anti-inflammatory; hepatotropic; virucide; anti-HIV;

KW arterial embolism; medicinal leech; cyclic.
 XX Synthetic.
 XX Key
 XX Modified-site 1 Location/Qualifiers
 FT /label= Orn
 FT /note= "side-chain amino group forms peptide linkage with
 FT Leu(6)"
 PT Modified-site 6
 PT /note= "forms peptide linkage with Orn(1)"
 PN EP482966-A.
 XX 29-APR-1992.
 XX 18-SEP-1991; 91EP-00402471.
 XX 26-SEP-1990; 90FR-00011842.
 XX (ADIR) ADIR & CIR.
 XX Fauchere JL, Thurielau C, Picard I, Verbeuren T;
 XX WPI; 1992-143016/18.
 XX New hirudin derivs. with non natural peptide features - are powerful, non
 PT -haemorrhagic anticoagulants, etc., stable against proteolysis.
 PS Example 10; Page 9; 27pp; French.
 XX This peptide is one specific example of a highly generic formula for
 CC hirudin derivatives. The derivs. are anticoagulant, antithrombotic and
 CC platelet-aggregation inhibiting agents. The derivs. have no haemorrhagic
 CC action and show anticoagulant activity at doses 10 times lower than known
 CC hirudin derivs. The derivs. are also stable against proteolysis
 XX
 SQ Sequence 6 AA;
 Query Match 40.0%; Score 4; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EHYL 4
 DB 3 EHYL 6
 RESULT 24
 AAY24186
 ID AAY24186 standard; peptide; 6 AA.
 XX AAY24186;
 AC 10-SEP-1999 (first entry)
 XX Human pepsinogen II and pepsin II assaying peptide #19.
 DE Human pepsinogen II; pepsin II; diagnosis; gastropathy; gastric cancer;
 KM Human; pepsinogen II; pepsin II; diagnosis; gastropathy; gastric cancer;
 KM gastric ulcer.
 XX Synthetic.
 OS Homo sapiens.
 XX Key
 XX Modified-site 5 Location/Qualifiers
 PT /note= "2-naphthylalanine"
 PT Modified-site 6
 PT /note= "modified C-terminal: Ala-pNA"
 XX MO9932511-A1.
 XX 01-JUL-1999.

XX 21-DEC-1998; 98WO-JP005780.
 PF 22-DEC-1997; 97JP-00364796.
 PR 13-JUL-1998; 98JP-00215113.
 XX (ONOY) ONO PHARM CO LTD.
 XX Hayashi A, Matsuo M;
 PI WPI; 1999-405156/34.
 XX New peptide substitutes useful in the diagnosis of gastric ulcers.
 PT Claim 5; Page 44; 56pp; English.
 XX AAY24168 to AAY2428 represents peptide (1) substitutes specific for
 CC human pepsin II. (1) may be used for assaying human pepsin II or human
 CC pepsinogen II useful in the diagnosis of gastropathies such as gastric
 CC cancer or gastric ulcer
 XX
 SQ Sequence 6 AA;
 Query Match 40.0%; Score 4; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 POGG 9
 DB 1 POGG 4
 RESULT 25
 AAU80407
 ID AAU80407 standard; peptide; 6 AA.
 XX AAU80407;
 AC 12-MAR-2002 (first entry)
 XX Positive cell selection associated peptide #4.
 DE Positive cell selection; cancer; immunosuppression; gene therapy;
 XX breast cancer; prostate cancer; colon cancer; lung cancer; lymphoma;
 KM myeloma; melanoma; leukaemia; ovarian cancer; pancreatic cancer;
 KM adrenal cancer; renal cancer; cell carcinoma; cervical cancer;
 KM hepatic cancer; stomach cancer; neuroblastoma; stem cell;
 KM cell-related disease.
 XX Synthetic.
 OS WO200190153-A2.
 XX 29-NOV-2001.
 PD 23-MAY-2001; 2001WO-US016840.
 PF 23-MAY-2000; 2000US-00578784.
 XX 11-SEP-2000; 2000US-00659469.
 PR (NEXB-) NEXEL THERAPEUTICS INC.
 XX Schaeffer AT, Tseng-Law J, Thornton JR, Van Epps DB;
 PI WPI; 2002-089920/12.
 DR New peptide-ligand conjugates, useful as reagents for cell selection,
 XX particularly for positively isolating stem cells, which are useful for
 PT transplantation, especially for treating a condition such cancer or
 PT immunosuppression.
 XX Disclosure; Page 15; 116pp; English.

OY 1 EBYL 4
 XX ||||
 DB 4 EBYL 7

RESULT 28

AAW91861 standard; peptide; 7 AA.

AAW91861;

28-NOV-1996 (first entry)

Reversible thrombin inhibitor for coating intravascular medical devices.

Anti-thrombotic; blood clot; prevention; intravascular; coating;
 medical equipment; surgical; dialysis; blood oxygenator; catheter;
 plasmapheresis.

Synthetic.

WO9611668-A1.

25-APR-1996.

13-OCT-1995; 95WO-US013171.

17-OCT-1994; 94US-00324413.

(SURF-) SURFACE GENESIS INC.

Subramaniam R;

WPI; 1996-221729/22.

Mfr. of medical device with biocompatible coating - by providing surface
 with first reactive group contacted with agent reactive with first gp.
 for covalent binding.

Claim 9; Page 13; 29pp; English.

AAW91861 is a reversible inhibitor of thrombosis. The peptide was
 covalently bonded to a surface for coating medical equipment for the
 prevention of thrombogenesis. Equipment in which this is useful includes
 intravascular catheters, blood oxygenators, dialysis and plasmapheresis
 machines. Also disclosed in the specification are uses of promoters of
 thrombosis in the same way which are useful to coat bandages, sutures,
 etc. to promote wound healing

Sequence 7 AA;

Query Match 40.0%; Score 4; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EBYL 4
 XX ||||
 DB 3 EBYL 6

RESULT 29

AAW59316 standard; peptide; 7 AA.

AAW59316;

24-SEP-1998 (first entry)

Non-polio enterovirus peptide fragment 40A.

Non-polio enterovirus; NPEV; enteroviral disease; aseptic meningitis;
 vaccination.

XX Enterovirus sp.

OS WO9814611-A2.

PN 09-APR-1998.

PD 01-OCT-1997; 97WO-US017734.

PF 02-OCT-1996; 96US-0027353P.

PR (USSH) US DEPT HEALTH & HUMAN SERVICES.

PA Kilpatrick D;

PI WPI; 1998-240106/21.

Identifying non-polio enteroviruses - using primers which hybridise to
 sense and antisense strands that encode conserved non-polio enterovirus
 peptide sequences.

Claim 4; Page 23; 47pp; English.

The peptide sequences AAW59298-W59344 are amplified by primers to detect
 the presence of a non-polio enterovirus (NPEV) in a sample. The primers
 CC and assays are used to detect NPEVs in a sample, to serotype these
 CC viruses, to diagnose enteroviral diseases and medical conditions, and to
 CC correlate (or disprove a correlation between) specific symptoms or
 CC combinations of symptoms with the presence of a particular enterovirus.
 CC They can be used for diseases such as aseptic meningitis. The detection
 CC of NPEV infections and their correlation with medical conditions will
 CC make possible vaccines and methods of treatment

Sequence 7 AA;

Query Match 40.0%; Score 4; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 LVPQ 7
 XX ||||
 DB 4 LVPQ 7

RESULT 30

AAW50074 standard; peptide; 7 AA.

AAW50074;

19-JAN-2000 (first entry)

Coxsackievirus A VP1 conserved epitope 40.

Virus; epitope; target; degenerate; PCR; primer; amplification; VP1;
 KM nonstructural protein 2A; conserved; base analogue; inosine;
 KM predetermined nucleotide; diagnosis; enterovirus; poliovirus.

Synthetic.

OS Coxsackievirus.

PN WO9553097-A2.

PD 21-OCT-1999.

PF 06-APR-1999; 99WO-US007513.

PR 15-APR-1998; 98US-0081944P.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Kilpatrick DR;

DR	WP1; 1999-620444/53.
DR	N-PSSB; AAZ30993.
PX	
PT	Designing degenerate polymerase chain reaction primers.
PS	Example 3; Page 18; 30pp; English.
XX	This sequence represents a conserved Coxsaekievirus A (serotype AI6) VP1 epitope. The invention relates to a novel method for designing degenerate PCR primers (AAZ30975-Z31000, AAZ32601-AAZ32611) for amplifying target polynucleotides. This method comprises identifying uniquely conserved amino acid sequences (e.g., this epitope) in target proteins; synthesizing degenerate polynucleotides encoding the conserved sequences; and substituting the synthesized polynucleotides with up to four predetermined nucleotides (e.g., inosine) at degenerate nucleotide positions. The nucleic acids comprise no more than 7 degenerate positions, have no more than 2 adjacent predetermined nucleotides and the predetermined nucleotides are 3 bases away from the 3' end of the synthesized strand. The degenerate primers are useful for amplifying target polynucleotides by the polymerase chain reaction (PCR). The use of the method of designing degenerate primers useful for the detection of polioviruses in clinical samples is described in US585477. The degenerate primers facilitate PCR amplification of unknown polynucleotides, where the amino acid sequence encoded is known. The primers also allow for the correlation of the subsequent molecular based diagnosis with a serologically derived diagnosis
SQ	Sequence 7 AA;
OY	Query Match 40.0%; Score 4; DB 2; Length 7; Best Local Similarity 100.0%; Pred.No. 2e+6; Mismatches 0; Gaps 0. Matches 4; Conservative 0; Indels 0; LVPQ 7 <div style="text-align:center;">4 LVPO 7 4 LPVQ 7</div>
DG	
ID	RESULT 31 AAZ24181 standard; peptide; 7 AA.
AC	AAZ24181;
DT	10-SEP-1999 (first entry)
DE	Human pepsinogen II and pepsin II assaying peptide #14.
KW	Human; pepsinogen II; pepsin II; diagnosis; gastritis; gastric cancer; gastric ulcer.
OS	Synthetic.
FX	Homo sapiens.
FH	Key Location/Qualifiers
FT	Modified-site 6 /note= "4-Iodo-phenylalanine"
PT	Modified-site 7 /note= "modified C-terminal: Ala-pyNA"
PN	WO9932511-A1.
PD	01-JUL-1999.
PF	21-DEC-1998; 98WO-TP005780.
PR	22-DEC-1997; 97UP-00364796.
PA	13-JUL-1998; 98JP-00213513.
PI	(ONOI) ONO PHARM CO LTD.
HA	Hayashi A, Matsuo M;
XX	

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DR WP1; 1999-405156/34.
XX
XX PT New peptide substitutes useful in the diagnosis of gastric ulcers.
XX
XX PS Claim 5; Page 43; 56pp; English.
XX
XX AY24168 to AY24238 represents peptide (I) substitutes specific for
CC human pepsin II. (I) may be used for assaying human pepsin II or human
CC pepsinogen II useful in the diagnosis of gastropathies such as gastric
CC cancer or gastric ulcer
XX
XX SQ Sequence 7 AA;
XX
XX Query Match 40.0%; Score 4; DB 2; Length 7;
XX Best Local Similarity 100.0%; Pred. No. 2e+06;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX
XX CY 5 VPOQ 8
XX ||||
XX DB 1 VPOQ 4
XX
XX RESULT 32
XX AAR23690
XX ID AAR23690 standard; protein; 8 AA.
XX
XX AC AAR23690;
XX
XX DT 03-NOV-1992 (first entry)
XX
XX DE Cyclic hirudin derivative #22.
XX
XX KW Blood clotting; platelet aggregation; inhibition; atherosclerosis;
XX myocardial infarction; pulmonary embolism; acute venous thrombosis;
XX arterial embolism; medicinal leech; cyclic.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX FH Modified-site 1
XX FT /label= OTHER
XX FT /note= "pyroglutamic acid"
XX FT Modified-site 3
XX FT /label= Orn
XX FT /note= "side-chain amino group forms peptide linkage with
XX FT Leu(8) "
XX FT Modified-site 8
XX FT /note= "forms peptide linkage with Orn(3) "
XX
XX PN EP482966-A.
XX
XX PD 29-APR-1992.
XX
XX PF 18-SEP-1991; 91EP-00402471.
XX
XX PR 26-SEP-1990; 90FR-00011842.
XX
XX PA (ADIR ) ADIR & CIE.
XX
XX PT Fauchere JL, Thuriere C, Picard I, Verbeuren T;
XX DR WPI; 1992-143016/18.
XX
XX PT New hirudin derivs. with non natural peptide features - are powerful, non
XX pt-haemorrhagic anticoagulants, etc., stable against proteolysis.
XX
XX PS Example 18; Page 10; 27pp; French.
XX
XX This peptide is one specific example of a highly generic formula for
XX hirudin derivatives. The derivs. are anticoagulant, antithrombotic and
XX platelet-aggregation inhibiting agents. The derivs. have no haemorrhagic
XX action and show anticoagulant activity at doses 10 times lower than known
XX hirudin derivs. The derivs. are also stable against proteolysis

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XX Sequence 8 AA;

Query Match 40.0%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYL 4
|||
5 EBYL 8

RESULT 33
AAR23691
ID AAR23691 standard; protein; 8 AA.

AC AAR23691;

DT 03-NOV-1992 (first entry)

XX Cyclic hirudin derivative #23.

XX Blood clotting; platelet aggregation; inhibition; atherosclerosis;
KM myocardial infarction; pulmonary embolism; acute venous thrombosis;
KW arterial embolism; medicinal leech; cyclic.

OS Synthetic.

Key Location/Qualifiers

FT Modified-site 1
/label= OTHER
/note= "3-((3-hydroxy-4-methoxycarbonyl)phenyl)
carbamoylmethylcarbamoyl(propionyl)"

FT Modified-site 3
/label= Orn
/note= "side-chain amino group forms peptide linkage with
Leu(8)"

FT Modified-site 8
/note= "forms peptide linkage with Orn(3)"

XX EP482966-A.

XX 29-APR-1992.

XX 18-SEP-1991; 91EP-00402471.

XX 26-SEP-1990; 90FR-00011842.

XX (ADIR) ADIR & CIE.

XX Fauchere JL, Thurleau C, Picard I, Verdeuren T;

XX WPI; 1992-143016/18.

XX New hirudin derivs. with non natural peptide features - are powerful, non
PT -haemorrhagic anticoagulants, etc., stable against proteolysis.

XX Example 19; Page 10; 27pp; French.

XX This peptide is one specific example of a highly generic formula for
CC hirudin derivatives. The derivs. are anticoagulant, antithrombotic and
CC platelet-aggregation inhibiting agents. The derivs. have no haemorrhagic
CC action and show anticoagulant activity at doses 10 times lower than known
CC hirudin derivs. The derivs. are also stable against proteolysis

XX Sequence 8 AA;

Query Match 40.0%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYL 4
|||

DB 5 EBYL 8

RESULT 34
AAV21534
ID AAV21534 standard; peptide; 8 AA.

XX AAV21534;

DT 02-AUG-1999 (first entry)

XX Hirudin peptide 2 (residues 57-64).

XX Platelet aggregation; hirudin; inhibitor; coagulation; leech;
KW heparin-induced thrombocytopenia.

XX Hirudo medicinalis.

XX US5256559-A.

XX 26-OCT-1993.

XX 27-MAR-1991; 91US-00677609.

XX 04-MAR-1988; 88US-00164178.

XX 29-SEP-1988; 88US-00251150.

XX 05-DEC-1988; 88US-00280618.

XX 28-FEB-1989; 89US-00314755.

XX (BIOJ) BIOGEN INC.

XX (UYBO-) UNIV BOSTON.

XX Maraganore JM, Jakubowski JA;

XX WPI; 1993-350828/44.

XX Platelet aggregation inhibition in vitro and in vivo - using specified
PT hirudin peptide(s).

XX Example; Fig 2; 22pp; English.

XX The invention relates to a method for inhibiting platelet aggregation in
CC stored platelets. The method comprises storing platelets in the presence
CC of a composition comprising a peptide and a carrier, where the peptide is
CC of formula Y-Phe-Glu-Glu-Ile-Pro-Glu-Glu-X-Z or Asn-Gly-Asp-Phe-Glu-Glu-
CC Ile-Pro-Glu-Glu-Tyr-Z, Y = H, an amino protecting group, Asp or sequence
CC of at least two C-terminal amino acids from the sequence Val-Thr-Gly-Glu-
CC Gly-Thr-Pro-Lys-Pro-Gln-Ser-His-Asn-Asp-Gly-Asp; Z = OH, Leu or Leu-Gln; X =
CC Thr-Pro-Asn-Pro-Glu-Ser-His-Asn-Asp-Gly-Asp; Z = OH, Leu or Leu-Gln; X =
CC Tyr with a negatively charged side gp. The peptides are derived from
CC hirudin, a natural inhibitor of coagulation, produced by the blood
CC sucking leech Hirudo medicinalis. The peptides may be used to treat
CC patients who are suffering from or have suffered from heparin-induced
CC thrombocytopenia

XX Sequence 8 AA;

Query Match 40.0%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYL 4
|||
5 EBYL 8

RESULT 35
AAW29068
ID AAW29068 standard; peptide; 8 AA.

XX AAW29068;

DT 25-MAR-2003 (revised)

DT 17-MAR-1998 (first entry)
 XX Peptide fragment of new thrombin inhibitor compound.
 DE
 XX alpha-ketoamide linkage; thrombin inhibitor; hirudin; thrombus.
 KW
 XX Synthetic.
 OS
 XX
 FT Key Location/Qualifiers
 FT Modified-site 7 /note= "optionally iodinated as Tyr(3-iodo) or Tyr(3,5-
 FT Modified-site 8 diiodo)"
 FT Modified-site 8 /note= "optionally in the form of a C-terminal amide"
 FT
 XX US5670479-A.
 PN 23-SEP-1997.
 XX 25-MAR-1994; 94US-00218329.
 XX 25-MAR-1993; 93US-00037574.
 XX (CORV-) CORVAS INT INC.
 XX Webb TR, Vlaeuk GP, Abelman MM, Pearson DA;
 PI WPI; 1997-479505/44.
 DR
 XX New peptide alpha-keto:amide analogues - useful as thrombin inhibitors
 XX for therapy and diagnosis of thrombosis.
 PT
 XX Claim 1; Col 196, 197; 116pp; English.
 XX
 CC The patent describes new thrombin inhibitor peptides consisting of an N-
 CC protected Asp-Pro-Arg (or analogue) tripeptide joined via an alpha-
 CC ketoamide linkage (-CO-CO-NH-) to a spacer peptide (preferably (Gly)5) in
 CC turn joined to a peptide which is homologous to amino acids 53-64 of
 CC hirudin. The peptides are effective at low doses for preventing or
 CC treating thrombus formation. The present sequence is a preferred fragment
 CC of the new peptides, consisting of a portion of the hirudin homologue.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 CC
 SQ Sequence 8 AA;
 Query Match 40.0%; Score 4; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2e+06; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0;
 QY 1 EBYL 4
 DB 5 EBYL 8
 RESULT 36
 AAY55243
 ID AAY55243 standard; peptide; 8 AA.
 AC AAY55243;
 XX
 DT 07-JAN-2000 (first entry)
 XX
 DE ATCC HB 11646 monoclonal antibody 9069 releasing peptide SEQ ID NO:137.
 XX
 KW Antibody releasing peptide; CD34; hybridoma; binding; antigen;
 KW cell surface antigen; identification; haematopoietic stem cell; tumour;
 KW cancer; immune system; therapy; displacement.
 XX
 OS Synthetic.
 OS Mus sp.
 XX
 XX US5968753-A.
 PN
 XX

PD 19-OCT-1999.
 XX
 XX 07-JUN-1995; 95US-00482228.
 XX
 XX 14-JUN-1994; 94US-00259427.
 XX
 XX (NEXE-) NEXELL THERAPEUTICS INC.
 XX
 XX Guillermo R, Helgerson SL, Deans RJ, Tseng-Law J, Kobori JA;
 PI Al-Abdaly FA;
 DR WPI; 1999-590399/50.
 XX
 XX Short peptides useful for displacing antibodies from cell surface
 PT antigens.
 PT
 XX Example 8; Col 27; 81pp; English.
 XX
 CC The present invention describes peptides of 4-17 amino acids which
 CC displace either the anti-CD34 monoclonal antibody designated 561, the
 CC anti-CD34 mouse monoclonal antibody produced by the hybridoma ATCC HB-
 CC 11646 (designated 9069), the anti-CD34 antibody produced by hybridoma
 CC ATCC HB-11885 (9079), or the anti-human breast cancer antibody produced
 CC by hybridoma ATCC HB-11884 (9187), from a cell surface antigen on a
 CC target cell. The peptides are useful for displacing antibodies bound to
 CC cell surfaces to release cells that have been positively selected by
 CC antibody-mediated binding to beads or other solid support. AAY5107 to
 CC AAY5319 represent peptides used in the exemplification of the present
 CC invention
 CC
 SQ Sequence 8 AA;
 Query Match 40.0%; Score 4; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2e+06; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0;
 QY 7 QGGF 10
 DB 1 QGGF 4
 RESULT 37
 AAY86989
 ID AAY86989 standard; peptide; 8 AA.
 AC AAY86989;
 XX
 DT 09-MAY-2000 (first entry)
 XX
 DE Human haematopoietic CD34+ cell binding peptide SEQ ID #137.
 XX
 KW Human; haematopoietic CD34+ cell; binding peptide; monoclonal antibody;
 KW non-enzymatic cell selection method; haematopoietic stem cell;
 KW haematopoietic progenitor cell; antibody 561; breast cancer cell;
 KW antibody 9187; cell surface determinant; diagnostic cell based assay.
 XX
 OS Homo sapiens.
 OS
 XX US6017719-A.
 PN 25-JAN-2000.
 XX
 PD 07-JUN-1995; 95US-00482528.
 XX
 PR 14-JUN-1994; 94US-00259427.
 XX
 PA (NEXE-) NEXELL THERAPEUTICS INC.
 XX
 PI Guillermo R, Helgerson SL, Deans RJ, Tseng-Law J, Kobori JA;
 PI Al-Abdaly FA;
 XX WPI; 2000-136676/12.
 XX

PT Non-enzymatic method for the positive selection of target cells from a
 PT heterogeneous cell suspension, useful for selecting human breast cancer
 PT cells from a patient's blood or bone marrow.

XX Example 8; Col 32; 82pp; English.

PS This sequence represents a human haematopoietic CD34+ cell binding
 CC peptide, and was used to test the method of the invention. The method is
 CC a non-enzymatic method for the positive selection of one or more target
 CC cells from a heterogeneous cell suspension, by using specific peptides
 CC which effect the displacement and release of a specific target cell from
 CC a specific monoclonal antibody. The method is useful for positive
 CC selection and specific release of target human haematopoietic
 CC stem/progenitor cells bound by the monoclonal anti-CD34 antibodies and
 CC the antibody 561. The method is also useful for positive selection and
 CC specific release of target human breast cancer cells, bound by the
 CC monoclonal anti-breast cancer antibody 9187, from a patient's blood or
 CC bone marrow. Identification of peptide epitopes for antibodies which
 CC recognize cell surface determinants also allows construction of
 CC diagnostic cell based assays. The peptide mediated release is enzyme free
 CC and thus leaves the cell surface proteins intact. Moreover, peptide
 CC mediated release leaves the target cell free of bound antibody or
 CC antibody fragments. The method also produces a high yield of functional
 CC target cells and is relatively inexpensive to carry out

SQ Sequence 8 AA;

Query Match 40.0%; Score 4; DB 3; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2e+06; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 OQGF 10
 ||||
 1 OQGF 4

DB

RESULT 39
 AAB82748
 ID AAB82748 standard; peptide; 8 AA.

AC AAB82748;

DT 29-OCT-2001 (first entry)

DE Wheat glutenin repeat peptide variant.

KW Tyrosine; di-tyrosine bond; crosslinking; glutenin; viscoelasticity;

KW wheat; grain; dough; baking; mutant; mutein.

OS Triticum aestivum.

OS Synthetic.

PH Key Location/Qualifiers

FT Misc-difference 4 /note= "Tyr in native peptide"

FT Misc-difference 5 /note= "Tyr in native peptide"

FT WO200154486-A1.

PN 02-AUG-2001.

PD 27-JAN-2000; 2000WO-US002106.

PF 26-JAN-2000; 2000US-00491259.

PR (UNITV) UNITV KANSAS STATE RES FOUND.

PA Tilley K;

PI WPI; 2001-536416/59.

DR N-PSDB; AAH26439.

PT Polymeric structure comprising a pair of discrete bio- or synthetic
 PT polymers coupled together via a tyrosine bond, useful when the polymer is

PT a plant (e.g. wheat) protein that can be used to, for e.g. modify
 PT physical properties of dough.

XX Example 32; Page 48; 104pp; English.

PS The present sequence is that of a variant of a conserved repeat peptide
 CC motif of wheat glutenin, and does not include the peptide-bonded tyrosine
 CC pair of the native peptide owing to the replacement of the native Tyr-4
 CC residue with Phe. Oligonucleotides (see AAH26436-45) coding for the
 CC native repeat and its variants (see AAB82746-54) were expressed in
 CC glutenin proteins in order to analyse the effect of the precise repeat
 CC amino acid sequence on di-tyrosine formation in doughs. The proteins were
 CC produced in *Escherichia coli*, purified and added to flour to test the
 CC effect of mutations on product quality. The proteins were also produced
 CC in transformed wheat plants. The invention is based on the discovery that
 CC a class of tyrosine-containing peptides, such as the glutenin repeat
 CC peptide, form tyrosine bonds in the protein fraction of wheat, wheat
 CC flour, wheat dough and its product. These tyrosine bonds have a profound
 CC and previously unrecognized effect on product quality. This discovery
 CC allows effective genetic manipulation of wheat and other grains in order
 CC to control tyrosine bond levels in the grain protein. It also leads to
 CC methods for monitoring and/or altering tyrosine bond levels during plant
 CC growth, flour manufacture and dough formation and processing

SQ Sequence 8 AA;

Query Match 40.0%; Score 4; DB 4; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2e+06; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 OQGF 10
 ||||
 1 OQGF 4

DB

RESULT 39
 AAB82746
 ID AAB82746 standard; peptide; 8 AA.

AC AAB82746;

DT 29-OCT-2001 (first entry)

DE Wheat glutenin repeat peptide variant.

KW Tyrosine; di-tyrosine bond; crosslinking; glutenin; viscoelasticity;

KW wheat; grain; dough; baking; mutant; mutein.

OS Triticum aestivum.

OS Synthetic.

PH Key Location/Qualifiers

FT Misc-difference 4 /note= "Tyr in native peptide"

FT Misc-difference 5 /note= "Tyr in native peptide"

FT WO200154486-A1.

PN 02-AUG-2001.

PD 27-JAN-2000; 2000WO-US002106.

PF 26-JAN-2000; 2000US-00491259.

PR (UNITV) UNITV KANSAS STATE RES FOUND.

PA Tilley K;

PI WPI; 2001-536416/59.

DR N-PSDB; AAH26437.

PT Polymeric structure comprising a pair of discrete bio- or synthetic


```
ID ADK37330 standard; peptide; 8 AA.
XX
XX ADK37330;
AC
XX 06-MAY-2004 (first entry)
DT
XX Hepatitis B virus (HBV) epitope #198.
DE
XX Hepatitis B virus (HBV) epitope #198.
DE
XX HBV, cytotoxic T-cell response; immunogenic activity;
KM human leukocyte antigen; HLA; HBV infection; HBV epitope;
KM antiinflammatory; hepatotropic; virucide.
XX
XX Hepatitis B virus.
OS
XX US6689363-B1.
PN
XX 10-FEB-2004.
PD
XX 27-JAN-1999; 99US-00239043.
PF
XX 29-JAN-1992; 92US-00827682.
XX 27-APR-1992; 92US-00874491.
PR 07-AUG-1992; 92US-00926666.
PR 26-AUG-1992; 92US-00935811.
PR 05-MAR-1993; 93US-00027146.
PR 05-MAR-1993; 93US-00027146.
PR 04-JUN-1993; 93US-00073205.
PR 06-AUG-1993; 93US-00103396.
PR 16-FEB-1994; 94US-00197484.
PR 04-MAR-1994; 94US-00205713.
PR 23-NOV-1994; 94US-00344824.
PR 01-DEC-1994; 94US-00347610.
PR 13-MAR-1996; 96US-0013363P.
PR 12-MAR-1997; 97US-00820360.
PR 25-NOV-1997; 97US-00978291.
XX 10-NOV-1998; 98US-00189702.
XX
XX (EPTM-) EPTMONE INC.
PA
XX Sette A, Sidney J, Southwood S, Vitello MA, Livingston BD;
PI Cells E, Kubo RT, Grey HM, Chestnut RW;
PI
XX WPI; 2004-141419/14.
DR
XX Hepatitis B virus (HBV) vaccine composition useful for inducing cellular
PT immune responses to HBV or for preventing and treating HBV infection.
PT
XX Disclosure; SEQ ID NO 198; 73pp; English.
PS
XX
XX The invention relates to a hepatitis B virus (HBV) vaccine composition
CC comprising a pharmaceutical carrier and an isolated peptide less than 25
CC or less than 15 amino acids in length. The invention also relates to a
CC method of inducing a cytotoxic T-cell response to HBV in a mammal and a
CC method of monitoring immunogenic activity of the vaccine in a patient
CC having a known human leukocyte antigen (HLA) type. The composition and
CC methods are useful for preventing and treating HBV infection. This
CC sequence represents an HBV epitope used in the scope of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format directly from USPTO
CC at seqdata.uspto.gov/sequence.html.
XX
XX Sequence 8 AA;
SQ
Query Match 40.0%; Score 4; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 EYLV 5
DB 5 EYLV 8
RESULT 43
```

```
ADK38478
ID ADK38478 standard; peptide; 8 AA.
XX
XX ADK38478;
AC
XX 06-MAY-2004 (first entry)
DT
XX Hepatitis B virus (HBV) epitope #1346.
DE
XX Hepatitis B virus (HBV) epitope #1346.
DE
XX HBV, cytotoxic T-cell response; immunogenic activity;
KM human leukocyte antigen; HLA; HBV infection; HBV epitope;
KM antiinflammatory; hepatotropic; virucide.
XX
XX Hepatitis B virus.
OS
XX US6689363-B1.
PN
XX 10-FEB-2004.
PD
XX 27-JAN-1999; 99US-00239043.
PF
XX 29-JAN-1992; 92US-00827682.
XX 27-APR-1992; 92US-00874491.
PR 07-AUG-1992; 92US-00926666.
PR 26-AUG-1992; 92US-00935811.
PR 05-MAR-1993; 93US-00027146.
PR 05-MAR-1993; 93US-00027146.
PR 04-JUN-1993; 93US-00073205.
PR 06-AUG-1993; 93US-00103396.
PR 16-FEB-1994; 94US-00197484.
PR 04-MAR-1994; 94US-00205713.
PR 23-NOV-1994; 94US-00344824.
PR 01-DEC-1994; 94US-00347610.
PR 13-MAR-1996; 96US-0013363P.
PR 12-MAR-1997; 97US-00820360.
PR 25-NOV-1997; 97US-00978291.
XX 10-NOV-1998; 98US-00189702.
XX
XX (EPTM-) EPTMONE INC.
PA
XX Sette A, Sidney J, Southwood S, Vitello MA, Livingston BD;
PI Cells E, Kubo RT, Grey HM, Chestnut RW;
PI
XX WPI; 2004-141419/14.
DR
XX Hepatitis B virus (HBV) vaccine composition useful for inducing cellular
PT immune responses to HBV or for preventing and treating HBV infection.
PT
XX Disclosure; SEQ ID NO 1346; 73pp; English.
PS
XX
XX The invention relates to a hepatitis B virus (HBV) vaccine composition
CC comprising a pharmaceutical carrier and an isolated peptide less than 25
CC or less than 15 amino acids in length. The invention also relates to a
CC method of inducing a cytotoxic T-cell response to HBV in a mammal and a
CC method of monitoring immunogenic activity of the vaccine in a patient
CC having a known human leukocyte antigen (HLA) type. The composition and
CC methods are useful for preventing and treating HBV infection. This
CC sequence represents an HBV epitope used in the scope of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format directly from USPTO
CC at seqdata.uspto.gov/sequence.html.
XX
XX Sequence 8 AA;
SQ
Query Match 40.0%; Score 4; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 EYLV 5
DB 5 EYLV 8
```

```
RESULT 44
ID AD205868 standard; peptide; 8 AA.
XX
AC AD205868;
XX
XX 02-JUN-2005 (first entry)
XX
DE Hepatitis B virus HLA restricted antigen #1346.
XX
KW antiinflammatory; hepatotropic; virucide; vaccine; gene therapy; epitope;
XX immune response; hepatitis B virus infection.
XX
OS Hepatitis B virus.
XX
PN US2005063983-A1.
XX
PD 24-MAR-2005.
XX
PE 04-SEP-2003; 2003US-00654601.
XX
PR 05-MAR-1993; 93US-00027146.
XX 04-JUN-1993; 93US-00073205.
PR 29-NOV-1993; 93US-00159184.
PR 04-MAR-1994; 94US-00205713.
PR 13-MAR-1996; 96US-0013363P.
PR 12-MAR-1997; 97US-00820360.
PR 10-NOV-1998; 98US-00189702.
PR 27-JAN-1999; 99US-00239043.
XX
XX (EPIM-) EPIMMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Vitiello MA, Livingston BD;
PI Cells E, Kubo RT, Grey HM, Cheenut RW;
XX
XX WPI; 2005-241251/25.
XX
XX New peptide and nucleic acid molecule composition for inducing an immune
XX response against hepatitis B virus (HBV) or for treating or preventing
XX HBV infection.
XX
XX Claim 47; SEQ ID NO 1346; 497bp; English.
XX
XX The invention relates to a peptide composition, or its analog, of less
XX than 100 amino acid residues comprising a peptide epitope useful for
XX inducing an immune response against hepatitis B virus (HBV). The peptide
XX or peptide epitope comprises an amino acid sequence of about 8-13 or 9-25
XX amino acid residues that have at least 65% identity with a native amino
XX acid sequence for HBV, and binds to at least one MHC class I or II HLA
XX allele with a dissociation constant of less than about 500 or 1000 nM.
XX The peptide is from the envelope region, polymerase region, protein X
XX region or nucleocapsid core region of HBV. The peptide bears one of the
XX HLA motifs (e.g. HLA A1, HLA A2, HLA A3, HLA A24, HLA B7, HLA B27, HLA
XX B44, HLA B58 or HLA B62 supermotif, or HLA A1, HLA A3, HLA A11 or HLA 24
XX motif) as listed in the specification. The composition is useful for
XX inducing cellular immune response to HBV or for treating or preventing
XX HBV infection.
XX
XX Sequence 8 AA:
SQ
Query Match 40.0%; Score 4; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
AC AD204720;
XX
XX 02-JUN-2005 (first entry)
XX
DE Hepatitis B virus HLA restricted antigen #198.
XX
KW antiinflammatory; hepatotropic; virucide; vaccine; gene therapy; epitope;
XX immune response; hepatitis B virus infection.
XX
OS Hepatitis B virus.
XX
PN US2005063983-A1.
XX
PD 24-MAR-2005.
XX
PE 04-SEP-2003; 2003US-00654601.
XX
PR 05-MAR-1993; 93US-00027146.
XX 04-JUN-1993; 93US-00073205.
PR 29-NOV-1993; 93US-00159184.
PR 04-MAR-1994; 94US-00205713.
PR 13-MAR-1996; 96US-0013363P.
PR 12-MAR-1997; 97US-00820360.
PR 10-NOV-1998; 98US-00189702.
PR 27-JAN-1999; 99US-00239043.
XX
XX (EPIM-) EPIMMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Vitiello MA, Livingston BD;
PI Cells E, Kubo RT, Grey HM, Cheenut RW;
XX
XX WPI; 2005-241251/25.
XX
XX New peptide and nucleic acid molecule composition for inducing an immune
XX response against hepatitis B virus (HBV) or for treating or preventing
XX HBV infection.
XX
XX Claim 47; SEQ ID NO 198; 497bp; English.
XX
XX The invention relates to a peptide composition, or its analog, of less
XX than 100 amino acid residues comprising a peptide epitope useful for
XX inducing an immune response against hepatitis B virus (HBV). The peptide
XX or peptide epitope comprises an amino acid sequence of about 8-13 or 9-25
XX amino acid residues that have at least 65% identity with a native amino
XX acid sequence for HBV, and binds to at least one MHC class I or II HLA
XX allele with a dissociation constant of less than about 500 or 1000 nM.
XX The peptide is from the envelope region, polymerase region, protein X
XX region or nucleocapsid core region of HBV. The peptide bears one of the
XX HLA motifs (e.g. HLA A1, HLA A2, HLA A3, HLA A24, HLA B7, HLA B27, HLA
XX B44, HLA B58 or HLA B62 supermotif, or HLA A1, HLA A3, HLA A11 or HLA 24
XX motif) as listed in the specification. The composition is useful for
XX inducing cellular immune response to HBV or for treating or preventing
XX HBV infection.
XX
XX Sequence 8 AA:
SQ
Query Match 40.0%; Score 4; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
RESULT 45
AD204720 standard; peptide; 8 AA.
ID AD204720 standard; peptide; 8 AA.
XX
```

```
RESULT 46
AEA22285
ID AEA22285 standard; peptide; 8 AA.
XX
XX AEA22285;
XX
XX 11-AUG-2005 (first entry)
XX
XX
```

DE Soybean activation oxygen inhibiting peptide #3.
 XX renal hypertension; adrenal hypertension; congestive cardiac failure;
 KM hypotensive; cardiant.
 XX Glycine max.
 OS JP2005139158-A.
 PN
 XX
 PD 02-JUN-2005.
 PF 07-NOV-2003; 2003JP-00413922.
 XX
 PR 07-NOV-2003; 2003JP-00413922.
 XX
 PA (SUET/) SUETSUNA Y.
 PA (ORIE-) ORIENTAL BIO KK.
 XX
 PI Sueetsuna K, Watanabe K;
 XX
 DR WPI; 2005-390541/40.
 XX
 PT Novel hexapeptide having sequence containing amino acids of L-form, and
 PT capable of inhibiting activity of angiotensin converting enzyme, useful
 PT as angiotensin converting enzyme inhibitor and antihypertensive.
 XX
 PS Disclosure; page 3; 10pp; Japanese.
 XX
 CC This invention relates to a novel hexapeptide containing amino acids in
 CC the L-form that can be used as an angiotensin converting enzyme (ACE)
 CC inhibitor. Specifically, it refers to a peptide that can be a long-acting
 CC ACE inhibitor as well as an antihypertensive. The present invention
 CC describes using this peptide in pharmaceutical compositions to prevent or
 CC treat hypertension, in particular renal hypertension and adrenal
 CC hypertension, as well as for treating congestive cardiac failure.
 CC Furthermore, the hexapeptide exhibits low toxicity as it does not induce
 CC antibody production and does not generate anaphylactic shock. It also
 CC exhibits hypotensive and cardiant activity in vivo and bradykinin
 CC inactivation inhibitory activity. This peptide sequence is a soybean
 CC activation oxygen inhibition peptide, given in an exemplification of the
 CC invention.
 CC
 SO Sequence 8 AA;
 QY
 Query Match 40.0%; Score 4; DB 9; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0;
 Db 4 LVPO 7
 1 LVPO 4
 RESULT 47
 AEA90023
 ID AEA90023 standard; peptide; 8 AA.
 XX
 AC AEA90023;
 XX
 DT 25-AUG-2005 (first entry)
 XX
 DE Phage display peptide, SEQ ID NO: 39, with ability to bind Salmonella.
 XX
 KM Phage display; surface display; diagnostic; prognosis;
 KM salmonella infection; antibacterial; gastrointestinal disease; infection;
 KM gastrointestinal infection; antimicrobial; biosensor.
 XX
 OS unidentified bacteriophage.
 XX
 XX US2005137136-A1.
 XX
 PD 23-JUN-2005.
 XX

PF 29-APR-2004; 2004US-00835405.
 XX
 PR 29-APR-2003; 2003US-0466485P.
 XX
 PA (AUBU) UNIV AUBURN.
 XX
 PI Petrenko VA, Sorokulova IB, Chin BA, Barbaree JM, Vodyanov VJ;
 PI Chen I, Samoylov AM;
 XX
 DR WPI; 2005-444162/45.
 XX
 PT New biospecific probes, which are synthetic peptides, useful for
 PT identifying bacterial cell surface markers to which the compositions
 PT containing the peptide binds.
 XX
 PS Disclosure; SEQ ID NO 39; 25pp; English.
 XX
 CC The present invention relates to compositions and methods for binding to
 CC Salmonella bacteria. The compositions comprise peptides which bind to
 CC Salmonella bacteria with high specificity and act as a biospecific probe.
 CC These peptides are cell-binding and cell entry peptides. The invention
 CC includes methods of selecting phages with enhanced binding properties.
 CC These phages display peptides that have stronger and more selective
 CC binding affinity to Salmonella cells. The compositions of the invention
 CC are useful for identifying bacterial cell surface markers to which the
 CC compositions containing the peptide bind. The peptides of the invention
 CC are useful for targeting compounds to Salmonella cells for diagnostic,
 CC prognostic and therapeutic purposes and in the therapy of various
 CC bacterial infections (particularly Salmonella infections which may also
 CC cause food poisoning). The invention is also useful as components of
 CC biosensors for detection and characterization of various cells and cell
 CC populations, in areas of health science and for the production of
 CC bioselective materials and nanomaterials such as biospecific filters,
 CC gene and drug delivery vehicles, hemostatics and molecular switches. The
 CC present sequence is a phage display peptide. This peptide is expressed by
 CC phage selected for ability to bind Salmonella.
 CC
 SO Sequence 8 AA;
 QY
 Query Match 40.0%; Score 4; DB 9; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0;
 Db 6 POOG 9
 4 POOG 7
 RESULT 48
 AEA90008
 ID AEA90008 standard; peptide; 8 AA.
 XX
 AC AEA90008;
 XX
 DT 25-AUG-2005 (first entry)
 XX
 DE Phage display peptide, SEQ ID NO: 24, with ability to bind Salmonella.
 XX
 KM Phage display; surface display; diagnostic; prognosis;
 KM salmonella infection; antibacterial; gastrointestinal disease; infection;
 KM gastrointestinal infection; antimicrobial; biosensor.
 XX
 OS unidentified bacteriophage.
 XX
 XX US2005137136-A1.
 XX
 PD 23-JUN-2005.
 XX
 PF 29-APR-2004; 2004US-00835405.
 XX
 PR 29-APR-2003; 2003US-0466485P.
 XX
 PA (AUBU) UNIV AUBURN.
 XX

XX Petrenko VA, Sorokulova IB, Chin BA, Barbaree JM, Vodyanov VU;
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 XX WPI; 2005-444162/45.
 XX
 PT New biospecific probes, which are synthetic peptides, useful for
 PT identifying bacterial cell surface markers to which the compositions
 PT containing the peptide binds.
 PS Disclosure; SEQ ID NO 24; 25pp; English.
 XX
 CC The present invention relates to compositions and methods for binding to
 CC Salmonella bacteria. The compositions comprise peptides which bind to
 CC Salmonella bacteria with high specificity and act as a biospecific probe.
 CC These peptides are cell-binding and cell entry peptides. The invention
 CC includes methods of selecting phages with enhanced binding properties.
 CC These phages display peptides that have stronger and more selective
 CC binding affinity to Salmonella cells. The compositions of the invention
 CC are useful for identifying bacterial cell surface markers to which the
 CC compositions containing the peptide bind. The peptides of the invention
 CC are useful for targeting compounds to Salmonella cells for diagnostic,
 CC prognostic and therapeutic purposes and in the therapy of various
 CC bacterial infections (particularly Salmonella infections which may also
 CC cause food poisoning). The invention is also useful as components of
 CC biosensors for detection and characterization of various cells and cell
 CC populations, in areas of health science and for the production of
 CC bioselective materials and nanomaterials such as biospecific filters,
 CC gene- and drug delivery vehicles, hemostatics and molecular switches. The
 CC present sequence is a phage display peptide. This peptide is expressed by
 CC phage selected for ability to bind Salmonella.
 SQ Sequence 8 AA;

Query Match 40.0%; Score 4; DB 9; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPOQ 8
 ||||
 Db 1 VPOQ 4

RESULT 49

AEA90030
 ID AEA90030 standard; peptide; 8 AA.

XX AEA90030;

XX 25-AUG-2005 (first entry)

XX Phage display peptide #1 with ability to bind Salmonella.

XX Phage display; surface display; diagnostic; prognosis;
 KW salmonella infection; antibacterial; gastrointestinal disease; infection;
 KW gastrointestinal infection; antimicrobial; biosensor.

XX unidentified bacteriophage.

XX US2005137136-A1.

XX 23-JUN-2005.

XX 29-APR-2004; 2004US-00835405.

XX 29-APR-2003; 2003US-0466485P.

XX (AUBU) UNTV AUBURN.

XX Petrenko VA, Sorokulova IB, Chin BA, Barbaree JM, Vodyanov VU;
 PI Chen I, Samoylov AM;

XX WPI; 2005-444162/45.

XX New biospecific probes, which are synthetic peptides, useful for
 PT identifying bacterial cell surface markers to which the compositions
 PT containing the peptide binds.
 PS Disclosure; Page 1; 25pp; English.

XX
 CC The present invention relates to compositions and methods for binding to
 CC Salmonella bacteria. The compositions comprise peptides which bind to
 CC Salmonella bacteria with high specificity and act as a biospecific probe.
 CC These peptides are cell-binding and cell entry peptides. The invention
 CC includes methods of selecting phages with enhanced binding properties.
 CC These phages display peptides that have stronger and more selective
 CC binding affinity to Salmonella cells. The compositions of the invention
 CC are useful for identifying bacterial cell surface markers to which the
 CC compositions containing the peptide bind. The peptides of the invention
 CC are useful for targeting compounds to Salmonella cells for diagnostic,
 CC prognostic and therapeutic purposes and in the therapy of various
 CC bacterial infections (particularly Salmonella infections which may also
 CC cause food poisoning). The invention is also useful as components of
 CC biosensors for detection and characterization of various cells and cell
 CC populations, in areas of health science and for the production of
 CC bioselective materials and nanomaterials such as biospecific filters,
 CC gene- and drug delivery vehicles, hemostatics and molecular switches. The
 CC present sequence is a phage display peptide. This peptide is expressed by
 CC phage selected for ability to bind Salmonella.
 SQ Sequence 8 AA;

Query Match 40.0%; Score 4; DB 9; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPOQ 8
 ||||
 Db 1 VPOQ 4

RESULT 50

AAR39927
 ID AAR39927 standard; peptide; 9 AA.

XX AAR39927;

XX 25-MAR-2003 (revised)

XX 23-DEC-1993 (first entry)

XX N-terminally guanidinoacyl-modified hirudin deriv. #26.

XX Hirudin analogue; hirulog; leech; anti-coagulant; anti-thrombotic;
 KW platelet aggregation inhibition; coagulation; blood clotting.

XX Synthetic.

XX Key Location/Qualifiers

XX Modified-site

XX /label= OTHER
 /note= "(4-guanidino-benzoyl)-Glu"

XX Modified-site

XX /label= OTHER
 /note= "2-aza-bicyclo(2,2,2)octane-3-carbonyl"

XX Modified-site

XX /label= OTHER
 /note= "Tyr(mPO3H2), i.e. PO3H2 in meta-position of ring"

XX Misc-difference

XX /note= "D-Glu"

XX EP552939-A1.

XX 28-JUL-1993.

XX 13-JAN-1993; 93BP-00400051.

PR 15-JAN-1992; 92FR-00000340.

XX (ADIR) ADIR & CIE.

XX Fauchere J, Thirleau C, Verbeuren T, Paladino J;

XX WPI; 1993-23668/30.

DR New stable hirudin deriva. - with increased anticoagulant, antithrombotic
PT and platelet aggregation inhibiting activities.

XX Example 30; Page 10; 28pp; French.

XX This peptide is a specific example of a highly generic formula for
CC hirudin analogues. The analogues have antithrombotic, anti-coagulant
CC and/or platelet aggregation inhibiting activities significantly better
CC than related known compounds (e.g. at least 30 times greater anti-
CC coagulant activity than the hirudin 55-65 fragment). Peptides of the
CC invention also have greater hydrolytic stability and are suitable for
CC preventing post-thrombotic complications and for inhibiting vascular
CC wall/platelet interactions implicated in thrombosis and atherosclerosis.
CC See AAR39903-R39936. (Updated on 25-MAR-2003 to correct PN field.)
XX

SQ Sequence 9 AA;

Query Match 40.0%; Score 4; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2e+06; Mismatches 0; Gaps 0;

Matches 4; Conservative 0; Indels 0;

QY 1 EEYL 4

DB 5 EEYL 8

Search completed: January 18, 2006, 21:03:09
Job time : 145 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 18, 2006, 20:45:40 ; Search time 16 Seconds
(without alignments)
1413.184 Million cell updates/sec

Title:	US-09-930-125-2_COPY_975_1209
Perfect score:	235
Sequence:	1 EFSRMADPQRFVVIQNE...AVENPEYLTGGAAPQHP 235

Scoring code: UNIV Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size: 0

Total number of hits satisfying chosen parameters: 121454

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Minimum DB seq length: 0
Maximum DB seq length: 235

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Post-processing: Listing first 200 summaries

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Database : PIR_80: *
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	7	3.0	68	2	E69489	LSU ribosomal prot
2	7	3.0	85	2	I78540	epidermal growth f
3	7	3.0	105	2	AF1985	nitrogen fixation
4	7	3.0	120	2	T35946	probable regulator
5	7	3.0	138	2	D97041	hypothetical prote
6	7	3.0	182	2	H95365	NADH2 dehydrogenas
7	7	3.0	197	2	AD2829	transcription regul
8	7	3.0	212	2	AD2595	conserved hypothet
9	7	3.0	213	2	B97607	regulatory protein
10	7	3.0	220	2	AE1802	phosphoglucomutase
11	7	3.0	224	2	E72704	hypothetical prote
12	7	3.0	229	2	F97377	hypothetical prote
13	7	3.0	233	2	H96694	hypothetical prote
14	6	2.6	24	2	I61491	seed protein ws-9
15	6	2.6	26	2	P00725	phospholipase A2 (
16	6	2.6	37	2	S39036	lipid transfer prot
17	6	2.6	54	2	B46281	tetraphydrofolylop
18	6	2.6	69	2	T04350	auxin-induced prot
19	6	2.6	73	2	C83650	hypothetical prote
20	6	2.6	73	2	B84020	hypothetical prote
21	6	2.6	88	2	JC5816	cytochrome c6 (val2
22	6	2.6	90	2	T42170	hypothetical prote
23	6	2.6	92	2	DB4330	hypothetical prote
24	6	2.6	93	2	SA42743	hypothetical prote
25	6	2.6	95	2	DS6912	hypothetical prote
26	6	2.6	96	2	F70379	hydroxylase
27	6	2.6	97	2	S11755	hypothetical prote
28	6	2.6	97	2	F97780	hypothetical prote
29	6	2.6	102	2	E72482	hypothetical prote

30	6	2.6	104	2	B4D074	hypothetical prote
31	6	2.6	105	1	RI052	somatostatin-22 pr
32	6	2.6	105	1	A45641	acidic ribosomal p
33	6	2.6	106	2	S31435	acidic ribosomal p
34	6	2.6	106	2	S25631	acidic ribosomal p
35	6	2.6	106	2	T48070	hypothetical prote
36	6	2.6	107	1	R5U728	acidic ribosomal p
37	6	2.6	107	1	R6K916	acidic ribosomal p
38	6	2.6	107	2	S59918	acidic ribosomal p
39	6	2.6	107	2	S59913	acidic ribosomal p
40	6	2.6	107	2	S59920	acidic ribosomal p
41	6	2.6	107	2	S59919	acidic ribosomal p
42	6	2.6	107	2	S40106	acidic ribosomal p
43	6	2.6	108	2	H66287	paii.29 protei
44	6	2.6	109	1	R6U7P1	acidic ribosomal p
45	6	2.6	109	1	QOE0ZG	conserved hypotet
46	6	2.6	109	2	AH0562	hypothetical prote
47	6	2.6	109	2	D90694	hypothetical prote
48	6	2.6	109	2	H85544	hypothetical prote
49	6	2.6	109	2	R81953	hypothetical prote
50	6	2.6	109	2	D81012	hypothetical prote
51	6	2.6	110	2	C71029	hypothetical prote
52	6	2.6	112	1	R6U728	acidic ribosomal p
53	6	2.6	113	1	R6FEP2	acidic ribosomal p
54	6	2.6	115	2	T03336	gene e31 protei
55	6	2.6	115	2	B70536	hypothetical prote
56	6	2.6	115	2	H72745	hypothetical prote
57	6	2.6	119	2	F60767	copla polypept
58	6	2.6	119	2	C84403	hypothetical prote
59	6	2.6	120	2	E95329	hypothetical prote
60	6	2.6	120	2	B72519	hypothetical prote
61	6	2.6	122	2	S52840	haloalkanoic acid
62	6	2.6	126	2	H82479	glycine cleavage s
63	6	2.6	127	2	A72488	hypothetical prote
64	6	2.6	130	2	F95976	hypothetical expor
65	6	2.6	130	2	C90503	conserved hypotet
66	6	2.6	130	2	I52612	Landsteiner-Wiene
67	6	2.6	132	2	A11084	hypothetical prote
68	6	2.6	134	2	T44984	methylmalonyl-CoA
69	6	2.6	134	2	H70814	hypothetical prote
70	6	2.6	136	2	T36547	hypothetical prote
71	6	2.6	142	2	JC4997	hypothetical 15.7M
72	6	2.6	144	2	B70111	V-type ATPase, sub
73	6	2.6	145	2	A70576	hypothetical prote
74	6	2.6	147	2	H84047	hypothetical prote
75	6	2.6	149	2	F87569	flagellar basal-D
76	6	2.6	150	2	A87323	chemotaxis protein
77	6	2.6	150	2	AG1585	hypothetical prote
78	6	2.6	150	2	AH1231	hypothetical prote
79	6	2.6	151	2	AE3643	adenasin a1dA-1 [m
80	6	2.6	153	2	T44492	phosphoenolpyruva
81	6	2.6	156	2	E84861	hypothetical prote
82	6	2.6	156	2	B72592	hypothetical prote
83	6	2.6	157	2	F71406	hypothetical prote
84	6	2.6	158	2	E87271	hypothetical prote
85	6	2.6	158	2	B71228	hypothetical prote
86	6	2.6	160	2	C72501	hypothetical prote
87	6	2.6	160	2	E82441	conserved hypotet
88	6	2.6	161	2	J50739	H+-transporting tw
89	6	2.6	161	2	F72593	hypothetical prote
90	6	2.6	163	2	B84731	hypothetical prote
91	6	2.6	164	2	F86895	RNA polymerase BCT
92	6	2.6	166	2	S13219	s18 protei
93	6	2.6	166	2	A45119	basic helix-loop-h
94	6	2.6	167	2	F84559	histone H1 [import
95	6	2.6	167	2	A55438	transcription fact
96	6	2.6	168	2	E87389	RNA polymerase sid
97	6	2.6	169	2	T18321	hypothetical prote
98	6	2.6	170	2	D87707	hypothetical prote
99	6	2.6	171	1	HJ0246	phosphonotritcin N
100	6	2.6	172	2	A13475	hypothetical peripl
101	6	2.6	173	2	S57617	inorganic diphosph
102	6	2.6	173	2	AG2762	single-strand DNA

A:Residues: 1-85 <RES>
A:Cross-references: UNIPROT:P55245; UNIPARC:UPI0000129DF2; GB:S75916; NID:9912829; PIDN:
C:Superfamily: Tyrosine-protein kinase, EGF receptor type; protein kinase homology
C:Keywords: ATP; growth factor receptor
P:1-83/Domains: protein kinase homology (fragment) <KIN>

Query Match 3.0%; Score 7; DB 2; Length 85;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 MARDPOR 11
DB 79 MARDPOR 85

RESULT 3
AF1985
nitrogen fixation protein [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C:Accession: AF1985
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21555285; PMID:11759840

A:Accession: AF1985

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-105 <KUR>

A:Cross-references: UNIPROT:Q44149; UNIPARC:UPI0000130133; GB:BA000019; PIDN:BAE73390.1;
A:Experimental source: strain PCC 7120

C:Genetics:

A:Gene: nifW

C:Superfamily: nitrogenase stabilizer NifW

Query Match 3.0%; Score 7; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 LVDAREY 49
DB 11 LVDAREY 17

RESULT 4
T35946
probable regulatory protein - Streptomyces coelicolor

C:Species: Streptomyces coelicolor

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C:Accession: T35946
R:Seeger, K.J.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrett, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, January 1999

A:Reference number: Z21551

A:Accession: T35946

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-120 <SEE>

A:Cross-references: UNIPROT:Q9ZBP4; UNIPARC:UPI00000DAEA2; EMBL:AL035206; PIDN:CAA22768.
A:Experimental source: strain A3(2)

C:Genetics:

A:Gene: SCOEDB:SC9B5.26c

Query Match 3.0%; Score 7; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 REGPLPA 185
DB 46 REGPLPA 52

RESULT 5
D97041
hypothetical protein CAC1147 [imported] - Clostridium acetobutylicum

C:Species: Clostridium acetobutylicum

C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004

C:Accession: D97041

R:Molling, J.; Breton, G.; Onelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J.; Daly, M.U.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001

A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo

A:Reference number: A96900; MUID:21359325; PMID:21359325

A:Accession: D97041

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-138 <KUR>

A:Cross-references: UNIPROT:Q97JY6; UNIPARC:UPI00000CA0DF; GB:AE001437; PIDN:AAK79119.1;
A:Experimental source: Clostridium acetobutylicum ATCC824

C:Genetics:

A:Gene: CAC1147

Query Match 3.0%; Score 7; DB 2; Length 138;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 LGLEPSE 93
DB 37 LGLEPSE 43

RESULT 6
H95365
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain C NuoC2 [imported] - Sinorhizobium me

C:Species: Sinorhizobium meliloti

C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 31-Dec-2004

C:Accession: H95365

R:Barnett, M.U.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows

.; Kaiman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yen, K.C.;
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9889, 2001

A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti

A:Reference number: A95262; MUID:21396509; PMID:11481432

A:Accession: H95365

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-182 <KUR>

A:Cross-references: UNIPROT:P56896; UNIPARC:UPI00001308AF; GB:AE006469; PIDN:AAK65490.1;
A:Experimental source: strain 1021, megaplasmid pSymA

R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001

A:Authors: Kahn, D.; Kahn, M.L.; Kaiman, S.; Keating, D.H.; Kiss, B.; Komp, C.; Lelaure,
Hebault, P.; Vandenberg, M.; Vorholter, F.U.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.C.

A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A:Reference number: A96039; MUID:21368234; PMID:11474104

A:Contents: annotation

C:Genetics:

A:Gene: nuoC2

A:Genome: plasmid

C:Superfamily: NADH:quinone oxidoreductase (complex I), subunit 30kD/Ndh/NuoC

C:Keywords: oxidoreductase

Query Match 3.0%; Score 7; DB 2; Length 182;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 213 FGGAIVEN 219
DB 16 FGGAIVEN 22

RESULT 7
AD2829
transcription regulator, TetR family beta [imported] - Agrobacterium tumefaciens (strain

```

C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AB2829
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Minks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Moo, I.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AD2829
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-197 <KUR>
A:Cross-references: UNIPROT:Q8UDR2; UNIPARC:UPI000016469C; GB:AE008668; PIDN:AAL43050.1;
A:Experimental source: strain C58 (Dupont)
A:Genetics:
A:Gene: betI
A:Map position: circular chromosome

Query Match      3.0%; Score 7; DB 2; Length 197;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      189 AGATLER 195
      |||||
      28 AGATLER 34

RESULT 8
AD2595
Conserved hypothetical protein Atu0154 [imported] - Agrobacterium tumefaciens (strain C5
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AD2595
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Minks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Moo, I.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AD2595
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-212 <KUR>
A:Cross-references: UNIPROT:Q8UIY7; UNIPARC:UPI0000164476; GB:AE008668; PIDN:AAL41178.1;
A:Experimental source: strain C58 (Dupont)
A:Genetics:
A:Gene: Atu0154
A:Map position: circular chromosome
A:Superfamily: hypothetical protein b1832

Query Match      3.0%; Score 7; DB 2; Length 212;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      118 MGAAGKL 124
      |||||
      104 MGAAGKL 110

RESULT 9
B97607
regulatory protein (U71857) [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C:Species: Agrobacterium tumefaciens
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C:Accession: B97607
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorllo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001

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A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: B97607
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-213 <KUR>
A:Cross-references: UNIPROT:Q8UDR2; UNIPARC:UPI00000DD1D7E; GB:AE007869; PIDN:AAK87811.1;
A:Genetics:
A:Gene: AGR_C 3729
A:Map position: circular chromosome

Query Match      3.0%; Score 7; DB 2; Length 213;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      189 AGATLER 195
      |||||
      44 AGATLER 50

RESULT 10
AE1802
phosphoglucosyltransferase homolog lin2964 [imported] - Listeria innocua (strain C11p1262)
C:Species: Listeria innocua
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AE1802
R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker,
; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fehli, H.;
D.; Jones, L.M.; Karet, U.
Science 294, 849-852, 2001
A:Authors: Kretz, U.; Kuhn, M.; Kunst, F.; Kurapat, G.; Madueno, E.; Maitournam, A.; Mat
ok, C.; Schueter, T.; Simoes, N.; Tiller, A.; Vazquez-Boland, J.A.; Voss, H.; Wehländ,
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AE1802
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-220 <GLA>
A:Cross-references: UNIPROT:Q926S7; UNIPARC:UPI00000CCA28; GB:AL592022; PIDN:CAC98189.1;
A:Experimental source: strain C11p1262
A:Genetics:
A:Gene: lin2964
A:Superfamily: hypothetical protein b2690

Query Match      3.0%; Score 7; DB 2; Length 220;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      87 LGLPSE 93
      |||||
      162 LGLPSE 168

RESULT 11
E72704
hypothetical protein APE1052 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: E72704
R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Hatake, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyru
A:Reference number: A72450; MUID:99310339; PMID:10382966
A:Accession: E72704
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-224 <KAW>
A:Cross-references: UNIPROT:Q9YD60; UNIPARC:UPI000005DDC2; DBJ:AF000060; NID:G5104188; I
A:Experimental source: strain K1
A:Genetics:
A:Gene: APE1052

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Query Match 3.0%; Score 7; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 PARGAG 67
|||||
DB 99 PARGAG 105

RESULT 12

P97377

hypothetical protein AGR_C_252 [imported] - Agrobacterium tumefaciens (strain C58, Cerec)
C/Species: Agrobacterium tumefaciens
C/Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #ext_change 09-Jul-2004

C/Accession: F97377
R/Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quirillo, B.; Goldman, A.; Liu, F.; Molism, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens
A/Reference number: A97359; MUID:21608551; PMID:11743194

A/Accession: F97377
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-229 <KUR>
A/Cross-references: UNIPROT:Q8UY7; UNIPARC:UPI00000D16F7; GB:AE007869; PIDN:AAK85975.1;
C/Genetics: AGR_C_252

A/Map position: circular chromosome
A/Superfamily: hypothetical protein b1832

Query Match 3.0%; Score 7; DB 2; Length 229;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 118 MGAAGL 124
|||||
DB 121 MGAAGL 127

RESULT 13

H96694

hypothetical protein F5A8.2 [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cross)

C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #ext_change 05-Oct-2004
C/Accession: H96694

R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chiu, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Hansen, N.F.; Hughes, B.; Hultzer, L. Nature 408, 816-820, 2000
A/Author: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Kuykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lurov, J.S.; Malt, R.; Marshall, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A/Author: Salzman, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A/Reference number: A86141; MUID:21016719; PMID:11130712

A/Accession: H96694
A/Status: preliminary
A/Molecule type: DNA

A/Residues: 1-223 <STO>
A/Cross-references: UNIPROT:Q9ZWS6; UNIPARC:UPI00000A7A4C; GB:AE005173; NID:94204277; PI
C/Genetics: A/Map position: 1

A/Map position: 1
C/Superfamily: LOB domain protein

Query Match 3.0%; Score 7; DB 2; Length 233;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 LTLGLEP 91
|||||
DB 189 LTLGLEP 195

RESULT 14

I61491

seed protein w8-9 - winged bean (fragment)
C/Species: Psophocarpus tetragonolobus (winged bean)

C/Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #ext_change 09-Jul-2004
C/Accession: I61491
R/Hirano, H.

A/Title: Protein Chem. 8, 115-130, 1989

A/Title: Microsequence analysis of winged bean seed proteins electrophoretically separated from two-dim
A/Reference number: A61491; MUID:89351606; PMID:2765119

A/Accession: I61491

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-24 <HR>
A/Cross-references: UNIPROT:Q43708; UNIPARC:UPI00001763AC

C/Superfamily: Plant Kunitz-type proteinase inhibitor
C/Keywords: seed

Query Match 2.6%; Score 6; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 DLVDAB 47
|||||
DB 3 DLVDAB 8

RESULT 15

PQ0725

phospholipase A2 (BC 3.1.1.4) 4.0/15K [imported] - rice (fragment)

C/Species: Oryza sativa (rice)
C/Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #ext_change 09-Jul-2004

C/Accession: PQ0725; PQ0724

R/Komatsu, S.; Kajiwara, H.; Hirano, H.

Theor. Appl. Genet. 86, 935-942, 1993

A/Title: A rice protein library; a data-file of rice proteins separated by two-dimension

A/Reference number: PQ0696

A/Accession: PQ0725

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-26 <KOM1>
A/Cross-references: UNIPROT:Q7MLV0; UNIPARC:UPI000017B114

A/Accession: PQ0724

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-10 <KOM2>
A/Cross-references: UNIPARC:UPI000017B115

C/Keywords: carboxylic ester hydrolase

Query Match 2.6%; Score 6; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 APGAG 67
|||||
DB 5 APGAG 10

RESULT 16

S39036

lipid transfer protein P3 - grape

C/Species: Vitis sp. (grape)

C/Date: 25-Dec-1994 #sequence_revision 19-Apr-1996 #ext_change 09-Jul-2004
C/Accession: S39036

R/Coutos-Thévenot, P.; Jouenne, T.; Maes, O.; Guerbette, F.; Grosbois, M.; le Caer, J.P.; Bur, J. Biochem. 217, 885-889, 1993

A/Title: Four 9-kDa proteins excreted by somatic embryos of grapevine are isoforms of 11f

A/Reference number: S39034; MUID:94039144; PMID:8223644

A/Accession: S39036

A/Status: preliminary

A/Molecule type: protein

A:Residues: 1-37 <PGR>
A:Cross-references: UNIPROT:P80273; UNIPARC:UPI00000330241
C:Superfamily: phospholipid transfer protein

Query Match 2.6%; Score 6; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 181 GPLPA 186
DB 21 GPLPA 26

RESULT 17

B46281
Leutrohydrofolylpolyglutamate synthase (EC 6.3.2.17) - pig (fragments)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 31-Dec-1993
C:Accession: B46281
R:Garrow, T.A.; Admon, A.; Shane, B.
Proc. Natl. Acad. Sci. U.S.A. 89, 9151-9155, 1992
A:Title: Expression cloning of a human cDNA encoding folylpoly(gamma-glutamate) synthetase
A:Reference number: A46281; MUID:93028422; PMID:1409616
A:Accession: B46281
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-54 <GAR>
A:Cross-references: UNIPARC:UPI0000088A64
C:Keywords: ligase

Query Match 2.6%; Score 6; DB 2; Length 54;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 LTLGLE 90
DB 28 LTLGLE 33

RESULT 18

T04350
auxin-induced protein IAA2 - tomato (fragment)
C:Species: Lycopersicon esculentum (tomato)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T04350
R:Nebentuehr, A.; Lomax, T.L.
Submitted to the EMBL Data Library, September 1997
A:Description: Auxin-regulated IeIAA genes of tomato.
A:Reference number: Z15303
A:Accession: T04350
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-69 <NEB>
A:Cross-references: UNIPROT:O64913; UNIPARC:UPI00000ACBAF; EMBL:AF022013; NID:G3043894;
A:Experimental source: tissue-type etiolated hypocotyls
C:Genetics:
A:Gene: IAA2
C:Superfamily: auxin-induced protein aux28

Query Match 2.6%; Score 6; DB 2; Length 69;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 148 SETDGY 153
DB 54 SETDGY 59

RESULT 19

C83650
hypothetical protein BH0003 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004

C:Accession: C83650
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hiran
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and 5
A:Reference number: A83650; MUID:20512582; PMID:11058132

A:Accession: C83650
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-73 <STO>
A:Cross-references: UNIPROT:Q9RC40; UNIPARC:UPI00000D4031; GB:AP001507; GB:BA000004; NID:
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH0003

Query Match 2.6%; Score 6; DB 2; Length 73;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 DLVDAE 47
DB 68 DLVDAE 73

RESULT 20

B84020
hypothetical protein BH2962 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: B84020
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hiran
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and 5
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: B84020
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-73 <STO>
A:Cross-references: UNIPROT:Q9K8P1; UNIPARC:UPI00000C4076; GB:AP001517; GB:BA000004; NID:
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH2962

Query Match 2.6%; Score 6; DB 2; Length 73;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 SLLEDD 38
DB 20 SLLEDD 25

RESULT 21

JC5816
cytochrome c6 [validated] - Chlorella vulgaris (strain CK-22)
C:Species: Chlorella vulgaris
C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004
C:Accession: JC5816
R:Yamada, S.; Nakamura, T.; Tanaka, Y.; Isegai, Y.; Nishio, T.; Oku, T.
Biosci. Biotechnol. Biochem. 64, 628-632, 2000
A:Title: Characterization and Amino Acid Sequences of Cytochromes c6 from Two Strains of
A:Reference number: JC5816
A:Accession: JC5816
A:Molecule type: protein
A:Residues: 1-88 <YAM>
A:Cross-references: UNIPROT:Q7M1S4; UNIPARC:UPI0000174C7B
C:Superfamily: cytochrome c6; cytochrome c6 homology
C:Keywords: acetylated amino end; chromoprotein; electron transfer; heme; iron; metallopro
F:4-79/Domain: cytochrome c6 homology <CY6>
F:14,17/Binding site: heme (Ys) (covalent) #status experimental
F:18,60/Binding site: heme iron (His, Met) (axial ligands) #status predicted

Query Match 2.6%; Score 6; DB 2; Length 88;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 83 GDLTIG 88
Db 1 GDLTIG 6

RESULT 22
T42170
hypothetical protein L7070 - Escherichia coli plasmid p0157

C/Spectrum: Escherichia coli
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C/Accession: T42170
R/Burkard, V.; Shao, Y.; Perna, N.T.; Plunkett, G.; Sofia, H.J.; Blattner, F.R.
Nucleic Acids Res. 26, 4196-4204, 1998
A/Title: The complete DNA sequence and analysis of the large virulence plasmid of Escherichia coli O157:H7
A/Reference number: Z22068; PMID:98391744; PMID:9722640
A/Accession: T42170
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-90 <BUR>
A/Cross-references: UNIPROT:Q9ZGGS; UNIPARC:UPI0000083811; EMBL:AF074613; PIDD:AACT0138.
A/Experimental source: strain EDJ933; serotype O157:H7
C/Genetics:
A/Genome: plasmid p0157
A/Note: L7070

Query Match 2.6%; Score 6; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 RSSSTR 79
Db 59 RSSSTR 64

RESULT 23
D84330
hypothetical protein Vng1786h [imported] - Halobacterium sp. NRC-1

C/Spectrum: Halobacterium sp. NRC-1
C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C/Accession: D84330
R/Ng, W.V.; Kennedy, S.P.; Mahalingam, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Laaky, S.; Leithauer, B.; Keller, K.; Cruz, R.; Danon, M.J.; Hough, D.W.; Maddocks, D.G.; Jabit Jung, K.H.; Alam, M.; Prells, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A/Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; Li
A/Title: Genome sequence of Halobacterium species NRC-1.
A/Reference number: A84160; PMID:20504483; PMID:11016950
A/Accession: D84330
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-92 <STO>
A/Cross-references: UNIPROT:Q9HP62; UNIPARC:UPI0000063985; GB:AE004437; NID:G10581240; F
C/Genetics:
A/Genome: VNG1786h

Query Match 2.6%; Score 6; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 DPORPV 13
Db 41 DPORPV 46

RESULT 24

S42743
hypothetical protein - Erwinia chrysanthemi (fragment)
C/Spectrum: Erwinia chrysanthemi
C/Date: 07-Oct-1994 #sequence_revision 26-May-1995 #text_change 31-Dec-2004
C/Accession: S42743
R/Moulard, M.; Condemine, G.; Robert-Baudouy, J.

Mol. Microbiol. 8, 685-695, 1993
A/Title: Characterization of the nuc gene coding for a nuclease of the phytopathogenic bacterium Erwinia chrysanthemi
A/Reference number: S34943; PMID:93323747; PMID:8332061
A/Accession: S42743
A/Status: preliminary; translation not shown
A/Molecule type: DNA
A/Residues: 1-93 <MOU>
A/Cross-references: UNIPROT:P37995; UNIPARC:UPI000013B096; EMBL:X73255; NID:G403001; PIDD:G403001

C/Superfamily: methyltransferase, b1r0722 type

Query Match 2.6%; Score 6; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 223 LTPQGG 228
Db 12 LTPQGG 17

RESULT 25

D69121
hypothetical protein MTH1905 - Methanobacterium thermoautotrophicum (strain Delta H)
C/Spectrum: Methanobacterium thermoautotrophicum
C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C/Accession: D69121
R/Smith, D.R.; Doucette-Stamm, L.A.; DeJonghery, C.; Lee, H.; Dubois, J.; Aldredge, T.; I
J. Bacteriol. 179, 7135-7155, 1997
A/Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: functi
A/Reference number: A69000; PMID:98037514; PMID:9371463
A/Accession: D69121
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-95 <MTH>
A/Cross-references: UNIPROT:Q27927; UNIPARC:UPI0000062C1A; GB:AE000941; GB:AE000666; NID:
A/Experimental source: strain Delta H
C/Genetics:
A/Genome: MTH1905
A/Start codon: GTG
C/Superfamily: hypothetical protein MTH1905

Query Match 2.6%; Score 6; DB 2; Length 95;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 SLLEDD 38
Db 62 SLLEDD 67

RESULT 26

F70379
ferredoxin [2Fe-2S] fdx1 [similarity] - Aquifex aeolicus
C/Spectrum: Aquifex aeolicus
C/Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C/Accession: F70379
R/Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.B.; Ove
V.

Nature 392, 353-358, 1998
A/Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A/Reference number: A70300; PMID:98196666; PMID:9537320
A/Accession: F70379
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-96 <AQF>
A/Cross-references: UNIPROT:Q67065; UNIPARC:UPI00000564A4; GB:AE000713; NID:G2983424; PIDD:G2983424

A/Experimental source: strain VFS
C/Genetics:
A/Genome: fdx1
C/Superfamily: ferredoxin (2Fe-2S)
C/Keywords: 2Fe-2S; iron-sulfur protein; metalloprotein
F/21-79/Domain: ferredoxin [2Fe-2S] homology <FER>

F,34,39,42,78/Binding site: 2Fe-2S cluster (Cys) (covalent) #status predicted

Query Match 2.6%; Score 6; DB 2; Length 96;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 90 EPSEEE 95
|||||
DB 55 EPSEEE 60

RESULT 27
S11755

hypothetical protein - Plasmodium vivax (fragment)

C.Species: Plasmodium vivax
C.Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

C.Accession: S11755

R.Campbell, J.R.; Franke, E.D.

submitted to the EMBL Data Library, April 1989

A.Description: A repetitive element found in Plasmodium vivax DNA.

A.Reference number: S11755

A.Accession: S11755

A.Molecule type: DNA

A.Residues: 1-97 <CAM>

A.Cross-references: UNIPROT:Q26168; UNIPARC:UPI000007CFDD; EMBL:X15129; NID:G10086; PID:

Query Match 2.6%; Score 6; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 APSEGA 107
|||||
DB 29 APSEGA 34

RESULT 28
F97780

hypothetical protein RC0646 [imported] - Rickettsia conorii (strain Malish 7)

C.Species: Rickettsia conorii

C.Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004

C.Accession: F97780

R.Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Ro

Science 293, 2093-2098, 2001

A.Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.

A.Reference number: A97700; MUID:21442074; PMID:11557893

A.Accession: F97780

A.Status: preliminary

A.Molecule type: DNA

A.Residues: 1-97 <KUR>

A.Cross-references: UNIPROT:Q92HX4; UNIPARC:UPI00000CBE59; GB:AE006914; PIDN:AAL03184.1;

A.Gene: RC0646

Query Match 2.6%; Score 6; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 TIGLEP 91
|||||
DB 37 TIGLEP 42

RESULT 29
E72482

hypothetical protein APE2501 - Aeropyrum pernix (strain K1)

C.Species: Aeropyrum pernix

C.Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004

C.Accession: E72482

R.Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah

awa, H.; Takamiya, M.; Maeda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K

DNA Res. 6, 83-101, 1999

A.Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr

A.Reference number: A74501; MUID:99310339; PMID:10382966

A.Accession: E72482

A.Status: preliminary

A.Molecule type: DNA

A.Residues: 1-102 <KMW>

A.Cross-references: UNIPROT:Q9Y8Y3; UNIPARC:UPI000005E389; DDBJ:AP000064; NID:G5105945; I

A.Experimental source: strain K1

C.Genetics:

A.Gene: APE2501

C.Superfamily: Aeropyrum pernix hypothetical protein APE2501

Query Match 2.6%; Score 6; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 TRSGGG 83
|||||
DB 12 TRSGGG 17

RESULT 30
E42074

hypothetical protein 2 (SMP1 gene region) - human

C.Species: Homo sapiens (man)

C.Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 09-Jul-2004

C.Accession: E42074

R.Schuchman, E.H.; Levran, O.; Pereira, L.V.; Deanick, R.U.

Genomics 12, 197-205, 1992

A.Title: Structural organization and complete nucleotide sequence of the gene encoding h

A.Reference number: A42074; MUID:92155708; PMID:1740330

A.Accession: E42074

A.Status: preliminary; not compared with conceptual translation

A.Molecule type: DNA

A.Residues: 1-104 <SCH>

A.Cross-references: UNIPROT:Q15495; UNIPARC:UPI00006D406; GB:M81780; NID:G972768; PIDN:J

C.Superfamily: human hypothetical protein 2 (SMP1 gene region)

Query Match 2.6%; Score 6; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 APGAGG 67
|||||
DB 6 APGAGG 11

RESULT 31
RIIDS2

somatostatin-22 precursor - channel catfish

N.Alternate names: somatostatin II; SST-22

N.Contains: somatostatin-22

C.Species: Ictalurus punctatus (channel catfish)

C.Date: 02-Apr-1982 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C.Accession: S00293; A92451; A92271; I50799; A01436

R.Magazin, M.; Minch, C.D.; Funke, C.L.; Deechene, R.; Tavlanli, M.A.; Dixon, J.E.

Proc. Natl. Acad. Sci. U.S.A. 79, 5152-5156, 1982

A.Title: Sequence of a cDNA encoding pancreatic preprosomatostatin-22.

A.Reference number: S00293; MUID:83039328; PMID:6127673

A.Accession: S00293

A.Molecule type: mRNA

A.Residues: 1-105 <MAG>

A.Cross-references: UNIPROT:P01172; UNIPARC:UPI0000135AD6; GB:J00945; NID:G213341; PIDN:J

R.Andrews, P.C.; Pubols, M.H.; Hermodson, M.A.; Shearer, B.T.; Dixon, J.E.

J. Biol. Chem. 259, 13267-13272, 1984

A.Title: Structure of the 22-residue somatostatin from catfish. An O-glycosylated peptide

A.Reference number: A92451; MUID:85030447; PMID:6149220

A.Accession: A92451

A.Molecule type: protein

A.Residues: 84-105 <AND>

A.Cross-references: UNIPARC:UPI00001733D5

A.Note: this is the major form of somatostatin-22

R.Oyama, H.; Bradshaw, R.A.; Bates, O.J.; Permutt, A.

J. Biol. Chem. 255, 2251-2254, 1980

A.Title: Amino acid sequence of catfish pancreatic somatostatin I.

A/Reference number: A92271; MUID:80137439; PMID:7358665
A/Accession: A92271
A/Molecule type: protein
A/Residues: 1-4, 'R', '6-18, 'S', '20-22 <OYA>
A/Cross-references: UNIPARC:UPI00001733D6
A/Experimental source: pancreatic islet D-cell
A/Note: the authors' designation of this form as somatostatin I may conflict with other
R./Dixon, J.E.; Andrews, P.C.
Adv. Exp. Med. Biol. 188, 19-29, 1985
A/Title: Somatostatin of the channel catfish.
A/Reference number: 150798; MUID:85303576; PMID:2863931
A/Accession: 150799
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-105 <DIX>
A/Cross-references: UNIPARC:UPI0000135AD6; GB:M25904; NID:G213343; PIDN:AAA49341.1; PID:
C/Superfamily: somatostatin
C/Keyword: glycoprotein; neuropeptide; pancreatic islet
F./1-25/Domain: signal sequence #status predicted <SIG>
F./26-83/Domain: propeptide #status predicted <PRO>
F./84-105/Product: somatostatin-22 #status experimental <MAT>
F./88/Binding site: carbohydrate (Thr) (covalent) #status experimental
F./94-105/Distal/Disulfide bonds: #status experimental

Query Match 2.6%; Score 6; DB 1; Length 105;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 94 EDAPRS 99
DB 71 EDAPRS 76

RESULT 32
A45641
acidic ribosomal protein P2 - Trypanosoma cruzi (fragment)
C/Species: Trypanosoma cruzi
C/Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
R./Matzger, D.A.; Reinos, R.F.; Hunter, C.A.; Donelson, J.E.
Mol. Biochem. Parasitol. 49, 325-328, 1991
A/Title: Patients infected with Leishmania donovani chagasi can have antibodies that rec
A/Reference number: A45641; MUID:92131069; PMID:1733150
A/Accession: A45641
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-105 <NRF>
A/Cross-references: UNIPROT:P23632; UNIPARC:UPI000016C0B3; GB:M72710; GB:M72712; NID:G14
A/Note: sequence extracted from NCBI backbone (NCBI:79052, NCBI:P:79054)
C/Superfamily: rat acidic ribosomal protein P1

Query Match 2.6%; Score 6; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 EDDDMG 41
DB 95 EDDDMG 100

RESULT 33
S31435
acidic ribosomal protein P2 isoform P-JL5 - Trypanosoma cruzi (fragment)
C/Species: Trypanosoma cruzi
C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004
C/Accession: S31435
R./Schijman, A.G.
Submitted to the EMBL Data Library, September 1992
A/Reference number: S31435
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-106 <SCH>

A/Cross-references: UNIPROT:P23632; UNIPARC:UPI000016C0B3; EMBL:X69508; NID:G10643; PIDN:
C/Superfamily: rat acidic ribosomal protein P1

Query Match 2.6%; Score 6; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 EDDDMG 41
DB 96 EDDDMG 101

RESULT 34
S25631
acidic ribosomal protein P2 isoform P2a-RA - Trypanosoma cruzi
C/Species: Trypanosoma cruzi
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
R./Vazquez, M.; Levin, M.J.
Submitted to the EMBL Data Library, September 1992
A/Reference number: S25631
A/Accession: S25631
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-106 <VAZ>
A/Cross-references: UNIPROT:Q26944; UNIPARC:UPI000007C407; EMBL:X68310; NID:G10631; PIDN:
C/Superfamily: rat acidic ribosomal protein P1

Query Match 2.6%; Score 6; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 EDDDMG 41
DB 97 EDDDMG 102

RESULT 35
T48070
hypothetical protein F26K9.240 - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C/Accession: T48070
R./Boeckler, H.; Mewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.; Querier, F.; Salanoubat
Submitted to the Protein Sequence Database, March 2000
A/Reference number: Z24465
A/Accession: T48070
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-106 <BLO>
A/Cross-references: UNIPROT:Q9LZ14; UNIPARC:UPI000000C46C; EMBL:AL162651
A/Experimental source: cultivar Columbia; BAC clone F26K9
C/Genetics:
A/Map position: 3
A/Introns: 81/1
A/Note: F26K9.240

Query Match 2.6%; Score 6; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 189 AGATLE 194
DB 89 AGATLE 94

RESULT 36
R5UTR28
acidic ribosomal protein P2-A - Trypanosoma cruzi
N/Alternate names: acidic ribosomal protein P-JL5; ribosomal protein TL12el; Tcp2-beta
C/Species: Trypanosoma cruzi
C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C/Accession: S12585; A60447; S59917

R;Schijman, A.G.; Dusecchi, N.J.; Vazquez, M.P.; Lafon, S.; Levy-Yeyati, P.; Levin, M.J.
Nucleic Acids Res. 18, 3399, 1990
A>Title: Nucleotide cDNA and complete deduced amino acid sequence of a Trypanosoma cruzi
A:Reference number: S12585; MUID:90287723; PMID:2192363
A:Accession: S12585
A:Molecule type: mRNA
A:Residues: 1-107 <SCH>
A:Cross-references: UNIPROT:P23632; UNIPARC:UPI0000134263; EMBL:X52323; NID:G10635; PIDN
R:Levin, M.J.; Meiri, E.; Benarous, R.; Levitus, G.; Schijman, A.; Levy-Yeyati, P.; Chis
Am. J. Trop. Med. Hyg. 41, 530-538, 1989
A>Title: Identification of major Trypanosoma cruzi antigenic determinants in chronic cha
A:Reference number: A60447; MUID:90053984; PMID:2479275
A:Accession: A60447
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 73-83, 'G', 85-107 <LEV>
A:Cross-references: UNIPARC:UPI0000173AB8
R;Schijman, A.G.; Vazquez, M.P.; Ben Dov, C.; Ghio, S.; Lorenzi, H.; Levin, M.J.
Biochim. Biophys. Acta 1264, 15-18, 1995
A>Title: Cloning and sequence analysis of the Tcp2-beta cDNA variants of Trypanosoma cru
A:Reference number: S59912; MUID:96038812; PMID:7578249
A:Accession: S59912
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-107 <SC2>
A:Cross-references: UNIPARC:UPI0000134263; EMBL:X52323; NID:G10635; PIDN:CAA36557.1; PID
C:Keywords: phosphoprotein; protein biosynthesis; ribosome

Query Match 2.6%; Score 6; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 EDDDMG 41
DB 97 EDDDMG 102

RESULT 37
REMIC
acidic ribosomal protein P1, cytosolic - Chlamydomonas reinhardtii
C:Species: Chlamydomonas reinhardtii
C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C:Accession: S24990
R:Dumont, F.
submitted to the EMBL Data Library, May 1992
A:Reference number: S24989
A:Accession: S24990
A:Molecule type: mRNA
A:Residues: 1-107 <DUM>
A:Cross-references: UNIPROT:P29763; UNIPARC:UPI0000134241; EMBL:X66411; NID:G18210; PIDN
C:Superfamily: rat acidic ribosomal protein P1
C:Keywords: phosphoprotein; protein biosynthesis; ribosome

Query Match 2.6%; Score 6; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 90 EPSSEER 95
DB 94 EPSSEER 99

RESULT 38
S59918
acidic ribosomal protein P2.beta (H1.5) - Trypanosoma cruzi
N:Alternate names: acidic ribosomal protein P.1J5 variant D
C:Species: Trypanosoma cruzi
C:Date: 24-Aug-1996 #sequence_revision 08-Nov-1996 #text_change 09-Jul-2004
C:Accession: S59918; S40100; S31434
R;Schijman, A.G.; Vazquez, M.P.; Ben Dov, C.; Ghio, S.; Lorenzi, H.; Levin, M.J.
Biochim. Biophys. Acta 1264, 15-18, 1995
A>Title: Cloning and sequence analysis of the Tcp2-beta cDNA variants of Trypanosoma cru

A:Reference number: S59912; MUID:96038812; PMID:7578249
A:Accession: S59918
A:Molecule type: mRNA
A:Residues: 1-107 <SCH>
A:Cross-references: UNIPROT:P23632; UNIPARC:UPI000016C0B8; EMBL:X69510; NID:G10639; PIDN
R:Vazquez, M.; Schijman, A.; Levin, M.
submitted to the EMBL Data Library, September 1993
A:Reference number: S40100
A:Accession: S40100
A:Molecule type: DNA
A:Residues: 1-107 <VAZ>
A:Cross-references: UNIPARC:UPI000016C0B8; EMBL:X75030; NID:G436137; PIDN:CAA52938.1; PII
C:Superfamily: rat acidic ribosomal protein P1
C:Keywords: phosphoprotein; protein biosynthesis; ribosome

Query Match 2.6%; Score 6; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 EDDDMG 41
DB 97 EDDDMG 102

RESULT 39
S59913
acidic ribosomal protein P2.beta (H1.3) - Trypanosoma cruzi
C:Species: Trypanosoma cruzi
C:Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S59913
R;Schijman, A.G.; Vazquez, M.P.; Ben Dov, C.; Ghio, S.; Lorenzi, H.; Levin, M.J.
Biochim. Biophys. Acta 1264, 15-18, 1995
A>Title: Cloning and sequence analysis of the Tcp2-beta cDNA variants of Trypanosoma cru
A:Reference number: S59912; MUID:96038812; PMID:7578249
A:Accession: S59913
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-107 <SCH>
A:Cross-references: UNIPROT:Q26959; UNIPARC:UPI00001772PE
C:Superfamily: rat acidic ribosomal protein P1
C:Keywords: phosphoprotein; protein biosynthesis; ribosome

Query Match 2.6%; Score 6; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 EDDDMG 41
DB 97 EDDDMG 102

RESULT 40
S59920
acidic ribosomal protein P2.beta (H6.4) - Trypanosoma cruzi
C:Species: Trypanosoma cruzi
C:Date: 24-Aug-1996 #sequence_revision 08-Nov-1996 #text_change 09-Jul-2004
C:Accession: S59920; S40103
R;Schijman, A.G.; Vazquez, M.P.; Ben Dov, C.; Ghio, S.; Lorenzi, H.; Levin, M.J.
Biochim. Biophys. Acta 1264, 15-18, 1995
A>Title: Cloning and sequence analysis of the Tcp2-beta cDNA variants of Trypanosoma cru
A:Reference number: S59912; MUID:96038812; PMID:7578249
A:Accession: S59920
A:Molecule type: mRNA
A:Residues: 1-107 <SCH>
A:Cross-references: UNIPROT:Q26957; UNIPARC:UPI00000817CC; EMBL:X75031; NID:G436141; PIDN
R:Vazquez, M.; Schijman, A.; Levin, M.
submitted to the EMBL Data Library, September 1993
A:Reference number: S40100
A:Accession: S40103
A:Molecule type: DNA
A:Residues: 1-107 <VAZ>
A:Cross-references: UNIPARC:UPI00000817CC; EMBL:X75031; NID:G436141; PIDN:CAA52941.1; PII
C:Superfamily: rat acidic ribosomal protein P1

C:Keywords: phosphoprotein; protein biosynthesis; ribosome

Query Match 2.6%; Score 6; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 36 EDDDMG 41
Db 97 EDDDMG 102

RESULT 41

559919

acidic ribosomal protein p2.beta (X) - Trypanosoma cruzi

N/Alternate names: acidic ribosomal protein P.315 variant C

C/Species: Trypanosoma cruzi

C/Date: 24-Aug-1996 #sequence_revision 08-Nov-1996 #text_change 09-Jul-2004

C/Accession: S59919; S31433

R/Schjman, A.G.; Vazquez, M.P.; Ben Dov, C.; Ghilo, S.; Lorenzi, H.; Levin, M.J.

A/Title: Cloning and sequence analysis of the Tcp2-beta cDNA variants of Trypanosoma cru

A/Reference number: S59912; PMID:96038812; PMID:7578249

A/Accession: S59919

A/Molecule type: mRNA

A/Residues: 1-107 <SCH>

A/Cross-references: UNIPROT:P23632; UNIPARC:UPI000016C0B7; EMBL:X65509; NID:G10637; PIDN

C/Superfamily: rat acidic ribosomal protein P1

C/Keywords: phosphoprotein; protein biosynthesis; ribosome

Query Match 2.6%; Score 6; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 36 EDDDMG 41
Db 97 EDDDMG 102

RESULT 42

S40106

acidic ribosomal protein p2.beta (H1.8) - Trypanosoma cruzi

N/Alternate names: gene Tcp2beta protein

C/Species: Trypanosoma cruzi

C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004

C/Accession: S40106; S59912; S40107

R/Vazquez, M.; Schjman, A.; Levin, M.

submitted to the EMBL Data Library, September 1993

A/Reference number: S40100

A/Accession: S40106

A/Molecule type: DNA

A/Residues: 1-107 <VAZ>

A/Cross-references: UNIPROT:Q27291; UNIPARC:UPI0000079E46; EMBL:X75033; NID:G436148; PIDN

R/Schjman, A.G.; Vazquez, M.P.; Ben Dov, C.; Ghilo, S.; Lorenzi, H.; Levin, M.J.

Biochim. Biophys. Acta 1264, 15-18, 1995

A/Title: Cloning and sequence analysis of the Tcp2-beta cDNA variants of Trypanosoma cru

A/Reference number: S59912; PMID:96038812; PMID:7578249

A/Accession: S59912

A/Status: not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-107 <SCH>

A/Cross-references: UNIPARC:UPI0000079E46

C/Superfamily: rat acidic ribosomal protein P1

C/Keywords: phosphoprotein; protein biosynthesis; ribosome

Query Match 2.6%; Score 6; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 36 EDDDMG 41
Db 97 EDDDMG 102

RESULT 43

H86287

P9L1.29 protein - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C/Accession: H86287

R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Hutzar, L.

Nature 408, 816-820, 2000

A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A/Reference number: A86141; PMID:21016719; PMID:11130712

A/Accession: H86287

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-108 <STO>

A/Cross-references: UNIPROT:Q9X135; UNIPARC:UPI000000BEB8; GB:AB005172; NID:G5103833; PIDN

C/Genetics:

A/Map position: 1

Query Match 2.6%; Score 6; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 163 PEYVNO 168
Db 32 PEYVNO 37

RESULT 44

R6UTP1

acidic ribosomal protein P1 - Trypanosoma cruzi

C/Species: Trypanosoma cruzi

C/Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004

C/Accession: S22644; S19924

R/Vazquez, M.P.; Schjman, A.G.; Levin, M.J.

Nucleic Acids Res. 20, 2599, 1992

A/Title: Nucleotide sequence of a cDNA encoding a Trypanosoma cruzi acidic ribosomal P1

A/Reference number: S22644; PMID:92285148; PMID:1598221

A/Accession: S22644

A/Status: nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-109 <VAZ>

A/Cross-references: UNIPROT:P26643; UNIPARC:UPI000013424B; EMBL:X65025; NID:G10629; PIDN:

C/Superfamily: rat acidic ribosomal protein P1

C/Keywords: phosphoprotein; protein biosynthesis; ribosome

Query Match 2.6%; Score 6; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 36 EDDDMG 41
Db 99 EDDDMG 104

RESULT 45

Q0BCZG

YbaB protein - Escherichia coli (strain K-12)

C/Species: Escherichia coli

C/Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 31-Dec-2004

C/Accession: A30371; C25549; F64777; Q00815

R/Mahdi, A.A.; Lloyd, R.G.

Nucleic Acids Res. 17, 6781-6794, 1989

A/Title: The rck locus of Escherichia coli K-12: molecular cloning, DNA sequencing and i

A/Reference number: A30371; PMID:89386036; PMID:2674903

A/Accession: A30371

A/Molecule type: DNA

A:Residues: 1-109 <MAH>
 A:Cross-references: UNIPROT:P17577; UNIPARC:UPI000005A1P2; GB:M38777; NID:G145295; PIDN:
 R:Flower, A.M.; McHenry, C.S.
 Nucleic Acids Res. 14, 8091-8101, 1986
 A:Title: The adjacent dna2 and dna3 genes of Escherichia coli are contained within one c
 A:Reference number: A25549; MUID:87040775; PMID:3534795
 A:Accession: C25549
 A:Molecule type: DNA
 A:Residues: 1-75 <ELO>
 A:Cross-references: UNIPARC:UPI000016F6F4; GB:X04487; NID:G43319; PIDN:CAA28176.1; PID:G
 A:Experimental source: strain K-12, substrain JM109
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
 A.; Rose, D.J.; Mau, B.; Shao, Y.
 Science 277, 1453-1462, 1997
 A:Title: The complete genome sequence of Escherichia coli K-12.
 A:Reference number: A64720; MUID:97426617; PMID:9278503
 A:Accession: F64777
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-109 <BLAT>
 A:Cross-references: UNIPARC:UPI000005A1P2; GB:AE000153; GB:U00096; NID:G1786671; PIDN:AF
 A:Experimental source: strain K-12, substrain MG1655
 C:Genetics:
 A:Gene: ybaB
 A:Map position: 11 min
 C:Superfamily: uncharacterized conserved protein

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 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 SLEDD 38
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 DB 60 SLEDD 65

RESULT 46
 AH0562
 conserved hypothetical protein STY0529 [imported] - Salmonella enterica subsp. enterica
 C:Species: Salmonella enterica subsp. enterica serovar Typh
 A:Note: this species has also been called Salmonella typh
 C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 31-Dec-2004
 C:Accession: AH0562
 R:Parhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
 th, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
 S.; Moule, S.; O'Garra, P.
 Nature 413, 848-852, 2001
 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
 A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
 A:Reference number: AB0502; MUID:21534947; PMID:11677608
 A:Accession: AH0562
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-109 <PAR>
 A:Cross-references: UNIPARC:UPI000005A1P2; GB:AL513382; PIDN:CAD04970.1; PID:G16501756;
 C:Genetics:
 A:Gene: STY0529
 C:Superfamily: uncharacterized conserved protein

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 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 SLEDD 38
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 DB 60 SLEDD 65

RESULT 47
 D90694
 hypothetical protein EG0524 [imported] - Escherichia coli (strain O157:H7, substrain R1
 C:Species: Escherichia coli
 C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 31-Dec-2004

C:Accession: D90694
 R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
 Gasaavara, N.; Yasunaga, T.; Kihara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
 DNA Res. 8, 11-22, 2001
 A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom
 A:Reference number: A9629; MUID:21156231; PMID:11258796
 A:Accession: D90694
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-109 <HAY>
 A:Cross-references: UNIPROT:P17577; UNIPARC:UPI000005A1P2; GB:BA000007; PIDN:BAB33947.1;
 A:Experimental source: strain O157:H7, substrain R1MD 0509952
 C:Genetics:
 A:Gene: EG0524
 C:Superfamily: uncharacterized conserved protein

Query Match 2.6%; Score 6; DB 2; Length 109;
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 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 SLEDD 38
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 DB 60 SLEDD 65

RESULT 48
 H85544
 hypothetical protein ybaB [imported] - Escherichia coli (strain O157:H7, substrain EDL933;
 C:Species: Escherichia coli
 C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Dec-2004
 C:Accession: H85544
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew,
 Miller, L.; Grobeck, E.J.; Davis, N.W.; Lam, A.; Diallantha, E.; Potamousis, K.; Apodaca,
 Nature 409, 529-533, 2001
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: A85480; MUID:21074935; PMID:11206551
 A:Accession: H85544
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-109 <STO>
 A:Cross-references: UNIPROT:P17577; UNIPARC:UPI000005A1P2; GB:AE005174; NID:G12513341; PJ
 A:Experimental source: strain O157:H7, substrain EDL933
 C:Genetics:
 A:Gene: ybaB
 C:Superfamily: uncharacterized conserved protein

Query Match 2.6%; Score 6; DB 2; Length 109;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 SLEDD 38
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 DB 60 SLEDD 65

RESULT 49
 F81953
 hypothetical protein MMA0376 [imported] - Neisseria meningitidis (strain Z2491 serogroup
 C:Species: Neisseria meningitidis
 C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
 C:Accession: F81953
 R:Parhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morell
 ; Holroyd, S.; Jagsis, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
 Nature 404, 502-506, 2000
 A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
 A:Reference number: A81775; MUID:20222556; PMID:10761919
 A:Accession: F81953
 A:Status: preliminary
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 A:Residues: 1-109 <PAR>
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 A:Experimental source: serogroup A, strain Z2491
 C:Genetics:

A:Gene: NMA0376

Query Match 2.6%; Score 6; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 YRSILE 36
|||
83 YRSILE 88

RESULT 50

D81012
hypothetical protein NMB2059 [imported] - *Neisseria meningitidis* (strain MCS8 serogroup
C/Species: *Neisseria meningitidis*
C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C/Accession: D81012
R/Tetcelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
rt, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A/Authors: Grand, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A/Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MCS8.
A/Reference number: A81000; WUID:20175755; PMID:10710307
A/Accession: D81012
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-109 <TE>
A/Cross-references: UNIPROT:Q9JXG7; UNIPARC:UPI00000C4858; GB:AE002555; GB:AE002098; NID
A/Experimental source: serogroup B, strain MCS8
C/Genetics:
A:Gene: NMB2059

Query Match 2.6%; Score 6; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 YRSILE 36
|||
83 YRSILE 88

Search completed: January 18, 2006, 20:49:39
Job time : 29 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: January 18, 2006, 21:06:00 : Search time 111 Seconds
(without alignments)
37.642 Million cell updates/sec

Title: US-09-930-125-3
Perfect score: 10
Sequence: 1 ERYLVPGQGF 10

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 1867569 seqs, 417829326 residues

Word size: 0
Total number of hits satisfying chosen parameters: 232507

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Listing first 200 summaries

Database : Published Applications AA Main:
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	90.0	90.0	9	US-10-149-138-1138	Sequence 1138, Appl1
5	90.0	90.0	9	US-10-149-138-3666	Sequence 3666, Appl1
6	90.0	90.0	9	US-10-253-286-607	Sequence 607, Appl1
7	90.0	90.0	9	US-10-149-138-1138	Sequence 1138, Appl1
8	90.0	90.0	9	US-10-149-138-3666	Sequence 3666, Appl1
9	90.0	90.0	10	US-10-149-138-1139	Sequence 1139, Appl1
10	90.0	90.0	10	US-10-149-138-3667	Sequence 3667, Appl1
11	90.0	90.0	10	US-10-149-138-1139	Sequence 1139, Appl1
12	90.0	90.0	10	US-10-149-138-1139	Sequence 1139, Appl1
13	80.0	80.0	8	US-10-149-138-15	Sequence 15, Appl1
14	80.0	80.0	8	US-10-149-138-1449	Sequence 1449, Appl1
15	80.0	80.0	8	US-10-149-138-2377	Sequence 2377, Appl1
16	80.0	80.0	8	US-10-149-138-3170	Sequence 3170, Appl1
17	80.0	80.0	8	US-10-149-138-15	Sequence 15, Appl1
18	80.0	80.0	8	US-10-149-138-1449	Sequence 1449, Appl1
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24	80.0	80.0	9	US-10-149-138-3171	Sequence 3171, Appl1
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42	50.0	50.0	9	US-10-149-138-506	Sequence 506, Appl1
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45	50.0	50.0	10	US-10-149-138-2046	Sequence 2046, Appl1
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54	40.0	40.0	8	US-10-149-138-1246	Sequence 1246, Appl1
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56	40.0	40.0	8	US-10-654-601-1346	Sequence 1346, Appl1
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106	4	40.0	9	4	US-10-643-888-71	Sequence 71, App1	179	3	30.0	4	4	US-10-654-578-1953	Sequence 1953, App
107	4	40.0	9	4	US-10-643-888-72	Sequence 72, App1	180	3	30.0	4	4	US-10-759-379-25	Sequence 25, App1
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114	4	40.0	9	4	US-10-736-640-41	Sequence 41, App1	187	3	30.0	4	4	US-10-946-789-11	Sequence 11, App1
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130	4	40.0	10	4	US-10-283-722-487	Sequence 487, App							
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136	4	40.0	10	4	US-10-283-903-178	Sequence 178, App							
137	4	40.0	10	4	US-10-283-903-200	Sequence 200, App							
138	4	40.0	10	4	US-10-283-903-475	Sequence 475, App							
139	4	40.0	10	4	US-10-283-903-481	Sequence 481, App							
140	4	40.0	10	4	US-10-283-903-487	Sequence 487, App							
141	4	40.0	10	4	US-10-283-903-603	Sequence 603, App							
142	4	40.0	10	4	US-10-283-903-611	Sequence 611, App							
143	4	40.0	10	4	US-10-371-260-200	Sequence 200, App							
144	4	40.0	10	4	US-10-149-138-642	Sequence 642, App							
145	4	40.0	10	4	US-10-634-262-22	Sequence 22, App1							
146	4	40.0	10	4	US-10-149-138-642	Sequence 642, App							
147	4	40.0	10	4	US-10-654-601-699	Sequence 699, App							
148	4	40.0	10	5	US-10-654-601-2019	Sequence 2019, App							
149	4	40.0	10	5	US-10-654-601-2462	Sequence 2462, App							
150	4	40.0	10	5	US-10-654-601-2549	Sequence 2549, App							
151	3	30.0	3	2	US-09-820-306-66	Sequence 66, App1							
152	3	30.0	4	2	US-08-424-550B-538	Sequence 538, App							
153	3	30.0	4	3	US-09-778-885-11	Sequence 11, App1							
154	3	30.0	4	3	US-09-234-395-25	Sequence 25, App1							
155	3	30.0	4	3	US-09-234-395-26	Sequence 26, App1							
156	3	30.0	4	3	US-09-305-928-25	Sequence 25, App1							
157	3	30.0	4	3	US-09-305-928-26	Sequence 26, App1							
158	3	30.0	4	3	US-09-819-136-6	Sequence 6, App1							
159	3	30.0	4	3	US-09-264-516A-51	Sequence 51, App1							
160	3	30.0	4	3	US-09-264-516A-52	Sequence 52, App1							
161	3	30.0	4	3	US-10-021-963-7	Sequence 7, App1							
162	3	30.0	4	4	US-10-006-869-86	Sequence 86, App1							
163	3	30.0	4	4	US-10-006-869-87	Sequence 87, App1							
164	3	30.0	4	4	US-10-006-869-142	Sequence 142, App							
165	3	30.0	4	4	US-10-006-869-144	Sequence 144, App							
166	3	30.0	4	4	US-10-006-869-362	Sequence 362, App							
167	3	30.0	4	4	US-10-006-869-364	Sequence 364, App							
168	3	30.0	4	4	US-10-141-357-51	Sequence 51, App1							
169	3	30.0	4	4	US-10-141-357-52	Sequence 52, App1							
170	3	30.0	4	4	US-10-395-032-86	Sequence 86, App1							
171	3	30.0	4	4	US-10-395-032-87	Sequence 87, App1							
172	3	30.0	4	4	US-10-395-032-142	Sequence 142, App							
173	3	30.0	4	4	US-10-395-032-144	Sequence 144, App							

APPLICANT: Hand-Zimmerman, Susan
TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND THERAPY OF HEMATOLOGICAL
FILE REFERENCE: 210121.483C3
CURRENT APPLICATION NUMBER: US/10/313,644
CURRENT FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
US-10-313-644-3

Query Match
Best Local Similarity 100.0%; Score 9; DB 4; Length 9;
Pred. No. 0.00028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYLVPOQGF 10
Db 1 EYLVPOQGF 10

RESULT 3
US-10-245-871-607
Sequence 607, Application US/10245871
Publication No. US20030235594A1
GENERAL INFORMATION:
APPLICANT: HUMPHREYS, ROBERT
APPLICANT: XU, MINZHEN
TITLE OF INVENTION: II-KEY/ANTIGENIC EPI TOPE HYBRID PEPTIDE VACCINES
FILE REFERENCE: RH-2013
CURRENT APPLICATION NUMBER: US/10/245,871
CURRENT FILING DATE: 2003-01-09
PRIOR APPLICATION NUMBER: 10/197,000
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: 09/396,813
PRIOR FILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 905
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 607
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-10-245-871-607

Query Match
Best Local Similarity 100.0%; Score 9; DB 4; Length 9;
Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EYLVPOQGF 10
Db 1 EYLVPOQGF 9

RESULT 4
US-10-149-138-1138
Sequence 1138, Application US/10149138
Publication No. US20040018971A1
GENERAL INFORMATION:
APPLICANT: Fikes, John
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Esben
APPLICANT: Keogh, Elissa
TITLE OF INVENTION: Inducing Cellular Immune Responses to
TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.0140001
CURRENT APPLICATION NUMBER: US/10/149,138
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: PCT/US00/33591

PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: US 09/458,299
PRIOR FILING DATE: 1999-12-11
NUMBER OF SEQ ID NOS: 4641
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1138
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-1138

Query Match
Best Local Similarity 100.0%; Score 9; DB 4; Length 9;
Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EYLVPOQGF 10
Db 1 EYLVPOQGF 9

RESULT 5
US-10-149-138-3666
Sequence 3666, Application US/10149138
Publication No. US20040018971A1
GENERAL INFORMATION:
APPLICANT: Fikes, John
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Esben
APPLICANT: Keogh, Elissa
TITLE OF INVENTION: Inducing Cellular Immune Responses to
TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.0140001
CURRENT APPLICATION NUMBER: US/10/149,138
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: PCT/US00/33591
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: US 09/458,299
PRIOR FILING DATE: 1999-12-11
NUMBER OF SEQ ID NOS: 4641
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3666
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-3666

Query Match
Best Local Similarity 100.0%; Score 9; DB 4; Length 9;
Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EYLVPOQGF 10
Db 1 EYLVPOQGF 9

RESULT 6
US-10-253-286-607
Sequence 607, Application US/10253286
Publication No. US20040058881A1
GENERAL INFORMATION:
APPLICANT: HUMPHREYS, ROBERT
APPLICANT: XU, MINZHEN
TITLE OF INVENTION: II-KEY/ANTIGENIC EPI TOPE HYBRID PEPTIDE VACCINES
FILE REFERENCE: RH-2015
CURRENT APPLICATION NUMBER: US/10/253,286
CURRENT FILING DATE: 2003-01-13

;; PRIOR APPLICATION NUMBER: 10/197,000
;; PRIOR FILING DATE: 2002-07-17
;; PRIOR APPLICATION NUMBER: 09/396,813
;; PRIOR FILING DATE: 1999-09-14
;; NUMBER OF SEQ ID NOS: 905
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO: 607
;; LENGTH: 9
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-253-286-607

Query Match 90.0%; Score 9; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EYLVPOQGF 10
DB 1 EYLVPOQGF 9

RESULT 7
US-10-149-138-1138
;; Sequence 1138, Application US/10149138
;; Publication No. US20040121946A9
;; GENERAL INFORMATION:
;; APPLICANT: Fikes, John
;; APPLICANT: Sette, Alessandro
;; APPLICANT: Sidney, John
;; APPLICANT: Southwood, Scott
;; APPLICANT: Chesnut, Robert
;; APPLICANT: Cells, Eteban
;; APPLICANT: Keogh, Elissa
;; TITLE OF INVENTION: Inducing Cellular Immune Responses to
;; TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
;; FILE REFERENCE: 2060.0140001
;; CURRENT APPLICATION NUMBER: US/10/149,138
;; CURRENT FILING DATE: 2002-06-10
;; PRIOR APPLICATION NUMBER: PCT/US00/33591
;; PRIOR FILING DATE: 2000-12-11
;; PRIOR APPLICATION NUMBER: US 09/458,299
;; PRIOR FILING DATE: 1999-12-11
;; NUMBER OF SEQ ID NOS: 4641
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO: 1138
;; LENGTH: 9
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-1138

Query Match 90.0%; Score 9; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EYLVPOQGF 10
DB 1 EYLVPOQGF 9

RESULT 8
US-10-149-138-3666
;; Sequence 3666, Application US/10149138
;; Publication No. US20040121946A9
;; GENERAL INFORMATION:
;; APPLICANT: Fikes, John
;; APPLICANT: Sette, Alessandro
;; APPLICANT: Sidney, John
;; APPLICANT: Southwood, Scott
;; APPLICANT: Chesnut, Robert
;; APPLICANT: Cells, Eteban
;; APPLICANT: Keogh, Elissa

;; TITLE OF INVENTION: Inducing Cellular Immune Responses to
;; TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
;; FILE REFERENCE: 2060.0140001
;; CURRENT APPLICATION NUMBER: US/10/149,138
;; CURRENT FILING DATE: 2002-06-10
;; PRIOR APPLICATION NUMBER: PCT/US00/33591
;; PRIOR FILING DATE: 2000-12-11
;; PRIOR APPLICATION NUMBER: US 09/458,299
;; PRIOR FILING DATE: 1999-12-11
;; NUMBER OF SEQ ID NOS: 4641
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO: 3666
;; LENGTH: 9
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-3666

Query Match 90.0%; Score 9; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EYLVPOQGF 10
DB 1 EYLVPOQGF 9

RESULT 9
US-10-149-138-1139
;; Sequence 1139, Application US/10149138
;; Publication No. US20040018971A1
;; GENERAL INFORMATION:
;; APPLICANT: Fikes, John
;; APPLICANT: Sette, Alessandro
;; APPLICANT: Sidney, John
;; APPLICANT: Southwood, Scott
;; APPLICANT: Chesnut, Robert
;; APPLICANT: Cells, Eteban
;; APPLICANT: Keogh, Elissa
;; TITLE OF INVENTION: Inducing Cellular Immune Responses to
;; TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
;; FILE REFERENCE: 2060.0140001
;; CURRENT APPLICATION NUMBER: US/10/149,138
;; CURRENT FILING DATE: 2002-06-10
;; PRIOR APPLICATION NUMBER: PCT/US00/33591
;; PRIOR FILING DATE: 2000-12-11
;; PRIOR APPLICATION NUMBER: US 09/458,299
;; PRIOR FILING DATE: 1999-12-11
;; NUMBER OF SEQ ID NOS: 4641
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO: 1139
;; LENGTH: 10
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-1139

Query Match 90.0%; Score 9; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EYLVPOQGF 10
DB 1 EYLVPOQGF 9

RESULT 10
US-10-149-138-3667
;; Sequence 3667, Application US/10149138
;; Publication No. US20040018971A1
;; GENERAL INFORMATION:


```

/ APPLICANT: Fikes, John
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Cells, Esteban
/ APPLICANT: Keogh, Eliesa
/ TITLE OF INVENTION: Inducing Cellular Immune Responses to
/ TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0140001
/ CURRENT APPLICATION NUMBER: US/10/149,138
/ PRIOR FILING DATE: 2002-06-10
/ PRIOR APPLICATION NUMBER: PCT/US00/33591
/ PRIOR FILING DATE: 2000-12-11
/ PRIOR APPLICATION NUMBER: US 09/458,299
/ PRIOR FILING DATE: 1999-12-11
/ NUMBER OF SEQ ID NOS: 4641
/ SOFTWARE: Patent version 3.1
/ SEQ ID NO 3667
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-3667

Query Match          90.0%; Score 9; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EYLVPOQGF 10
Db 1 EYLVPOQGF 9

RESULT 11
US-10-149-138-1139
/ Sequence 1139, Application US/10149138
/ Publication No. US20040121946A9
/ GENERAL INFORMATION:
/ APPLICANT: Fikes, John
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Cells, Esteban
/ APPLICANT: Keogh, Eliesa
/ TITLE OF INVENTION: Inducing Cellular Immune Responses to
/ TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0140001
/ CURRENT APPLICATION NUMBER: US/10/149,138
/ CURRENT FILING DATE: 2002-06-10
/ PRIOR APPLICATION NUMBER: PCT/US00/33591
/ PRIOR FILING DATE: 2000-12-11
/ PRIOR APPLICATION NUMBER: US 09/458,299
/ PRIOR FILING DATE: 1999-12-11
/ NUMBER OF SEQ ID NOS: 4641
/ SOFTWARE: Patent version 3.1
/ SEQ ID NO 1139
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-1139

Query Match          90.0%; Score 9; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EYLVPOQGF 10
Db 1 EYLVPOQGF 9
```

```

RESULT 12
US-10-149-138-3667
/ Sequence 3667, Application US/10149138
/ Publication No. US20040121946A9
/ GENERAL INFORMATION:
/ APPLICANT: Fikes, John
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Cells, Esteban
/ APPLICANT: Keogh, Eliesa
/ TITLE OF INVENTION: Inducing Cellular Immune Responses to
/ TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0140001
/ CURRENT APPLICATION NUMBER: US/10/149,138
/ CURRENT FILING DATE: 2002-06-10
/ PRIOR APPLICATION NUMBER: PCT/US00/33591
/ PRIOR FILING DATE: 2000-12-11
/ PRIOR APPLICATION NUMBER: US 09/458,299
/ PRIOR FILING DATE: 1999-12-11
/ NUMBER OF SEQ ID NOS: 4641
/ SOFTWARE: Patent version 3.1
/ SEQ ID NO 3667
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-3667

Query Match          90.0%; Score 9; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EYLVPOQGF 10
Db 1 EYLVPOQGF 9

RESULT 13
US-10-149-138-15
/ Sequence 15, Application US/10149138
/ Publication No. US20040018971A1
/ GENERAL INFORMATION:
/ APPLICANT: Fikes, John
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Cells, Esteban
/ APPLICANT: Keogh, Eliesa
/ TITLE OF INVENTION: Inducing Cellular Immune Responses to
/ TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0140001
/ CURRENT APPLICATION NUMBER: US/10/149,138
/ CURRENT FILING DATE: 2002-06-10
/ PRIOR APPLICATION NUMBER: PCT/US00/33591
/ PRIOR FILING DATE: 2000-12-11
/ PRIOR APPLICATION NUMBER: US 09/458,299
/ PRIOR FILING DATE: 1999-12-11
/ NUMBER OF SEQ ID NOS: 4641
/ SOFTWARE: Patent version 3.1
/ SEQ ID NO 15
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-15
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Query Match 80.0%; Score 8; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLVPQGGF 10
|||
Db 1 YLVPQGGF 8

RESULT 14
US-10-149-138-1449
; Sequence 1449, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:

; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1449
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-1449

Query Match 80.0%; Score 8; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLVPQGGF 10
|||
Db 1 YLVPQGGF 8

RESULT 15
US-10-149-138-2377
; Sequence 2377, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:

; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2377

; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-2377

Query Match 80.0%; Score 8; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLVPQGGF 10
|||
Db 1 YLVPQGGF 8

RESULT 16
US-10-149-138-3170
; Sequence 3170, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:

; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3170
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-3170

Query Match 80.0%; Score 8; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLVPQGGF 10
|||
Db 1 YLVPQGGF 8

RESULT 17
US-10-149-138-15
; Sequence 15, Application US/10149138
; Publication No. US20040121946A9
; GENERAL INFORMATION:

; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; PRIOR FILING DATE: 2002-06-10

PRIOR APPLICATION NUMBER: PCT/US00/33591
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: US 09/458,299
PRIOR FILING DATE: 1999-12-11
NUMBER OF SEQ ID NOS: 4641
SOFTWARE: PatentIn version 3.1
SEQ ID NO 15
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-15

Query Match 80.0%; Score 8; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLVPOQGF 10
Db 1 YLVPOQGF 8

RESULT 18
US-10-149-138-1449
Sequence 1449, Application US/10149138
Publication No. US20040121946A9
GENERAL INFORMATION:
APPLICANT: Fikes, John
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Chesnut, Robert
APPLICANT: Cellis, Esteban
APPLICANT: Keogh, Elissa
TITLE OF INVENTION: Inducing Cellular Immune Responses to
TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.0140001
CURRENT FILING DATE: 2002-06-10
CURRENT APPLICATION NUMBER: US/10/149,138
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: PCT/US00/33591
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: US 09/458,299
PRIOR FILING DATE: 1999-12-11
NUMBER OF SEQ ID NOS: 4641
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1449
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-1449

Query Match 80.0%; Score 8; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLVPOQGF 10
Db 1 YLVPOQGF 8

RESULT 19
US-10-149-138-2377
Sequence 2377, Application US/10149138
Publication No. US20040121946A9
GENERAL INFORMATION:
APPLICANT: Fikes, John
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Chesnut, Robert

US-10-149-138-45
Sequence 45, Application US/10149138

APPLICANT: Cellis, Esteban
APPLICANT: Keogh, Elissa
TITLE OF INVENTION: Inducing Cellular Immune Responses to
TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.0140001
CURRENT FILING DATE: 2002-06-10
CURRENT APPLICATION NUMBER: PCT/US00/33591
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: US 09/458,299
PRIOR FILING DATE: 1999-12-11
NUMBER OF SEQ ID NOS: 4641
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2377
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-2377

Query Match 80.0%; Score 8; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLVPOQGF 10
Db 1 YLVPOQGF 8

RESULT 20
US-10-149-138-3170
Sequence 3170, Application US/10149138
Publication No. US20040121946A9
GENERAL INFORMATION:
APPLICANT: Fikes, John
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Chesnut, Robert
APPLICANT: Cellis, Esteban
APPLICANT: Keogh, Elissa
TITLE OF INVENTION: Inducing Cellular Immune Responses to
TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.0140001
CURRENT FILING DATE: 2002-06-10
CURRENT APPLICATION NUMBER: US/10/149,138
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: PCT/US00/33591
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: US 09/458,299
PRIOR FILING DATE: 1999-12-11
NUMBER OF SEQ ID NOS: 4641
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3170
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-3170

Query Match 80.0%; Score 8; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLVPOQGF 10
Db 1 YLVPOQGF 8

RESULT 21
US-10-149-138-45
Sequence 45, Application US/10149138

```
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-45
```

```
Query Match      80.0%; Score 8; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      3 YLVPOQGF 10
        |||||
Db      1 YLVPOQGF 8

RESULT 22
US-10-149-138-1450
; Sequence 1450, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1450
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-1450
```

```
Query Match      80.0%; Score 8; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
,Oy      3 YLVPOQGF 10
```

```
Db      1 YLVPOQGF 8
        |||||
```

```
RESULT 23
US-10-149-138-2378
; Sequence 2378, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2378
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-2378
```

```
Query Match      80.0%; Score 8; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      3 YLVPOQGF 10
        |||||
Db      1 YLVPOQGF 8
```

```
RESULT 24
US-10-149-138-3171
; Sequence 3171, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3171
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptide
```

```
,Oy      3 YLVPOQGF 10
```

US-10-149-138-3171

Query Match 80.0%; Score 8; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLVPOQGF 10
DB 1 YLVPOQGF 8

RESULT 25

US-10-149-138-45
Sequence 45, Application US/10149138
Publication No. US20040121946A9
GENERAL INFORMATION:
APPLICANT: Fikes, John
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Bsteban
APPLICANT: Keogh, Elissa
TITLE OF INVENTION: Inducing Cellular Immune Responses to
TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.0140001
CURRENT APPLICATION NUMBER: US/10/149,138
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: PCT/US00/33591
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: US 09/458,299
PRIOR FILING DATE: 1999-12-11
NUMBER OF SEQ ID NOS: 4641
SOFTWARE: PatentIn version 3.1
SEQ ID NO 45
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-45

Query Match 80.0%; Score 8; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLVPOQGF 10
DB 1 YLVPOQGF 8

RESULT 26

US-10-149-138-1450
Sequence 1450, Application US/10149138
Publication No. US20040121946A9
GENERAL INFORMATION:
APPLICANT: Fikes, John
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Bsteban
APPLICANT: Keogh, Elissa
TITLE OF INVENTION: Inducing Cellular Immune Responses to
TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.0140001
CURRENT APPLICATION NUMBER: US/10/149,138
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: PCT/US00/33591
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: US 09/458,299
PRIOR FILING DATE: 1999-12-11
NUMBER OF SEQ ID NOS: 4641

SOFTWARE: PatentIn version 3.1
SEQ ID NO 1450
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-1450

Query Match 80.0%; Score 8; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLVPOQGF 10
DB 1 YLVPOQGF 8

RESULT 27

US-10-149-138-2378
Sequence 2378, Application US/10149138
Publication No. US20040121946A9
GENERAL INFORMATION:
APPLICANT: Fikes, John
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Bsteban
APPLICANT: Keogh, Elissa
TITLE OF INVENTION: Inducing Cellular Immune Responses to
TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.0140001
CURRENT APPLICATION NUMBER: US/10/149,138
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: PCT/US00/33591
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: US 09/458,299
PRIOR FILING DATE: 1999-12-11
NUMBER OF SEQ ID NOS: 4641
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2378
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-2378

Query Match 80.0%; Score 8; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLVPOQGF 10
DB 1 YLVPOQGF 8

RESULT 28

US-10-149-138-3171
Sequence 3171, Application US/10149138
Publication No. US20040121946A9
GENERAL INFORMATION:
APPLICANT: Fikes, John
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Bsteban
APPLICANT: Keogh, Elissa
TITLE OF INVENTION: Inducing Cellular Immune Responses to
TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.0140001

```
/ CURRENT APPLICATION NUMBER: US/10/149,138
/ CURRENT FILING DATE: 2002-06-10
/ PRIOR APPLICATION NUMBER: PCT/US00/33591
/ PRIOR FILING DATE: 2000-12-11
/ PRIOR APPLICATION NUMBER: US 09/458,299
/ PRIOR FILING DATE: 1999-12-11
/ NUMBER OF SEQ ID NOS: 4641
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO: 3171
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-3171

Query Match      80.0%; Score 8; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 YLVPOQGF 10
DB      1 YLVPOQGF 8

RESULT 29
US-10-333-430-64
/ Sequence 64, Application US/10/333430
/ Publication No. US20040072240A1
/ GENERAL INFORMATION:
/ APPLICANT: INSERM
/ APPLICANT: INSTITUT GUSTAVE ROUSSY
/ APPLICANT: KOSMOTOPOULOS, Kostae
/ APPLICANT: TOUPDOT, Sophie
/ APPLICANT: SCARDINO, Antonio
/ APPLICANT: GROSS, David, Alexandre
/ TITLE OF INVENTION: METHOD FOR SCREENING PEPTIDES FOR USE IN
/ FILE REFERENCE: 33339/259034
/ CURRENT APPLICATION NUMBER: US/10/333,430
/ CURRENT FILING DATE: 2003-10-02
/ PRIOR APPLICATION NUMBER: FR 0009591
/ PRIOR FILING DATE: 2000-07-21
/ NUMBER OF SEQ ID NOS: 70
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO: 64
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic peptide
US-10-333-430-64

Query Match      80.0%; Score 8; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 YLVPOQGF 10
DB      1 YLVPOQGF 8

RESULT 30
US-10-149-138-25
/ Sequence 25, Application US/10/149138
/ Publication No. US20040018971A1
/ GENERAL INFORMATION:
/ APPLICANT: Fikes, John
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Cells, Esteban
```

```
/ APPLICANT: Keogh, Elissa
/ TITLE OF INVENTION: Inducing Cellular Immune Responses to
/ FILE REFERENCE: 2060.0140001
/ CURRENT APPLICATION NUMBER: US/10/149,138
/ CURRENT FILING DATE: 2002-06-10
/ PRIOR APPLICATION NUMBER: PCT/US00/33591
/ PRIOR FILING DATE: 2000-12-11
/ PRIOR APPLICATION NUMBER: US 09/458,299
/ PRIOR FILING DATE: 1999-12-11
/ NUMBER OF SEQ ID NOS: 4641
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO: 25
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-25

Query Match      70.0%; Score 7; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 LVPQQGF 10
DB      1 LVPQQGF 7

RESULT 31
US-10-149-138-1249
/ Sequence 1249, Application US/10/149138
/ Publication No. US20040018971A1
/ GENERAL INFORMATION:
/ APPLICANT: Fikes, John
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Cells, Esteban
/ APPLICANT: Keogh, Elissa
/ TITLE OF INVENTION: Inducing Cellular Immune Responses to
/ FILE REFERENCE: 2060.0140001
/ CURRENT APPLICATION NUMBER: US/10/149,138
/ CURRENT FILING DATE: 2002-06-10
/ PRIOR APPLICATION NUMBER: PCT/US00/33591
/ PRIOR FILING DATE: 2000-12-11
/ PRIOR APPLICATION NUMBER: US 09/458,299
/ PRIOR FILING DATE: 1999-12-11
/ NUMBER OF SEQ ID NOS: 4641
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO: 1249
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-1249

Query Match      70.0%; Score 7; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 LVPQQGF 10
DB      1 LVPQQGF 7

RESULT 32
US-10-149-138-2188
/ Sequence 2188, Application US/10/149138
/ Publication No. US20040018971A1
```

```
/ GENERAL INFORMATION:
/ APPLICANT: Pike, John
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Celis, Eteban
/ APPLICANT: Keogh, Elissa
/ TITLE OF INVENTION: Inducing Cellular Immune Responses to
/ FILE REFERENCE: 2060.0140001
/ CURRENT APPLICATION NUMBER: US/10/149,138
/ PRIOR FILING DATE: 2002-06-10
/ PRIOR APPLICATION NUMBER: PCT/US00/33591
/ PRIOR FILING DATE: 2000-12-11
/ PRIOR APPLICATION NUMBER: US 09/458,299
/ PRIOR FILING DATE: 1999-12-11
/ NUMBER OF SEQ ID NOS: 4641
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 2188
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-2188
```

```
Query Match          70.0%; Score 7; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 4 LVPOQGF 10
    |||||
Db 1 LVPOQGF 7
```

```
RESULT 33
US-10-149-138-2859
/ Sequence 2859, Application US/10149138
/ Publication No. US20040018971A1
/ GENERAL INFORMATION:
/ APPLICANT: Pike, John
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Celis, Eteban
/ APPLICANT: Keogh, Elissa
/ TITLE OF INVENTION: Inducing Cellular Immune Responses to
/ FILE REFERENCE: 2060.0140001
/ CURRENT APPLICATION NUMBER: US/10/149,138
/ PRIOR FILING DATE: 2002-06-10
/ PRIOR APPLICATION NUMBER: PCT/US00/33591
/ PRIOR FILING DATE: 2000-12-11
/ PRIOR APPLICATION NUMBER: US 09/458,299
/ PRIOR FILING DATE: 1999-12-11
/ NUMBER OF SEQ ID NOS: 4641
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 2859
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-2859
```

```
Query Match          70.0%; Score 7; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 4 LVPOQGF 10
    |||||
```

```
Db 1 LVPOQGF 7

RESULT 34
US-10-149-138-25
/ Sequence 25, Application US/10149138
/ Publication No. US20040121946A9
/ GENERAL INFORMATION:
/ APPLICANT: Pike, John
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Celis, Eteban
/ APPLICANT: Keogh, Elissa
/ TITLE OF INVENTION: Inducing Cellular Immune Responses to
/ FILE REFERENCE: 2060.0140001
/ CURRENT APPLICATION NUMBER: US/10/149,138
/ PRIOR FILING DATE: 2002-06-10
/ PRIOR APPLICATION NUMBER: PCT/US00/33591
/ PRIOR FILING DATE: 2000-12-11
/ PRIOR APPLICATION NUMBER: US 09/458,299
/ PRIOR FILING DATE: 1999-12-11
/ NUMBER OF SEQ ID NOS: 4641
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 25
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-25
```

```
Query Match          70.0%; Score 7; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 4 LVPOQGF 10
    |||||
Db 1 LVPOQGF 7
```

```
RESULT 35
US-10-149-138-1249
/ Sequence 1249, Application US/10149138
/ Publication No. US20040121946A9
/ GENERAL INFORMATION:
/ APPLICANT: Pike, John
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Celis, Eteban
/ APPLICANT: Keogh, Elissa
/ TITLE OF INVENTION: Inducing Cellular Immune Responses to
/ FILE REFERENCE: 2060.0140001
/ CURRENT APPLICATION NUMBER: US/10/149,138
/ PRIOR FILING DATE: 2002-06-10
/ PRIOR APPLICATION NUMBER: PCT/US00/33591
/ PRIOR FILING DATE: 2000-12-11
/ PRIOR APPLICATION NUMBER: US 09/458,299
/ PRIOR FILING DATE: 1999-12-11
/ NUMBER OF SEQ ID NOS: 4641
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 1249
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-1249
```

Query Match 70.0%; Score 7; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LVPOQGF 10
|||||
DB 1 LVPOQGF 7

RESULT 36
US-10-149-138-2188
; Sequence 2188, Application US/10149138
; Publication No. US20040121946A9
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Keogh, Elisea
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2188
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-2188

Query Match 70.0%; Score 7; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LVPOQGF 10
|||||
DB 1 LVPOQGF 7

RESULT 37
US-10-149-138-2859
; Sequence 2859, Application US/10149138
; Publication No. US20040121946A9
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Keogh, Elisea
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 2859
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-2859

Query Match 70.0%; Score 7; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LVPOQGF 10
|||||
DB 1 LVPOQGF 7

RESULT 38
US-10-149-138-4152
; Sequence 4152, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Keogh, Elisea
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4152
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-4152

Query Match 60.0%; Score 6; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 BEYLVP 6
|||||
DB 4 BEYLVP 9

RESULT 39
US-10-149-138-4152
; Sequence 4152, Application US/10149138
; Publication No. US20040121946A9
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Keogh, Elisea
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138


```
/ CURRENT FILING DATE: 2002-06-10
/ PRIOR APPLICATION NUMBER: PCT/US00/33591
/ PRIOR FILING DATE: 2000-12-11
/ PRIOR APPLICATION NUMBER: US 09/458,299
/ PRIOR FILING DATE: 1999-12-11
/ NUMBER OF SEQ ID NOS: 4641
/ SOFTWARE: Patent version 3.1
/ SEQ ID NO 4152
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-4152

Query Match
Best Local Similarity 100.0%; Score 6; DB 4; Length 9;
Pred. No. 1.7e+06; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0;

QY 1 EBYLV 6
DB 4 EBYLV 9

RESULT 40
US-10-149-138-506
/ Sequence 506, Application US/10149138
/ Publication No. US20040018971A1
/ GENERAL INFORMATION:
/ APPLICANT: Fikes, John
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Celis, Steban
/ APPLICANT: Keogh, Elissa
/ TITLE OF INVENTION: Inducing Cellular Immune Responses to
/ TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0140001
/ CURRENT APPLICATION NUMBER: US/10/149,138
/ CURRENT FILING DATE: 2002-06-10
/ PRIOR APPLICATION NUMBER: PCT/US00/33591
/ PRIOR FILING DATE: 2000-12-11
/ PRIOR APPLICATION NUMBER: US 09/458,299
/ PRIOR FILING DATE: 1999-12-11
/ NUMBER OF SEQ ID NOS: 4641
/ SOFTWARE: Patent version 3.1
/ SEQ ID NO 506
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-506

Query Match
Best Local Similarity 100.0%; Score 5; DB 4; Length 9;
Pred. No. 1.7e+06; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0;

QY 1 EBYLV 5
DB 5 EBYLV 9

RESULT 41
US-10-149-138-2183
/ Sequence 2183, Application US/10149138
/ Publication No. US20040018971A1
/ GENERAL INFORMATION:
/ APPLICANT: Fikes, John
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
```

```
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Celis, Steban
/ APPLICANT: Keogh, Elissa
/ TITLE OF INVENTION: Inducing Cellular Immune Responses to
/ TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0140001
/ CURRENT APPLICATION NUMBER: US/10/149,138
/ CURRENT FILING DATE: 2002-06-10
/ PRIOR APPLICATION NUMBER: PCT/US00/33591
/ PRIOR FILING DATE: 2000-12-11
/ PRIOR APPLICATION NUMBER: US 09/458,299
/ PRIOR FILING DATE: 1999-12-11
/ NUMBER OF SEQ ID NOS: 4641
/ SOFTWARE: Patent version 3.1
/ SEQ ID NO 2183
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-2183

Query Match
Best Local Similarity 100.0%; Score 5; DB 4; Length 9;
Pred. No. 1.7e+06; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0;

QY 1 EBYLV 5
DB 5 EBYLV 9

RESULT 42
US-10-149-138-506
/ Sequence 506, Application US/10149138
/ Publication No. US20040121946A3
/ GENERAL INFORMATION:
/ APPLICANT: Fikes, John
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Celis, Steban
/ APPLICANT: Keogh, Elissa
/ TITLE OF INVENTION: Inducing Cellular Immune Responses to
/ TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0140001
/ CURRENT APPLICATION NUMBER: US/10/149,138
/ CURRENT FILING DATE: 2002-06-10
/ PRIOR APPLICATION NUMBER: PCT/US00/33591
/ PRIOR FILING DATE: 2000-12-11
/ PRIOR APPLICATION NUMBER: US 09/458,299
/ PRIOR FILING DATE: 1999-12-11
/ NUMBER OF SEQ ID NOS: 4641
/ SOFTWARE: Patent version 3.1
/ SEQ ID NO 506
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-506

Query Match
Best Local Similarity 100.0%; Score 5; DB 4; Length 9;
Pred. No. 1.7e+06; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0;

QY 1 EBYLV 5
DB 5 EBYLV 9

RESULT 43
US-10-149-138-2183
```

```
/ Sequence 2183, Application US/10149138
/ Publication No. US20040121946A9
/ GENERAL INFORMATION:
/ APPLICANT: Fikes, John
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Cells, Esteban
/ APPLICANT: Keogh, Elissa
/ TITLE OF INVENTION: Inducing Cellular Immune Responses to
/ TITLE OF INVENTION: HER2/new Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0140001
/ CURRENT APPLICATION NUMBER: US/10/149,138
/ PRIOR FILING DATE: 2002-06-10
/ PRIOR APPLICATION NUMBER: PCT/US00/33591
/ PRIOR FILING DATE: 2000-12-11
/ PRIOR APPLICATION NUMBER: US 09/458,299
/ PRIOR FILING DATE: 1999-12-11
/ NUMBER OF SEQ ID NOS: 4641
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO: 2183
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-2183
```

```
Query Match 50.0%; Score 5; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 EBYLV 5
Db 5 EBYLV 9
```

```
RESULT 44
US-10-149-138-220
/ Sequence 220, Application US/10149138
/ Publication No. US20040018971A1
/ GENERAL INFORMATION:
/ APPLICANT: Fikes, John
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Cells, Esteban
/ APPLICANT: Keogh, Elissa
/ TITLE OF INVENTION: Inducing Cellular Immune Responses to
/ TITLE OF INVENTION: HER2/new Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0140001
/ CURRENT APPLICATION NUMBER: US/10/149,138
/ PRIOR FILING DATE: 2002-06-10
/ PRIOR APPLICATION NUMBER: PCT/US00/33591
/ PRIOR FILING DATE: 2000-12-11
/ PRIOR APPLICATION NUMBER: US 09/458,299
/ PRIOR FILING DATE: 1999-12-11
/ NUMBER OF SEQ ID NOS: 4641
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO: 220
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-220
```

```
Query Match 50.0%; Score 5; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 EBYLV 5
Db 6 EBYLV 10
```

```
RESULT 45
US-10-149-138-2046
/ Sequence 2046, Application US/10149138
/ Publication No. US20040018971A1
/ GENERAL INFORMATION:
/ APPLICANT: Fikes, John
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Cells, Esteban
/ APPLICANT: Keogh, Elissa
/ TITLE OF INVENTION: Inducing Cellular Immune Responses to
/ TITLE OF INVENTION: HER2/new Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0140001
/ CURRENT APPLICATION NUMBER: US/10/149,138
/ PRIOR FILING DATE: 2002-06-10
/ PRIOR APPLICATION NUMBER: PCT/US00/33591
/ PRIOR FILING DATE: 2000-12-11
/ PRIOR APPLICATION NUMBER: US 09/458,299
/ PRIOR FILING DATE: 1999-12-11
/ NUMBER OF SEQ ID NOS: 4641
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO: 2046
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-2046
```

```
Query Match 50.0%; Score 5; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 EBYLV 5
Db 6 EBYLV 10
```

```
RESULT 46
US-10-149-138-220
/ Sequence 220, Application US/10149138
/ Publication No. US20040121946A9
/ GENERAL INFORMATION:
/ APPLICANT: Fikes, John
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Cells, Esteban
/ APPLICANT: Keogh, Elissa
/ TITLE OF INVENTION: Inducing Cellular Immune Responses to
/ TITLE OF INVENTION: HER2/new Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0140001
/ CURRENT APPLICATION NUMBER: US/10/149,138
/ PRIOR FILING DATE: 2002-06-10
/ PRIOR APPLICATION NUMBER: PCT/US00/33591
/ PRIOR FILING DATE: 2000-12-11
/ PRIOR APPLICATION NUMBER: US 09/458,299
/ PRIOR FILING DATE: 1999-12-11
/ NUMBER OF SEQ ID NOS: 4641
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO: 220
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
```

OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-220

Query Match 50.0%; Score 5; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYLV 5
| | | | |
Db 6 EBYLV 10

RESULT 47
US-10-149-138-2046

Sequence 2046, Application US/10149138
Publication No. US20040121946A9
GENERAL INFORMATION:
APPLICANT: Fikes, John
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Belderb
APPLICANT: Keogh, Elissa
TITLE OF INVENTION: Inducing Cellular Immune Responses to
TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.0140001
CURRENT APPLICATION NUMBER: US/10/149,138
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: PCT/US00/33591
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: US 09/458,299
PRIOR FILING DATE: 1999-12-11
NUMBER OF SEQ ID NOS: 4641
SOFTWARE: Patentin version 3.1
SEQ ID NO 2046
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-2046

Query Match 50.0%; Score 5; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYLV 5
| | | | |
Db 6 EBYLV 10

RESULT 48
US-09-912-733-4

Sequence 4, Application US/09912733
Publication No. US20030092131A1
GENERAL INFORMATION:
APPLICANT: Ward, Michael
APPLICANT: Power, Scott D.
TITLE OF INVENTION: DNA SEQUENCES, VECTORS, AND FUSION POLYPEPTIDES FOR SECRETION OF
TITLE OF INVENTION: POLYPEPTIDES IN FILAMENTOUS FUNGI
FILE REFERENCE: A-62926-1
CURRENT APPLICATION NUMBER: US/09/912,733
CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 08/785,668
PRIOR FILING DATE: 1997-01-17
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
LENGTH: 5
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Synthetic.
US-09-912-733-4

Query Match 40.0%; Score 4; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYL 4
| | | |
Db 2 EBYL 5

RESULT 49
US-10-209-323-4

Sequence 4, Application US/10209323
Publication No. US20030119070A1
GENERAL INFORMATION:
APPLICANT: Schaeffer, Andrew T.
APPLICANT: Tseng-Law, Janet
APPLICANT: Thornton, Jeffrey R.
APPLICANT: Van Bpps, Dennis R.
TITLE OF INVENTION: Reagents for Cell Selection and Methods
TITLE OF INVENTION: of Use
FILE REFERENCE: P-N74360
CURRENT APPLICATION NUMBER: US/10/209,323
CURRENT FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: US/09/659,469A
PRIOR FILING DATE: 2000-09-11
PRIOR APPLICATION NUMBER: US 09/578,784
PRIOR FILING DATE: 2000-05-23
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic peptide
US-10-209-323-4

Query Match 40.0%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 QOGF 10
| | | | |
Db 1 QOGF 4

RESULT 50
US-10-256-277-4

Sequence 4, Application US/10256277
Publication No. US20030219445A1
GENERAL INFORMATION:
APPLICANT: Schaeffer, Andrew T.
APPLICANT: Tseng-Law, Janet
APPLICANT: Thornton, Jeffrey R.
TITLE OF INVENTION: Reagents for Cell Selection and Methods
TITLE OF INVENTION: of Use
FILE REFERENCE: P-NT 3773
CURRENT APPLICATION NUMBER: US/10/256,277
CURRENT FILING DATE: 2002-09-25
PRIOR APPLICATION NUMBER: US/09/578,784
PRIOR FILING DATE: 2000-05-23
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic peptide
US-10-256-277-4

Query Match 40.0%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 QGGF 10
|||
Db 1 QGGF 4

Search completed: January 18, 2006, 21:17:06
Job time : 113 secs

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OM protein - protein search, using SW model

Run on: January 18, 2006, 21:00:09 ; Search time 44 Seconds
(without alignments)
18.790 Million cell updates/sec

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Title: US-09-930-125-3
Perfect score: 10
Sequence: 1 EBYLVPPQGF 10

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Scoring table: U180 Gapop 60.0 , Gapext 60.0

Searched: 572060 seqs, 82675679 residues

Word size : 0

Total number of hits satisfying chosen parameters: 130918

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Minimum DB seq length: 0
Maximum DB seq length: 10
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Post-processing: Listing first 200 summaries

Database : Issued_Patents_AA:*

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4: /cgn2_6/ptodataa/1/1aa/PCTUS_COMB.pcp.*
5: /cgn2_6/ptodataa/1/1aa/RE_COMB.pcp.*
6: /cgn2_6/ptodataa/1/1aa/backfiles.pcp.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID                 | Description        |
|------------|-------|-------------|--------|----|--------------------|--------------------|
| 1          | 5     | 50.0        | 6      | 4  | PCT-US93-01669-28  | Sequence 28, App1  |
| 2          | 5     | 50.0        | 9      | 4  | PCT-US93-01669-56  | Sequence 56, App1  |
| 3          | 4     | 40.0        | 5      | 2  | US-08-785-668-4    | Sequence 4, App1   |
| 4          | 4     | 40.0        | 5      | 2  | US-09-912-733-4    | Sequence 4, App1   |
| 5          | 4     | 40.0        | 6      | 2  | US-03-581-944A-25  | Sequence 25, App1  |
| 6          | 4     | 40.0        | 7      | 2  | US-09-147-933-19   | Sequence 19, App1  |
| 7          | 4     | 40.0        | 7      | 2  | US-09-581-944A-20  | Sequence 20, App1  |
| 8          | 4     | 40.0        | 7      | 6  | 5422249-15         | Patent No. 5422249 |
| 9          | 4     | 40.0        | 8      | 1  | US-08-037-574A-7   | Sequence 7, App1   |
| 10         | 4     | 40.0        | 8      | 1  | US-08-037-574A-9   | Sequence 9, App1   |
| 11         | 4     | 40.0        | 8      | 1  | US-08-037-574A-13  | Sequence 13, App1  |
| 12         | 4     | 40.0        | 8      | 1  | US-08-037-574A-17  | Sequence 17, App1  |
| 13         | 4     | 40.0        | 8      | 1  | US-08-037-574A-79  | Sequence 79, App1  |
| 14         | 4     | 40.0        | 8      | 1  | US-08-037-574A-81  | Sequence 81, App1  |
| 15         | 4     | 40.0        | 8      | 1  | US-08-037-574A-83  | Sequence 83, App1  |
| 16         | 4     | 40.0        | 8      | 1  | US-08-037-574A-100 | Sequence 100, App1 |
| 17         | 4     | 40.0        | 8      | 1  | US-08-037-574A-106 | Sequence 106, App1 |
| 18         | 4     | 40.0        | 8      | 1  | US-08-037-574A-114 | Sequence 114, App1 |
| 19         | 4     | 40.0        | 8      | 1  | US-08-037-574A-118 | Sequence 118, App1 |
| 20         | 4     | 40.0        | 8      | 1  | US-08-037-574A-151 | Sequence 151, App1 |
| 21         | 4     | 40.0        | 8      | 1  | US-08-037-574A-157 | Sequence 157, App1 |
| 22         | 4     | 40.0        | 8      | 1  | US-08-037-574A-163 | Sequence 163, App1 |
| 23         | 4     | 40.0        | 8      | 1  | US-08-218-329-7    | Sequence 7, App1   |
| 24         | 4     | 40.0        | 8      | 1  | US-08-218-329-9    | Sequence 9, App1   |
| 25         | 4     | 40.0        | 8      | 1  | US-08-218-329-13   | Sequence 13, App1  |
| 26         | 4     | 40.0        | 8      | 1  | US-08-218-329-17   | Sequence 17, App1  |
| 27         | 4     | 40.0        | 8      | 1  | US-08-218-329-79   | Sequence 79, App1  |

|     |   |      |    |           |                     |                     |
|-----|---|------|----|-----------|---------------------|---------------------|
| 28  | 4 | 40.0 | 8  | 1         | US-08-218-329-81    | Sequence 81, Appl   |
| 29  | 4 | 40.0 | 8  | 1         | US-08-218-329-83    | Sequence 83, Appl   |
| 30  | 4 | 40.0 | 8  | 1         | US-08-218-329-98    | Sequence 99, Appl   |
| 31  | 4 | 40.0 | 8  | 1         | US-08-218-329-105   | Sequence 105, Appl  |
| 32  | 4 | 40.0 | 8  | 1         | US-08-218-329-113   | Sequence 111, Appl  |
| 33  | 4 | 40.0 | 8  | 1         | US-08-218-329-117   | Sequence 117, Appl  |
| 34  | 4 | 40.0 | 8  | 1         | US-08-218-329-150   | Sequence 150, Appl  |
| 35  | 4 | 40.0 | 8  | 1         | US-08-218-329-156   | Sequence 156, Appl  |
| 36  | 4 | 40.0 | 8  | 1         | US-08-218-329-162   | Sequence 162, Appl  |
| 37  | 4 | 40.0 | 8  | 1         | US-08-482-228-137   | Sequence 137, Appl  |
| 38  | 4 | 40.0 | 8  | 2         | US-08-482-528-137   | Sequence 137, Appl  |
| 39  | 4 | 40.0 | 8  | 2         | US-09-239-043D-198  | Sequence 198, Appl  |
| 40  | 4 | 40.0 | 8  | 2         | US-09-239-043D-1346 | Sequence 1346, Appl |
| 41  | 4 | 40.0 | 6  | 5196404-2 | Patent No. 5196404  |                     |
| 42  | 4 | 40.0 | 9  | 1         | US-08-467-083-23    | Sequence 23, Appl   |
| 43  | 4 | 40.0 | 9  | 1         | US-08-414-41B-23    | Sequence 23, Appl   |
| 44  | 4 | 40.0 | 9  | 1         | US-08-486-348A-23   | Sequence 23, Appl   |
| 45  | 4 | 40.0 | 9  | 1         | US-08-466-545B-23   | Sequence 23, Appl   |
| 46  | 4 | 40.0 | 9  | 2         | US-08-466-680B-23   | Sequence 23, Appl   |
| 47  | 4 | 40.0 | 9  | 2         | US-09-692-170C-40   | Sequence 40, Appl   |
| 48  | 4 | 40.0 | 9  | 2         | US-09-692-170C-41   | Sequence 41, Appl   |
| 49  | 4 | 40.0 | 9  | 2         | US-09-692-325-37    | Sequence 37, Appl   |
| 50  | 4 | 40.0 | 9  | 2         | US-09-692-325-38    | Sequence 38, Appl   |
| 51  | 4 | 40.0 | 9  | 2         | US-09-692-325-59    | Sequence 59, Appl   |
| 52  | 4 | 40.0 | 9  | 2         | US-09-692-325-60    | Sequence 60, Appl   |
| 53  | 4 | 40.0 | 9  | 2         | US-09-692-325-61    | Sequence 61, Appl   |
| 54  | 4 | 40.0 | 9  | 2         | US-09-692-325-62    | Sequence 62, Appl   |
| 55  | 4 | 40.0 | 9  | 2         | US-09-692-325-63    | Sequence 63, Appl   |
| 56  | 4 | 40.0 | 9  | 2         | US-09-692-325-64    | Sequence 64, Appl   |
| 57  | 4 | 40.0 | 9  | 2         | US-09-692-325-69    | Sequence 69, Appl   |
| 58  | 4 | 40.0 | 9  | 2         | US-09-692-325-70    | Sequence 70, Appl   |
| 59  | 4 | 40.0 | 9  | 2         | US-09-692-325-71    | Sequence 71, Appl   |
| 60  | 4 | 40.0 | 9  | 2         | US-09-692-325-72    | Sequence 72, Appl   |
| 61  | 4 | 40.0 | 9  | 2         | US-09-354-533-23    | Sequence 23, Appl   |
| 62  | 4 | 40.0 | 9  | 2         | US-09-239-043D-698  | Sequence 698, Appl  |
| 63  | 4 | 40.0 | 9  | 2         | US-09-239-043D-1313 | Sequence 1313, Appl |
| 64  | 4 | 40.0 | 9  | 2         | US-09-239-043D-2018 | Sequence 2018, Appl |
| 65  | 4 | 40.0 | 9  | 2         | US-10-405-231A-40   | Sequence 40, Appl   |
| 66  | 4 | 40.0 | 9  | 2         | US-10-405-231A-41   | Sequence 41, Appl   |
| 67  | 4 | 40.0 | 9  | 2         | US-10-238-607-40    | Sequence 40, Appl   |
| 68  | 4 | 40.0 | 9  | 2         | US-10-238-607-41    | Sequence 41, Appl   |
| 69  | 4 | 40.0 | 9  | 2         | US-09-984-365-40    | Sequence 40, Appl   |
| 70  | 4 | 40.0 | 9  | 2         | US-09-984-365-41    | Sequence 41, Appl   |
| 71  | 4 | 40.0 | 9  | 2         | US-10-697-055-40    | Sequence 40, Appl   |
| 72  | 4 | 40.0 | 9  | 2         | US-10-697-055-41    | Sequence 41, Appl   |
| 73  | 4 | 40.0 | 9  | 2         | US-10-643-888-37    | Sequence 37, Appl   |
| 74  | 4 | 40.0 | 9  | 2         | US-10-643-888-38    | Sequence 38, Appl   |
| 75  | 4 | 40.0 | 9  | 2         | US-10-643-888-59    | Sequence 59, Appl   |
| 76  | 4 | 40.0 | 9  | 2         | US-10-643-888-60    | Sequence 60, Appl   |
| 77  | 4 | 40.0 | 9  | 2         | US-10-643-888-61    | Sequence 61, Appl   |
| 78  | 4 | 40.0 | 9  | 2         | US-10-643-888-62    | Sequence 62, Appl   |
| 79  | 4 | 40.0 | 9  | 2         | US-10-643-888-64    | Sequence 64, Appl   |
| 80  | 4 | 40.0 | 9  | 2         | US-10-643-888-66    | Sequence 66, Appl   |
| 81  | 4 | 40.0 | 9  | 2         | US-10-643-888-69    | Sequence 69, Appl   |
| 82  | 4 | 40.0 | 9  | 2         | US-10-643-888-70    | Sequence 70, Appl   |
| 83  | 4 | 40.0 | 9  | 2         | US-10-643-888-71    | Sequence 71, Appl   |
| 84  | 4 | 40.0 | 9  | 2         | US-10-643-888-72    | Sequence 72, Appl   |
| 85  | 4 | 40.0 | 10 | 1         | US-08-325-253-11    | Sequence 11, Appl   |
| 86  | 4 | 40.0 | 10 | 1         | US-08-968-542C-22   | Sequence 22, Appl   |
| 87  | 4 | 40.0 | 10 | 2         | US-09-475-316A-40   | Sequence 40, Appl   |
| 88  | 4 | 40.0 | 10 | 2         | US-09-311-784A-200  | Sequence 200, Appl  |
| 89  | 4 | 40.0 | 10 | 2         | US-09-704-66A-40    | Sequence 40, Appl   |
| 90  | 4 | 40.0 | 10 | 2         | US-09-554-467A-22   | Sequence 22, Appl   |
| 91  | 4 | 40.0 | 10 | 2         | US-09-239-043D-659  | Sequence 659, Appl  |
| 92  | 4 | 40.0 | 10 | 2         | US-09-239-043D-2019 | Sequence 2019, Appl |
| 93  | 4 | 40.0 | 10 | 2         | US-09-239-043D-2462 | Sequence 2462, Appl |
| 94  | 4 | 40.0 | 10 | 2         | US-09-239-043D-2549 | Sequence 2549, Appl |
| 95  | 4 | 40.0 | 10 | 2         | US-09-660-302A-24   | Sequence 24, Appl   |
| 96  | 4 | 40.0 | 10 | 2         | US-09-660-302A-32   | Sequence 32, Appl   |
| 97  | 4 | 40.0 | 4  | 1         | US-07-906-349E-16   | Sequence 16, Appl   |
| 98  | 3 | 30.0 | 4  | 1         | US-08-384-618-6     | Sequence 6, Appl    |
| 99  | 3 | 30.0 | 4  | 1         | US-08-102-757-23    | Sequence 23, Appl   |
| 100 | 3 | 30.0 | 4  | 1         | US-08-167-035-16    | Sequence 16, Appl   |

|     |   |      |   |   |                    |                   |     |   |      |   |   |                    |                    |
|-----|---|------|---|---|--------------------|-------------------|-----|---|------|---|---|--------------------|--------------------|
| 101 | 3 | 30.0 | 4 | 1 | US-08-255-272-21   | Sequence 21, Appl | 174 | 3 | 30.0 | 5 | 2 | US-09-020-880-45   | Sequence 45, Appl  |
| 102 | 3 | 30.0 | 4 | 1 | US-08-208-887A-16  | Sequence 16, Appl | 175 | 3 | 30.0 | 5 | 2 | US-09-273-565-63   | Sequence 63, Appl  |
| 103 | 3 | 30.0 | 4 | 1 | US-08-625-322-5    | Sequence 5, Appl  | 176 | 3 | 30.0 | 5 | 2 | US-08-505-250-31   | Sequence 31, Appl  |
| 104 | 3 | 30.0 | 4 | 1 | US-07-963-538B-8   | Sequence 8, Appl  | 177 | 3 | 30.0 | 5 | 2 | US-08-605-430-51   | Sequence 51, Appl  |
| 105 | 3 | 30.0 | 4 | 1 | US-08-539-005-15   | Sequence 15, Appl | 178 | 3 | 30.0 | 5 | 2 | US-08-505-250-31   | Sequence 31, Appl  |
| 106 | 3 | 30.0 | 4 | 2 | US-09-039-308A-17  | Sequence 17, Appl | 179 | 3 | 30.0 | 5 | 2 | US-09-565-538-63   | Sequence 63, Appl  |
| 107 | 3 | 30.0 | 4 | 2 | US-09-320-095-11   | Sequence 11, Appl | 180 | 3 | 30.0 | 5 | 2 | US-09-368-449B-41  | Sequence 41, Appl  |
| 108 | 3 | 30.0 | 4 | 2 | US-09-523-487-11   | Sequence 11, Appl | 181 | 3 | 30.0 | 5 | 2 | US-09-020-065A-3   | Sequence 3, Appl   |
| 109 | 3 | 30.0 | 4 | 2 | US-09-187-859-86   | Sequence 86, Appl | 182 | 3 | 30.0 | 5 | 2 | US-09-187-859-68   | Sequence 88, Appl  |
| 110 | 3 | 30.0 | 4 | 2 | US-09-187-859-87   | Sequence 87, Appl | 183 | 3 | 30.0 | 5 | 2 | US-09-187-859-69   | Sequence 89, Appl  |
| 111 | 3 | 30.0 | 4 | 2 | US-09-187-859-142  | Sequence 142, App | 184 | 3 | 30.0 | 5 | 2 | US-09-187-859-91   | Sequence 91, Appl  |
| 112 | 3 | 30.0 | 4 | 2 | US-09-187-859-144  | Sequence 144, App | 185 | 3 | 30.0 | 5 | 2 | US-09-187-859-143  | Sequence 143, App  |
| 113 | 3 | 30.0 | 4 | 2 | US-09-187-859-362  | Sequence 362, App | 186 | 3 | 30.0 | 5 | 2 | US-09-187-859-145  | Sequence 145, App  |
| 114 | 3 | 30.0 | 4 | 2 | US-09-187-859-364  | Sequence 364, App | 187 | 3 | 30.0 | 5 | 2 | US-09-187-859-147  | Sequence 147, App  |
| 115 | 3 | 30.0 | 4 | 2 | US-09-388-183-7    | Sequence 7, Appl  | 188 | 3 | 30.0 | 5 | 2 | US-09-187-859-363  | Sequence 363, App  |
| 116 | 3 | 30.0 | 4 | 2 | US-09-280-598-16   | Sequence 16, Appl | 189 | 3 | 30.0 | 5 | 2 | US-09-187-859-165  | Sequence 365, App  |
| 117 | 3 | 30.0 | 4 | 2 | US-09-578-303-15   | Sequence 15, Appl | 190 | 3 | 30.0 | 5 | 2 | US-09-187-859-367  | Sequence 367, App  |
| 118 | 3 | 30.0 | 4 | 2 | US-09-240-179-32   | Sequence 32, Appl | 191 | 3 | 30.0 | 5 | 2 | US-09-187-859-736  | Sequence 736, App  |
| 119 | 3 | 30.0 | 4 | 2 | US-09-305-927-51   | Sequence 51, Appl | 192 | 3 | 30.0 | 5 | 2 | US-09-187-859-751  | Sequence 751, App  |
| 120 | 3 | 30.0 | 4 | 2 | US-09-305-927-52   | Sequence 52, Appl | 193 | 3 | 30.0 | 5 | 2 | US-09-187-859-766  | Sequence 766, App  |
| 121 | 3 | 30.0 | 4 | 2 | US-08-469-260A-538 | Sequence 538, App | 194 | 3 | 30.0 | 5 | 2 | US-09-187-859-796  | Sequence 796, App  |
| 122 | 3 | 30.0 | 4 | 2 | US-09-584-001C-17  | Sequence 17, Appl | 195 | 3 | 30.0 | 5 | 2 | US-09-187-859-811  | Sequence 811, App  |
| 123 | 3 | 30.0 | 4 | 2 | US-09-584-001C-28  | Sequence 28, Appl | 196 | 3 | 30.0 | 5 | 2 | US-09-187-859-812  | Sequence 812, App  |
| 124 | 3 | 30.0 | 4 | 2 | US-09-584-001C-43  | Sequence 43, Appl | 197 | 3 | 30.0 | 5 | 2 | US-09-187-859-814  | Sequence 814, App  |
| 125 | 3 | 30.0 | 4 | 2 | US-08-488-446-538  | Sequence 538, App | 198 | 3 | 30.0 | 5 | 2 | US-09-187-859-1050 | Sequence 1050, App |
| 126 | 3 | 30.0 | 4 | 2 | US-09-839-542B-86  | Sequence 86, Appl | 199 | 3 | 30.0 | 5 | 2 | US-09-187-859-1094 | Sequence 1094, App |
| 127 | 3 | 30.0 | 4 | 2 | US-09-839-542B-87  | Sequence 87, Appl | 200 | 3 | 30.0 | 5 | 2 | US-09-187-859-1138 | Sequence 1138, App |

## ALIGNMENTS

RESULT 1  
PCT-US93-01669-28  
Sequence 28, Application PC/TUS9301669  
GENERAL INFORMATION:  
APPLICANT: Trowbridge, Ian S.  
APPLICANT: Collawn, J.T., James F.  
APPLICANT: Talmey, John A.  
APPLICANT: Kuhn, Leslie A.  
TITLE OF INVENTION: RECEPTOR INTERNALIZATION SIGNALS  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Spensley Horn Ubae & Lubitz  
STREET: 1880 Century Park East, Suite 500  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90067  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/01669  
CLASSIFICATION:  
FILING DATE: 01-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/844,852  
FILING DATE: 03-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Wetherell, Jr. Ph.D., John R.  
REGISTRATION NUMBER: 31,678  
REFERENCE/DOCKET NUMBER: PD-1636  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 455-5100  
TELEFAX: (619) 455-5110  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown

MOLECULE TYPE: peptide  
PCT-US93-01669-28

Query Match 50.0%; Score 5; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 P00GF 10  
DB 1 P00GF 5

## RESULT 2

PCT-US93-01669-56  
Sequence 56, Application PC/TUS9301669  
GENERAL INFORMATION:  
APPLICANT: Trowbridge, Ian S.  
APPLICANT: Collawn, Jr., James F.  
APPLICANT: Tainer, John A.  
APPLICANT: Kuhn, Leslie A.  
TITLE OF INVENTION: RECEPTOR INTERNALIZATION SIGNALS  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Spensley Horn Jubas & Lubitz  
STREET: 1880 Century Park East, Suite 500  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90067  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/01669  
FILING DATE: 01-MAR-1993  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/844,852  
FILING DATE: 03-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Wetherell, Jr. Ph.D., John R.  
REGISTRATION NUMBER: 31,678  
REFERENCE/DOCKET NUMBER: PD-1636  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 455-5100  
TELEFAX: (619) 455-5110  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
PCT-US93-01669-56

Query Match 50.0%; Score 5; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 P00GF 10  
DB 3 P00GF 7

## RESULT 3

US-08-785-668-4  
Sequence 4, Application US/08785668  
Patent No. 6265204  
GENERAL INFORMATION:  
APPLICANT: Ward et al.  
TITLE OF INVENTION: DNA SEQUENCES, VECTORS, AND FUSION  
TITLE OF INVENTION: POLYPEPTIDES FOR SECRETION OF FILAMENTOUS

TITLE OF INVENTION: FUNGI  
NUMBER OF SEQUENCES: 41  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genencor International, Inc.  
STREET: 925 Page Mill Road  
CITY: Palo Alto  
STATE: CA

COUNTRY: USA  
ZIP: 94304-1013  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/785,668  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/785,668  
FILING DATE: 17-JAN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Stone, Christopher L.  
REGISTRATION NUMBER: 35,696  
REFERENCE/DOCKET NUMBER: GC-284  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-846-7620  
TELEFAX: 650-845-6504  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

US-08-785-668-4

Query Match 40.0%; Score 4; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYL 4  
DB 2 EBYL 5

## RESULT 4

US-09-912-733-4  
Sequence 4, Application US/09912733  
Patent No. 6590078  
GENERAL INFORMATION:  
APPLICANT: Ward, Michael D.  
TITLE OF INVENTION: DNA SEQUENCES, VECTORS, AND FUSION POLYPEPTIDES FOR SECRETION OF  
FILE REFERENCE: A-62926-1  
CURRENT APPLICATION NUMBER: US/09/912,733  
CURRENT FILING DATE: 2001-07-23  
PRIOR APPLICATION NUMBER: US 08/785,668  
PRIOR FILING DATE: 1997-01-17  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 4  
LENGTH: 5  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic.

US-09-912-733-4

Query Match 40.0%; Score 4; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYL 4

Db 2 EBYL 5

RESULT 5  
US-09-581-944A-25  
Sequence 25, Application US/09581944A  
Patent No. 6441131

GENERAL INFORMATION:

APPLICANT: Ono Pharmaceutical Co., Ltd.

TITLE OF INVENTION: PEPTIDES, METHOD FOR ASSAYING HUMAN PEPSINOGEN II OR HUMAN PEPSIN

FILE REFERENCE: Q59565

CURRENT APPLICATION NUMBER: US/09/581,944A

PRIOR FILING DATE: 2000-06-20

PRIOR APPLICATION NUMBER: P. Hel. 9-364796

PRIOR FILING DATE: 1997-12-22

PRIOR APPLICATION NUMBER: P. Hel. 10-213513

PRIOR FILING DATE: 1998-07-13

PRIOR APPLICATION NUMBER: PCT/JP98/05780

PRIOR FILING DATE: 1998-12-21

NUMBER OF SEQ ID NOS: 92

SOFTWARE: PatentIn version 3.1

SEQ ID NO 25

LENGTH: 6

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: substrate for human pepsin II or pepsinogen II

NAME/KEY: MISC\_FEATURE

LOCATION: (5)..(5)

FEATURE: OTHER INFORMATION: 2-naphthyl Ala

NAME/KEY: MISC\_FEATURE

LOCATION: (6)..(6)

OTHER INFORMATION: Ala which binds to p-nitroaniline

US-09-581-944A-25

Query Match 40.0%; Score 4; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PQQ 9  
Db 1 PQQ 4

RESULT 6  
US-09-147-933-19  
Sequence 19, Application US/09147933A  
Patent No. 6168917

GENERAL INFORMATION:

APPLICANT: Kilpatrick, David

TITLE OF INVENTION: DETECTION AND IDENTIFICATION OF

FILE REFERENCE: 62242/US

CURRENT APPLICATION NUMBER: US/09/147,933A

PRIOR FILING DATE: 1999-07-09

PRIOR APPLICATION NUMBER: PCT/US97/17734

PRIOR FILING DATE: 1997-10-01

PRIOR APPLICATION NUMBER: U. S. 60/027,353

PRIOR FILING DATE: 1996-10-02

NUMBER OF SEQ ID NOS: 96

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 19

LENGTH: 7

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: peptide

US-09-147-933-19

Query Match 40.0%; Score 4; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LVPO 7  
Db 4 LVPO 7

RESULT 7  
US-09-581-944A-20  
Sequence 20, Application US/09581944A  
Patent No. 6441131

GENERAL INFORMATION:

APPLICANT: Ono Pharmaceutical Co., Ltd.

TITLE OF INVENTION: PEPTIDES, METHOD FOR ASSAYING HUMAN PEPSINOGEN II OR HUMAN PEPSIN

FILE REFERENCE: Q59565

CURRENT APPLICATION NUMBER: US/09/581,944A

PRIOR FILING DATE: 2000-06-20

PRIOR APPLICATION NUMBER: P. Hel. 9-364796

PRIOR FILING DATE: 1997-12-22

PRIOR APPLICATION NUMBER: P. Hel. 10-213513

PRIOR FILING DATE: 1998-07-13

PRIOR APPLICATION NUMBER: PCT/JP98/05780

PRIOR FILING DATE: 1998-12-21

NUMBER OF SEQ ID NOS: 92

SOFTWARE: PatentIn version 3.1

SEQ ID NO 20

LENGTH: 7

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: substrate for human pepsin II or pepsinogen II

NAME/KEY: MISC\_FEATURE

LOCATION: (6)..(6)

OTHER INFORMATION: 4-Iodo-Phenyl Ala

NAME/KEY: MISC\_FEATURE

LOCATION: (7)..(7)

OTHER INFORMATION: Ala which binds to p-nitroaniline

US-09-581-944A-20

Query Match 40.0%; Score 4; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VPOQ 8  
Db 1 VPOQ 4

RESULT 8  
542249-15  
Patent No. 542249  
APPLICANT: LIRSCH, MANFRED; RINK, HANS; MARKI, WALTER; GRUTTER,

MARKUS G.; MEYHACK, BERND

TITLE OF INVENTION: PROCESS FOR THE MANUFACTURE OF THROMBIN

NUMBER OF SEQUENCES: 15

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/121,974

FILING DATE: 15-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 700,9978

FILING DATE: 10-MAY-1991

APPLICATION NUMBER: 582,816

FILING DATE: 13-SEP-1990

APPLICATION NUMBER: 211,065

FILING DATE: 20-JUN-1988

APPLICATION NUMBER: 744,453

FILING DATE: 13-JUN-1985



SEQ ID NO:15:  
LENGTH: 7  
5422249-15

Query Match 40.0%; Score 4; DB 6; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYL 4  
|||  
Db 3 EBYL 6

RESULT 9  
US-08-037-574A-7  
Sequence 7, Application US/08037574A

PATENT INFORMATION:  
PATENT NO. 5656600  
APPLICANT: MATTHEW M. ABELMAN, DANIEL A.  
APPLICANT: PEASON, GEORGE P. VLASUK,  
APPLICANT: THOMAS R. WEBB  
TITLE OF INVENTION: ALPHA-KETAMIDE DERIVATIVES AS  
TITLE OF INVENTION: INHIBITORS OF THROMBOSIS  
NUMBER OF SEQUENCES: 166  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM M.S. DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/037,574A  
FILING DATE: 25 MARCH 1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA: No. 5656600e  
PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, Suzanne L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 200/188  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
FEATURE:  
OTHER INFORMATION:  
US-08-037-574A-7

Query Match 40.0%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYL 4  
|||  
Db 5 EBYL 8

RESULT 10

US-08-037-574A-9  
Sequence 9, Application US/08037574A

PATENT INFORMATION:  
PATENT NO. 5656600  
APPLICANT: MATTHEW M. ABELMAN, DANIEL A.  
APPLICANT: PEASON, GEORGE P. VLASUK,  
APPLICANT: THOMAS R. WEBB  
TITLE OF INVENTION: ALPHA-KETAMIDE DERIVATIVES AS  
TITLE OF INVENTION: INHIBITORS OF THROMBOSIS  
NUMBER OF SEQUENCES: 166  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM M.S. DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/037,574A  
FILING DATE: 25 MARCH 1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA: No. 5656600e  
PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, Suzanne L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 200/188  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
FEATURE:  
OTHER INFORMATION:  
US-08-037-574A-9

Query Match 40.0%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYL 4  
|||  
Db 5 EBYL 8

RESULT 11  
US-08-037-574A-13  
Sequence 13, Application US/08037574A

PATENT INFORMATION:  
PATENT NO. 5656600  
APPLICANT: MATTHEW M. ABELMAN, DANIEL A.  
APPLICANT: PEASON, GEORGE P. VLASUK,  
APPLICANT: THOMAS R. WEBB  
TITLE OF INVENTION: ALPHA-KETAMIDE DERIVATIVES AS  
TITLE OF INVENTION: INHIBITORS OF THROMBOSIS  
NUMBER OF SEQUENCES: 166  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles

STATE: California  
COUNTRY: USA  
ZIP: 90017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM M.S. DOS (Version 5.0)  
SOFTWARE: Wordperfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/037,574A  
FILING DATE: 25 MARCH 1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA: No. 5656600e  
PRIOR APPLICATION DATA: including application  
APPLICATION NUMBER: described below:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, Suzanne L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 200/188  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
FEATURE:  
OTHER INFORMATION:  
US-08-037-574A-13

Query Match 40.0%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYVL 4  
Db 5 EYVL 8

RESULT 12  
US-08-037-574A-17  
Sequence 17, Application US/08037574A  
Patent No. 5656600  
GENERAL INFORMATION:  
APPLICANT: MATTHEW M. ABELMAN, DANIEL A.  
APPLICANT: PEASON, GEORGE P. VLASUK,  
APPLICANT: THOMAS R. WEBB  
TITLE OF INVENTION: ALPHA-KETAMIDE DERIVATIVES AS  
TITLE OF INVENTION: INHIBITORS OF THROMBOSIS  
NUMBER OF SEQUENCES: 166  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM M.S. DOS (Version 5.0)  
SOFTWARE: Wordperfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/037,574A  
FILING DATE: 25 MARCH 1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA: No. 5656600e  
PRIOR APPLICATION DATA: including application

PRIOR APPLICATION DATA: described below:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, Suzanne L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 200/188  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
FEATURE:  
OTHER INFORMATION:  
US-08-037-574A-17

Query Match 40.0%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYVL 4  
Db 5 EYVL 8

RESULT 13  
US-08-037-574A-79  
Sequence 79, Application US/08037574A  
Patent No. 5656600  
GENERAL INFORMATION:  
APPLICANT: MATTHEW M. ABELMAN, DANIEL A.  
APPLICANT: PEASON, GEORGE P. VLASUK,  
APPLICANT: THOMAS R. WEBB  
TITLE OF INVENTION: ALPHA-KETAMIDE DERIVATIVES AS  
TITLE OF INVENTION: INHIBITORS OF THROMBOSIS  
NUMBER OF SEQUENCES: 166  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM M.S. DOS (Version 5.0)  
SOFTWARE: Wordperfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/037,574A  
FILING DATE: 25 MARCH 1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA: No. 5656600e  
PRIOR APPLICATION DATA: including application  
APPLICATION NUMBER: described below:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, Suzanne L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 200/188  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 79:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 AMINO ACIDS

TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
FEATURE:  
OTHER INFORMATION:  
US-08-037-574A-79

Query Match 40.0%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EBYL 4  
|||  
Db 5 EBYL 8

RESULT 14  
US-08-037-574A-81  
Sequence 81, Application US/08037574A  
Patent No. 5656600  
GENERAL INFORMATION:  
APPLICANT: MATTHEW M. ABELMAN, DANIEL A.  
APPLICANT: PEASON, GEORGE P. VLASUK,  
APPLICANT: THOMAS R. WEBB  
TITLE OF INVENTION: ALPHA-KETAMIDE DERIVATIVES AS  
TITLE OF INVENTION: INHIBITORS OF THROMBOSIS  
NUMBER OF SEQUENCES: 166  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM M.S. DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/037,574A  
FILING DATE: 25 MARCH 1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA: No. 5656600e  
PRIOR APPLICATION DATA: Including application  
PRIOR APPLICATION DATA: described below:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, Suzanne L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 200/188  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 81:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
FEATURE:  
OTHER INFORMATION:  
US-08-037-574A-81

Query Match 40.0%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EBYL 4  
|||  
Db 5 EBYL 8

RESULT 15  
US-08-037-574A-83  
Sequence 83, Application US/08037574A  
Patent No. 5656600

GENERAL INFORMATION:  
APPLICANT: MATTHEW M. ABELMAN, DANIEL A.  
APPLICANT: PEASON, GEORGE P. VLASUK,  
APPLICANT: THOMAS R. WEBB  
TITLE OF INVENTION: ALPHA-KETAMIDE DERIVATIVES AS  
TITLE OF INVENTION: INHIBITORS OF THROMBOSIS  
NUMBER OF SEQUENCES: 166  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90017

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM M.S. DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/037,574A  
FILING DATE: 25 MARCH 1993  
CLASSIFICATION: 435

PRIOR APPLICATION DATA: No. 5656600e  
PRIOR APPLICATION DATA: Including application  
PRIOR APPLICATION DATA: described below:  
APPLICATION NUMBER:  
FILING DATE:

ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, Suzanne L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 200/188  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 83:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
FEATURE:  
OTHER INFORMATION:  
US-08-037-574A-83

Query Match 40.0%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EBYL 4  
|||  
Db 5 EBYL 8

RESULT 16  
US-08-037-574A-100  
Sequence 100, Application US/08037574A  
Patent No. 5656600  
GENERAL INFORMATION:  
APPLICANT: MATTHEW M. ABELMAN, DANIEL A.  
APPLICANT: PEASON, GEORGE P. VLASUK,  
APPLICANT: THOMAS R. WEBB  
TITLE OF INVENTION: ALPHA-KETAMIDE DERIVATIVES AS  
TITLE OF INVENTION: INHIBITORS OF THROMBOSIS  
NUMBER OF SEQUENCES: 166  
CORRESPONDENCE ADDRESS:

ADDRESSER: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM M.S. DOS (Version 5.0)  
SOFTWARE: Wordperfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/037,574A  
FILING DATE: 25 MARCH 1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA: No. 5656600e  
PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, Suzanne L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 200/188  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 100:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
FEATURE:  
OTHER INFORMATION:  
US-08-037-574A-100

Query Match 40.0%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EBYL 4  
Db 5 EBYL 8

RESULT 17  
US-08-037-574A-106  
Sequence 106, Application US/08037574A  
Patent No. 5656600  
GENERAL INFORMATION:  
APPLICANT: MATTHEW M. ABELMAN, DANIEL A.  
APPLICANT: PEARSON, GEORGE P. VLASUK,  
APPLICANT: THOMAS R. WEBB  
TITLE OF INVENTION: ALPHA-KETOMIDE DERIVATIVES AS  
TITLE OF INVENTION: INHIBITORS OF THROMBOSIS  
NUMBER OF SEQUENCES: 166  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM M.S. DOS (Version 5.0)  
SOFTWARE: Wordperfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/037,574A  
FILING DATE: 25 MARCH 1993

CLASSIFICATION: 435  
PRIOR APPLICATION DATA: No. 5656600e  
PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, Suzanne L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 200/188  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 106:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
FEATURE:  
OTHER INFORMATION:  
US-08-037-574A-106

Query Match 40.0%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EBYL 4  
Db 5 EBYL 8

RESULT 18  
US-08-037-574A-114  
Sequence 114, Application US/08037574A  
Patent No. 5656600  
GENERAL INFORMATION:  
APPLICANT: MATTHEW M. ABELMAN, DANIEL A.  
APPLICANT: PEARSON, GEORGE P. VLASUK,  
APPLICANT: THOMAS R. WEBB  
TITLE OF INVENTION: ALPHA-KETOMIDE DERIVATIVES AS  
TITLE OF INVENTION: INHIBITORS OF THROMBOSIS  
NUMBER OF SEQUENCES: 166  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM M.S. DOS (Version 5.0)  
SOFTWARE: Wordperfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/037,574A  
FILING DATE: 25 MARCH 1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA: No. 5656600e  
PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, Suzanne L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 200/188  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 114:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
FEATURE:  
OTHER INFORMATION:  
US-08-037-574A-114

Query Match 40.0%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYL 4  
|||||  
DB 5 EBYL 8

RESULT 19  
US-08-037-574A-118  
; Sequence 118, Application US/08037574A  
; Patent No. 5656600  
; GENERAL INFORMATION:  
; APPLICANT: MATTHEW M. ABELMAN, DANIEL A.  
; APPLICANT: PEASON, GEORGE P. VLASUK,  
; TITLE OF INVENTION: ALPHA-KETOAMIDE DERIVATIVES AS  
; TITLE OF INVENTION: INHIBITORS OF THROMBOSIS  
; NUMBER OF SEQUENCES: 166  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 611 West Sixth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90017  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM M.S. DOS (Version 5.0)  
; SOFTWARE: WordPerfect (Version 5.1)  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; FILING DATE: 25 MARCH 1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA: No. 5656600e  
; PRIOR APPLICATION DATA: including application  
; PRIOR APPLICATION DATA: described below:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BIGGS, Suzanne L.  
; REGISTRATION NUMBER: 30,158  
; REFERENCE/DOCKET NUMBER: 200/188  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 118:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 AMINO ACIDS  
; TYPE: AMINO ACID  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE: PEPTIDE  
; FEATURE:  
; OTHER INFORMATION:  
; US-08-037-574A-118

Query Match 40.0%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYL 4  
|||||  
DB 5 EBYL 8

RESULT 20  
US-08-037-574A-151  
; Sequence 151, Application US/08037574A  
; Patent No. 5656600  
; GENERAL INFORMATION:  
; APPLICANT: MATTHEW M. ABELMAN, DANIEL A.  
; APPLICANT: PEASON, GEORGE P. VLASUK,  
; TITLE OF INVENTION: ALPHA-KETOAMIDE DERIVATIVES AS  
; TITLE OF INVENTION: INHIBITORS OF THROMBOSIS  
; NUMBER OF SEQUENCES: 166  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 611 West Sixth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90017  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM M.S. DOS (Version 5.0)  
; SOFTWARE: WordPerfect (Version 5.1)  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; FILING DATE: 25 MARCH 1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA: No. 5656600e  
; PRIOR APPLICATION DATA: including application  
; PRIOR APPLICATION DATA: described below:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BIGGS, Suzanne L.  
; REGISTRATION NUMBER: 30,158  
; REFERENCE/DOCKET NUMBER: 200/188  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 151:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 AMINO ACIDS  
; TYPE: AMINO ACID  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE: PEPTIDE  
; FEATURE:  
; OTHER INFORMATION:  
; US-08-037-574A-151

Query Match 40.0%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYL 4  
|||||  
DB 5 EBYL 8

RESULT 21  
US-08-037-574A-157  
; Sequence 157, Application US/08037574A  
; Patent No. 5656600  
; GENERAL INFORMATION:  
; APPLICANT: MATTHEW M. ABELMAN, DANIEL A.  
; APPLICANT: PEASON, GEORGE P. VLASUK,  
; TITLE OF INVENTION: ALPHA-KETOAMIDE DERIVATIVES AS

;; TITLE OF INVENTION: INHIBITORS OF THROMBOSIS  
;; NUMBER OF SEQUENCES: 166  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Lyon & Lyon  
;; STREET: 611 West Sixth Street  
;; CITY: Los Angeles  
;; STATE: California  
;; COUNTRY: USA  
;; ZIP: 90017  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: IBM M.S. DOS (Version 5.0)  
;; SOFTWARE: Wordperfect (Version 5.1)  
;;  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/037,574A  
;; FILING DATE: 25 MARCH 1993  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA: No. 5656600e  
;; PRIOR APPLICATION DATA: including application  
;; PRIOR APPLICATION DATA: described below:  
;; APPLICATION NUMBER:  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: BIGGS, Suzanne L.  
;; REGISTRATION NUMBER: 30,158  
;; REFERENCE/DOCKET NUMBER: 200/188  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (213) 489-1600  
;; TELEFAX: (213) 955-0440  
;; TELEX: 67-3510  
;; INFORMATION FOR SEQ ID NO: 157:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 8 AMINO ACIDS  
;; TYPE: AMINO ACID  
;; TOPOLOGY: LINEAR  
;; MOLECULE TYPE: PEPTIDE  
;; FEATURE:  
;; OTHER INFORMATION:  
;;  
US-08-037-574A-157  
;  
Query Match 40.0%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
;  
QY 1 EBYL 4  
|||  
Db 5 EBYL 8  
;  
RESULT 22  
US-08-037-574A-163  
; Sequence 163, Application US/08037574A  
; Patent No. 5656600  
; GENERAL INFORMATION:  
; APPLICANT: MATTHEW M. ABELMAN, DANIEL A.  
; APPLICANT: PEASON, GEORGE P. VLASUK,  
; APPLICANT: THOMAS R. WEBB  
; TITLE OF INVENTION: ALPHA-KETOAMIDE DERIVATIVES AS  
; TITLE OF INVENTION: INHIBITORS OF THROMBOSIS  
; NUMBER OF SEQUENCES: 166  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 611 West Sixth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90017  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM M.S. DOS (Version 5.0)  
; SOFTWARE: Wordperfect (Version 5.1)  
;  
;

;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/037,574A  
;; FILING DATE: 25 MARCH 1993  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA: No. 5656600e  
;; PRIOR APPLICATION DATA: including application  
;; PRIOR APPLICATION DATA: described below:  
;; APPLICATION NUMBER:  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: BIGGS, Suzanne L.  
;; REGISTRATION NUMBER: 30,158  
;; REFERENCE/DOCKET NUMBER: 200/188  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (213) 489-1600  
;; TELEFAX: (213) 955-0440  
;; TELEX: 67-3510  
;; INFORMATION FOR SEQ ID NO: 163:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 8 AMINO ACIDS  
;; TYPE: AMINO ACID  
;; TOPOLOGY: LINEAR  
;; MOLECULE TYPE: PEPTIDE  
;; FEATURE:  
;; OTHER INFORMATION:  
;;  
US-08-037-574A-163  
;  
Query Match 40.0%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
;  
QY 1 EBYL 4  
|||  
Db 5 EBYL 8  
;  
RESULT 23  
US-08-218-329-7  
; Sequence 7, Application US/08218329  
; Patent No. 5670479  
; GENERAL INFORMATION:  
; APPLICANT: MATTHEW M. ABELMAN, ET AL.  
; TITLE OF INVENTION: ALPHA-KETOAMIDE DERIVATIVES AS  
; TITLE OF INVENTION: INHIBITORS OF THROMBOSIS  
; NUMBER OF SEQUENCES: 165  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 611 West Sixth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90017  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM M.S. DOS (Version 5.0)  
; SOFTWARE: Wordperfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/218,329  
; FILING DATE: 25-MAR-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/037,574  
; FILING DATE: 25-MAR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BIGGS, Suzanne L.  
; REGISTRATION NUMBER: 30,158  
; REFERENCE/DOCKET NUMBER: 206/222  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 7:  
;  
;

SEQUENCE CHARACTERISTICS:  
LENGTH: 8 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
FEATURE:  
OTHER INFORMATION:

US-08-218-329-7

Query Match 40.0%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYL 4  
DB 5 EBYL 8

RESULT 24

US-08-218-329-9

Sequence 9, Application US/08218329

Patent No. 5670479

GENERAL INFORMATION:

APPLICANT: MATTHEW M. ABELMAN, ET AL.

TITLE OF INVENTION: ALPHA-KETOAMIDE DERIVATIVES AS

TITLE OF INVENTION: INHIBITORS OF THROMBOSIS

NUMBER OF SEQUENCES: 165

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 611 West Sixth Street

CITY: Los Angeles

STATE: California

COUNTRY: USA

ZIP: 90017

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM M.S. DOS (Version 5.0)

SOFTWARE: Wordperfect (Version 5.1)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/218,329

FILING DATE: 25-MAR-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/037,574

FILING DATE: 25-MAR-1993

ATTORNEY/AGENT INFORMATION:

NAME: BIGGS, Suzanne L.

REGISTRATION NUMBER: 30,158

REFERENCE/DOCKET NUMBER: 206/222

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 AMINO ACIDS

TYPE: AMINO ACID

TOPOLOGY: LINEAR

MOLECULE TYPE: PEPTIDE

FEATURE:

OTHER INFORMATION:

US-08-218-329-9

Query Match 40.0%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYL 4  
DB 5 EBYL 8

RESULT 25

US-08-218-329-13

Sequence 13, Application US/08218329

Patent No. 5670479

GENERAL INFORMATION:

APPLICANT: MATTHEW M. ABELMAN, ET AL.

TITLE OF INVENTION: ALPHA-KETOAMIDE DERIVATIVES AS

TITLE OF INVENTION: INHIBITORS OF THROMBOSIS

NUMBER OF SEQUENCES: 165

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 611 West Sixth Street

CITY: Los Angeles

STATE: California

COUNTRY: USA

ZIP: 90017

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM M.S. DOS (Version 5.0)

SOFTWARE: Wordperfect (Version 5.1)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/218,329

FILING DATE: 25-MAR-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/037,574

FILING DATE: 25-MAR-1993

ATTORNEY/AGENT INFORMATION:

NAME: BIGGS, Suzanne L.

REGISTRATION NUMBER: 30,158

REFERENCE/DOCKET NUMBER: 206/222

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 AMINO ACIDS

TYPE: AMINO ACID

TOPOLOGY: LINEAR

MOLECULE TYPE: PEPTIDE

FEATURE:

OTHER INFORMATION:

US-08-218-329-13

Query Match 40.0%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYL 4  
DB 5 EBYL 8

RESULT 26

US-08-218-329-17

Sequence 17, Application US/08218329

Patent No. 5670479

GENERAL INFORMATION:

APPLICANT: MATTHEW M. ABELMAN, ET AL.

TITLE OF INVENTION: ALPHA-KETOAMIDE DERIVATIVES AS

TITLE OF INVENTION: INHIBITORS OF THROMBOSIS

NUMBER OF SEQUENCES: 165

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 611 West Sixth Street

CITY: Los Angeles

STATE: California

COUNTRY: USA

ZIP: 90017

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage

COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM M.S. DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/218,329  
FILING DATE: 25-MAR-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/037,574  
FILING DATE: 25-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, Suzanne L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 206/222  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
FEATURE:  
OTHER INFORMATION:  
US-08-218-329-17

Query Match 40.0%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYL 4  
DB 5 EBYL 8

RESULT 27  
US-08-218-329-79  
Sequence 79, Application US/08218329  
Patent No. 5670479  
GENERAL INFORMATION:  
APPLICANT: MATTHEW M. ABELMAN, ET AL.  
TITLE OF INVENTION: ALPHA-KETAMIDE DERIVATIVES AS  
TITLE OF INVENTION: INHIBITORS OF THROMBOSIS  
NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM M.S. DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/218,329  
FILING DATE: 25-MAR-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/037,574  
FILING DATE: 25-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, Suzanne L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 206/222  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 79:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
FEATURE:  
OTHER INFORMATION:  
US-08-218-329-79

Query Match 40.0%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYL 4  
DB 5 EBYL 8

RESULT 28  
US-08-218-329-81  
Sequence 81, Application US/08218329  
Patent No. 5670479  
GENERAL INFORMATION:  
APPLICANT: MATTHEW M. ABELMAN, ET AL.  
TITLE OF INVENTION: ALPHA-KETAMIDE DERIVATIVES AS  
TITLE OF INVENTION: INHIBITORS OF THROMBOSIS  
NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM M.S. DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/218,329  
FILING DATE: 25-MAR-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/037,574  
FILING DATE: 25-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, Suzanne L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 206/222  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 81:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
FEATURE:  
OTHER INFORMATION:  
US-08-218-329-81

Query Match 40.0%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYL 4  
DB 5 EBYL 8



RESULT 29  
US-08-218-329-83  
Sequence 83, Application US/08218329  
Patent No. 5670479  
GENERAL INFORMATION:  
APPLICANT: MATTHEW M. ABELMAN, ET AL.  
TITLE OF INVENTION: ALPHA-KETOMIDE DERIVATIVES AS  
INHIBITORS OF THROMBOSIS  
NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM M.S. DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/218,329  
FILING DATE: 25-MAR-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/037,574  
FILING DATE: 25-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, Suzanne L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 206/222  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ. ID NO: 83:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
FEATURE:  
OTHER INFORMATION:  
US-08-218-329-83

Query Match 40.0%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4,6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYL 4  
|||  
DB 5 EBYL 8

RESULT 30  
US-08-218-329-99  
Sequence 99, Application US/08218329  
Patent No. 5670479  
GENERAL INFORMATION:  
APPLICANT: MATTHEW M. ABELMAN, ET AL.  
TITLE OF INVENTION: ALPHA-KETOMIDE DERIVATIVES AS  
INHIBITORS OF THROMBOSIS  
NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90017  
COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM M.S. DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/218,329  
FILING DATE: 25-MAR-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/037,574  
FILING DATE: 25-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, Suzanne L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 206/222  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ. ID NO: 99:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
FEATURE:  
OTHER INFORMATION:  
US-08-218-329-99

Query Match 40.0%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4,6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYL 4  
|||  
DB 5 EBYL 8

RESULT 31  
US-08-218-329-105  
Sequence 105, Application US/08218329  
Patent No. 5670479  
GENERAL INFORMATION:  
APPLICANT: MATTHEW M. ABELMAN, ET AL.  
TITLE OF INVENTION: ALPHA-KETOMIDE DERIVATIVES AS  
INHIBITORS OF THROMBOSIS  
NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM M.S. DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/218,329  
FILING DATE: 25-MAR-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/037,574  
FILING DATE: 25-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, Suzanne L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 206/222  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440

TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 105:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 AMINO ACIDS  
; TYPE: AMINO ACID  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE: PEPTIDE  
; FEATURE:  
; OTHER INFORMATION:  
US-08-218-329-105

Query Match 40.0%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYL 4  
|||  
Db 5 EBYL 8

RESULT 32  
US-08-218-329-113  
; Sequence 113, Application US/08218329  
; Patent No. 5670479  
; GENERAL INFORMATION:  
; APPLICANT: MATTHEW M. ABELMAN, ET AL.  
; TITLE OF INVENTION: ALPHA-KETAMIDE DERIVATIVES AS  
; NUMBER OF SEQUENCES: 165  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 611 West Sixth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90017  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM M.S. DOS (Version 5.0)  
; SOFTWARE: Wordperfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/218,329  
; FILING DATE: 25-MAR-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/037,574  
; FILING DATE: 25-MAR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BIGGS, Suzanne L.  
; REGISTRATION NUMBER: 30,158  
; REFERENCE/DOCKET NUMBER: 206/222  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 113:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 AMINO ACIDS  
; TYPE: AMINO ACID  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE: PEPTIDE  
; FEATURE:  
; OTHER INFORMATION:  
US-08-218-329-113

Query Match 40.0%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYL 4  
|||  
,Db 5 EBYL 8

RESULT 33  
US-08-218-329-117  
; Sequence 117, Application US/08218329  
; Patent No. 5670479  
; GENERAL INFORMATION:  
; APPLICANT: MATTHEW M. ABELMAN, ET AL.  
; TITLE OF INVENTION: ALPHA-KETAMIDE DERIVATIVES AS  
; NUMBER OF SEQUENCES: 165  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 611 West Sixth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90017  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM M.S. DOS (Version 5.0)  
; SOFTWARE: Wordperfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/218,329  
; FILING DATE: 25-MAR-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/037,574  
; FILING DATE: 25-MAR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BIGGS, Suzanne L.  
; REGISTRATION NUMBER: 30,158  
; REFERENCE/DOCKET NUMBER: 206/222  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 117:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 AMINO ACIDS  
; TYPE: AMINO ACID  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE: PEPTIDE  
; FEATURE:  
; OTHER INFORMATION:  
US-08-218-329-117

Query Match 40.0%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYL 4  
|||  
Db 5 EBYL 8

RESULT 34  
US-08-218-329-150  
; Sequence 150, Application US/08218329  
; Patent No. 5670479  
; GENERAL INFORMATION:  
; APPLICANT: MATTHEW M. ABELMAN, ET AL.  
; TITLE OF INVENTION: ALPHA-KETAMIDE DERIVATIVES AS  
; NUMBER OF SEQUENCES: 165  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 611 West Sixth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90017

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM M.S. DOS (Version 5.0)  
SOFTWARE: Wordperfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/218,329  
FILING DATE: 25-MAR-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/037,574  
FILING DATE: 25-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, Suzanne L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 206/222  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 150:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
FEATURE:  
OTHER INFORMATION:  
US-08-218-329-150

Query Match 40.0%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYL 4  
||||  
DB 5 EBYL 8

RESULT 35  
US-08-218-329-156  
Sequence 156, Application US/08218329  
Patent No. 5670479  
GENERAL INFORMATION:  
APPLICANT: MATTHEW M. ABELMAN, ET AL.  
TITLE OF INVENTION: ALPHA-KETAMIDE DERIVATIVES AS  
INHIBITORS OF THROMBOSIS  
NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM M.S. DOS (Version 5.0)  
SOFTWARE: Wordperfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/218,329  
FILING DATE: 25-MAR-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/037,574  
FILING DATE: 25-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, Suzanne L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 206/222  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 489-1600

TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 156:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
FEATURE:  
OTHER INFORMATION:  
US-08-218-329-156

Query Match 40.0%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYL 4  
||||  
DB 5 EBYL 8

RESULT 36  
US-08-218-329-162  
Sequence 162, Application US/08218329  
Patent No. 5670479  
GENERAL INFORMATION:  
APPLICANT: MATTHEW M. ABELMAN, ET AL.  
TITLE OF INVENTION: ALPHA-KETAMIDE DERIVATIVES AS  
INHIBITORS OF THROMBOSIS  
NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM M.S. DOS (Version 5.0)  
SOFTWARE: Wordperfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/218,329  
FILING DATE: 25-MAR-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/037,574  
FILING DATE: 25-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, Suzanne L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 206/222  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 162:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
FEATURE:  
OTHER INFORMATION:  
US-08-218-329-162

Query Match 40.0%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYL 4  
||||

Db 5 EBYL 8

## RESULT 37

US-08-482-228-137

Sequence 137, Application US/08482228  
Patent No. 5968753

## GENERAL INFORMATION:

APPLICANT: Teeng-law, Janet

APPLICANT: Kobori, Joan A.

APPLICANT: Al-Abdaly, Fahad A.

APPLICANT: Guillermo, Roy

APPLICANT: Helgeson, Sam L.

APPLICANT: Deans, Robert J.

TITLE OF INVENTION: POSITIVE AND NEGATIVE CELL

TITLE OF INVENTION: SELECTION MEDIATED BY PEPTIDE RELEASE

NUMBER OF SEQUENCES: 215

CORRESPONDENCE ADDRESSES:

ADDRESSER: Janice Guthrie, Ph.D.

STREET: P.O. Box 15210

CITY: Irvine

STATE: California

COUNTRY: USA

ZIP: 92713-5210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/482,228

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Guthrie, Janice

REGISTRATION NUMBER: 35,170

REFERENCE/DOCKET NUMBER: IT-4630CIP3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (714) 440-5353

TELEFAX: (714) 553-1952

INFORMATION FOR SEQ ID NO: 137:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-482-228-137

Query Match 40.0%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 QOGF 10

Db 1 QOGF 4

## RESULT 38

US-08-482-528-137

Sequence 137, Application US/08482528

Patent No. 6017719

## GENERAL INFORMATION:

APPLICANT: Teeng-law, Janet

APPLICANT: Kobori, Joan A.

APPLICANT: Al-Abdaly, Fahad A.

APPLICANT: Guillermo, Roy

APPLICANT: Helgeson, Sam L.

APPLICANT: Deans, Robert J.

TITLE OF INVENTION: POSITIVE AND NEGATIVE CELL

TITLE OF INVENTION: SELECTION MEDIATED BY PEPTIDE RELEASE

NUMBER OF SEQUENCES: 215

CORRESPONDENCE ADDRESSES:

ADDRESSER: Janice Guthrie, Ph.D.

STREET: P.O. Box 15210

CITY: Irvine

STATE: California

COUNTRY: USA

ZIP: 92713-5210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/482,528

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Guthrie, Janice

REGISTRATION NUMBER: 35,170

REFERENCE/DOCKET NUMBER: IT-4630CIP4

TELECOMMUNICATION INFORMATION:

TELEPHONE: (714) 440-5353

TELEFAX: (714) 553-1952

INFORMATION FOR SEQ ID NO: 137:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-482-528-137

Query Match 40.0%; Score 4; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 QOGF 10

Db 1 QOGF 4

## RESULT 39

US-09-239-043D-198

Sequence 198, Application US/09239043D

Patent No. 6689363

## GENERAL INFORMATION:

APPLICANT: Sette, Alessandro

APPLICANT: Sidney, John

APPLICANT: Southwood, Scott

APPLICANT: Vitiello, Maria A.

APPLICANT: Livingston, Brian D.

APPLICANT: Cells, Esteban

APPLICANT: Kubo, Ralph T.

APPLICANT: Grey, Howard M.

APPLICANT: Chesebunt, Robert

APPLICANT: Epiimmune Inc.

TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus

TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions

FILE REFERENCE: 2060.006007

CURRENT APPLICATION NUMBER: US/09/239,043D

CURRENT FILING DATE: 1999-01-27

PRIOR APPLICATION NUMBER: US 09/189,702

PRIOR FILING DATE: 1998-11-10

PRIOR APPLICATION NUMBER: US 08/978,291

PRIOR FILING DATE: 1997-11-25

PRIOR APPLICATION NUMBER: US 08/820,360

PRIOR FILING DATE: 1997-03-12

PRIOR APPLICATION NUMBER: US 60/013,363

PRIOR FILING DATE: 1996-03-13

PRIOR APPLICATION NUMBER: US 08/461,603

PRIOR FILING DATE: 1995-06-05

PRIOR APPLICATION NUMBER: US 08/347,610

PRIOR FILING DATE: 1994-12-01

PRIOR APPLICATION NUMBER: US 08/344,824

PRIOR FILING DATE: 1994-11-23

PRIOR APPLICATION NUMBER: US 08/278,634

PRIOR FILING DATE: 1994-07-21  
PRIOR APPLICATION NUMBER: US 08/205,713  
PRIOR FILING DATE: 1994-03-04  
PRIOR APPLICATION NUMBER: US 08/197,484  
PRIOR FILING DATE: 1994-02-16  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 2579  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 198  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Orthohepadnaviridae hepatitis B virus  
US-09-239-043D-198

Query Match 40.0%; Score 4; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EYLV 5  
DB 5 EYLV 8

RESULT 40  
US-09-239-043D-1346  
Sequence 1346, Application US/09239043D  
Patent No. 6689363  
GENERAL INFORMATION:  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Vitello, Maria A.  
APPLICANT: Livingston, Brian D.  
APPLICANT: Kubo, Esteban  
APPLICANT: Kubo, Ralph T.  
APPLICANT: Grey, Howard M.  
APPLICANT: Chesnut, Robert  
APPLICANT: Eptimmune Inc.  
TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus  
FILE REFERENCE: 2060.0060007  
CURRENT APPLICATION NUMBER: US/09/239,043D  
PRIORITY FILING DATE: 1999-01-27  
PRIORITY FILING DATE: 1999-01-27  
PRIORITY FILING DATE: 1998-11-10  
PRIORITY FILING DATE: 1997-11-25  
PRIORITY FILING DATE: 1997-11-25  
PRIORITY FILING DATE: 1997-03-12  
PRIORITY FILING DATE: 1997-03-12  
PRIORITY FILING DATE: 1996-03-13  
PRIORITY FILING DATE: 1995-06-05  
PRIORITY FILING DATE: 1994-12-01  
PRIORITY FILING DATE: 1994-12-01  
PRIORITY FILING DATE: 1994-11-23  
PRIORITY FILING DATE: 1994-07-21  
PRIORITY FILING DATE: 1994-07-21  
PRIORITY FILING DATE: 1994-03-04  
PRIORITY FILING DATE: 1994-03-04  
PRIORITY FILING DATE: 1994-02-16  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 2579  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 1346  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Orthohepadnaviridae hepatitis B virus  
US-09-239-043D-1346  
Query Match 40.0%; Score 4; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EYLV 5  
DB 5 EYLV 8

RESULT 41  
5196404-2  
Patent No. 5196404  
APPLICANT: MARGANORE, JOHN M., FENTON II, JOHN M., KLINE, TONI  
TITLE OF INVENTION: INHIBITORS OF THROMBIN  
NUMBER OF SEQUENCES: 18  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/549,388  
FILING DATE: 06-JUN-1990  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 395,482  
FILING DATE: 18-AUG-1989  
SEQ ID NO: 2  
LENGTH: 8  
5196404-2

Query Match 40.0%; Score 4; DB 6; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYLV 4  
DB 5 EYLV 8

RESULT 42  
US-08-467-083-23  
Sequence 23, Application US/08467083  
Patent No. 5726023  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
APPLICANT: Disis, Mary L.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN  
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Seed and Berry  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,083  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 424  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/414,417  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C2  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
TELEX: 3723836 SEEDANBERRY  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-467-083-23

Query Match 40.0%; Score 4; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred.No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EBYL 4  
|||  
DB 6 EBYL 9

RESULT 43  
US-08-414-417B-23

Sequence 23, Application US/08414417B  
Patent No. 5801005  
GENERAL INFORMATION:

APPLICANT: Cheever, Martin A.

TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN

TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
NUMBER OF SEQUENCES: 69  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/414,417B  
FILING DATE: 31-MAR-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Sharkey, Richard G.

REGISTRATION NUMBER: 32,629

REFERENCE/DOCKET NUMBER: 920010.448C2

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-414-417B-23

Query Match 40.0%; Score 4; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred.No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EBYL 4  
|||  
DB 6 EBYL 9

RESULT 44  
US-08-486-348A-23

Sequence 23, Application US/08486348A  
Patent No. 5846538  
GENERAL INFORMATION:

APPLICANT: Cheever, Martin A.

TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN

TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
NUMBER OF SEQUENCES: 69  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/468,348A  
FILING DATE: 06-JUN-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Sharkey, Richard G.

REGISTRATION NUMBER: 32,629

REFERENCE/DOCKET NUMBER: 920010.448C5

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-486-348A-23

Query Match 40.0%; Score 4; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred.No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EBYL 4  
|||  
DB 6 EBYL 9

RESULT 45  
US-08-468-545B-23

Sequence 23, Application US/08468545B  
Patent No. 5876712  
GENERAL INFORMATION:

APPLICANT: Cheever, Martin A.

TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN

TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
NUMBER OF SEQUENCES: 69  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/468,545B  
FILING DATE: 06-JUN-1995

TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED

NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:

ADDRESS: Seed and Berry LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: US

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/468,348A

FILING DATE: 07-JUN-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Sharkey, Richard G.

REGISTRATION NUMBER: 32,629

REFERENCE/DOCKET NUMBER: 920010.448C6

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-468-348A-23

Query Match 40.0%; Score 4; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred.No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EBYL 4  
|||  
DB 6 EBYL 9

RESULT 45  
US-08-468-545B-23

Sequence 23, Application US/08468545B  
Patent No. 5876712  
GENERAL INFORMATION:

APPLICANT: Cheever, Martin A.

TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN

TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
NUMBER OF SEQUENCES: 69  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/468,545B  
FILING DATE: 06-JUN-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Sharkey, Richard G.

REGISTRATION NUMBER: 32,629

REFERENCE/DOCKET NUMBER: 920010.448C5

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-468-545B-23

Query Match 40.0%; Score 4; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred.No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EBYL 4  
|||  
DB 6 EBYL 9

RESULT 45  
US-08-468-545B-23

Sequence 23, Application US/08468545B  
Patent No. 5876712  
GENERAL INFORMATION:

APPLICANT: Cheever, Martin A.

TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN

TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
NUMBER OF SEQUENCES: 69  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/468,545B  
FILING DATE: 06-JUN-1995

TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-468-545B-23

Query Match 40.0%; Score 4; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYL 4  
Db 6 EBYL 9

RESULT 46  
US-08-466-680B-23  
Sequence 23, Application US/08466680B

PATENT INFORMATION:  
PATENT NO. 6075122  
APPLICANT: Cheever, Martin A.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/466,680B  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-466-680B-23

Query Match 40.0%; Score 4; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYL 4  
Db 6 EBYL 9

RESULT 47  
US-09-692-170C-40  
Sequence 40, Application US/09692170C  
Patent No. 6562345  
GENERAL INFORMATION:

APPLICANT: Diamond, Don J.  
TITLE OF INVENTION: IMMUNO-REACTIVE PEPTIDE CTL EPITOPES OF HUMAN CYTOMEGALOVIRUS  
FILE REFERENCE: 1954-346  
CURRENT APPLICATION NUMBER: US/09/692,170C  
CURRENT FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: US 09/534,639  
PRIOR FILING DATE: 2000-03-27  
PRIOR APPLICATION NUMBER: US 09/075,257  
PRIOR FILING DATE: 1998-05-11  
PRIOR APPLICATION NUMBER: US 09/021,298  
PRIOR FILING DATE: 1998-02-10  
PRIOR APPLICATION NUMBER: US 08/950,064  
PRIOR FILING DATE: 1997-10-14  
PRIOR APPLICATION NUMBER: US 08/747,488  
PRIOR FILING DATE: 1996-11-12  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 40  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: Amidated variant human cytomegalovirus peptide epitope  
NAME/KEY: MOD RRS  
LOCATION: (9)-(9)  
OTHER INFORMATION: AMIDATION  
US-09-692-170C-40

Query Match 40.0%; Score 4; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLVP 6  
Db 1 YLVP 4

RESULT 48  
US-09-692-170C-41  
Sequence 41, Application US/09692170C  
Patent No. 6562345  
GENERAL INFORMATION:  
APPLICANT: Diamond, Don J.  
TITLE OF INVENTION: IMMUNO-REACTIVE PEPTIDE CTL EPITOPES OF HUMAN CYTOMEGALOVIRUS  
FILE REFERENCE: 1954-346  
CURRENT APPLICATION NUMBER: US/09/692,170C  
CURRENT FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: US 09/534,639  
PRIOR FILING DATE: 2000-03-27  
PRIOR APPLICATION NUMBER: US 09/075,257  
PRIOR FILING DATE: 1998-05-11  
PRIOR APPLICATION NUMBER: US 09/021,298  
PRIOR FILING DATE: 1998-02-10  
PRIOR APPLICATION NUMBER: US 08/950,064  
PRIOR FILING DATE: 1997-10-14  
PRIOR APPLICATION NUMBER: US 08/747,488  
PRIOR FILING DATE: 1996-11-12  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 41  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: Amidated variant human cytomegalovirus peptide epitope  
NAME/KEY: MOD RRS  
LOCATION: (9)-(9)  
OTHER INFORMATION: AMIDATION  
US-09-692-170C-41

Query Match 40.0%; Score 4; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 YLVP 4

Search completed: January 18, 2006, 21.07.29  
Job time : 46 secs

QY 3 YLVP 6  
1 YLVP 4

RESULT 49

US-09-692-325-37  
; Sequence 37, Application US/09692325  
; Patent No. 6632435  
; GENERAL INFORMATION:  
; APPLICANT: Diamond, Don  
; TITLE OF INVENTION: CTL Epitope Analogs  
; FILE REFERENCE: 1954-314  
; CURRENT APPLICATION NUMBER: US/09/692,325  
; CURRENT FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: US 60/160633  
; PRIOR FILING DATE: 1999-10-20  
; PRIOR APPLICATION NUMBER: US 60/187871  
; NUMBER OF SEQ ID NOS: 78  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 37  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: HCMV vaccine peptide  
; NAME/KEY: MOD\_RES  
; LOCATION: (9)..(9)  
; OTHER INFORMATION: AMIDATION  
US-09-692-325-37

Query Match 40.0%; Score 4; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLVP 6  
1 YLVP 4

RESULT 50

US-09-692-325-38  
; Sequence 38, Application US/09692325  
; Patent No. 6632435  
; GENERAL INFORMATION:  
; APPLICANT: Diamond, Don  
; TITLE OF INVENTION: CTL Epitope Analogs  
; FILE REFERENCE: 1954-314  
; CURRENT APPLICATION NUMBER: US/09/692,325  
; CURRENT FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: US 60/160633  
; PRIOR FILING DATE: 1999-10-20  
; PRIOR APPLICATION NUMBER: US 60/187871  
; PRIOR FILING DATE: 2000-03-08  
; NUMBER OF SEQ ID NOS: 78  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 38  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: HCMV vaccine peptide  
US-09-692-325-38

Query Match 40.0%; Score 4; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLVP 6



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 18, 2006, 20:56:58 ; Search time 157 Seconds  
(without alignments)  
44.938 Million cell updates/sec

Title: US-09-930-125-3

Perfect score: 10

Sequence: 1 BEEYLPQGGF 10

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3063

Minimum DB seq length: 0  
Maximum DB seq length: 10

Post-processing: Listing first 200 summaries

Database : UniProt 05.80:\*

1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description   |
|------------|-------|-------------|--------|-------|---------------|
| 1          | 3     | 30.0        | 7      | 1     | PAP2_ASCSU    |
| 2          | 3     | 30.0        | 7      | 1     | PAP2_PANRE    |
| 3          | 3     | 30.0        | 8      | 1     | LCK3_LEUMA    |
| 4          | 3     | 30.0        | 8      | 1     | PPK3_PPRAM    |
| 5          | 3     | 30.0        | 8      | 2     | Q83332_GCCORO |
| 6          | 3     | 30.0        | 9      | 1     | FAR1_CALVO    |
| 7          | 3     | 30.0        | 9      | 1     | UPAT_HUMAN    |
| 8          | 3     | 30.0        | 9      | 2     | P78484_HUMAN  |
| 9          | 3     | 30.0        | 10     | 1     | GPCR_MOUSE    |
| 10         | 3     | 30.0        | 10     | 2     | Q8WGD2_9EUBCA |
| 11         | 3     | 30.0        | 10     | 2     | Q7MIF6_9POLA  |
| 12         | 3     | 30.0        | 10     | 2     | Q7MIF7_9POLA  |
| 13         | 3     | 30.0        | 10     | 2     | Q8L7F5_HEYBR  |
| 14         | 3     | 30.0        | 10     | 2     | Q53VQ3_MOUSE  |
| 15         | 3     | 30.0        | 10     | 2     | Q53VQ7_MOUSE  |
| 16         | 3     | 30.0        | 10     | 2     | Q53VRI_MOUSE  |
| 17         | 3     | 30.0        | 10     | 2     | Q83978_9INPA  |
| 18         | 2     | 20.0        | 4      | 1     | ACR1_ACFU     |
| 19         | 2     | 20.0        | 4      | 1     | PARG_HIRME    |
| 20         | 2     | 20.0        | 4      | 1     | OCPI_OCTMI    |
| 21         | 2     | 20.0        | 5      | 1     | PAP2_PPRAM    |
| 22         | 2     | 20.0        | 5      | 1     | PRCT_CARMA    |
| 23         | 2     | 20.0        | 5      | 1     | PRCT_LIMO     |
| 24         | 2     | 20.0        | 5      | 1     | PRCT_PPRAM    |
| 25         | 2     | 20.0        | 5      | 1     | RB33_LITRU    |
| 26         | 2     | 20.0        | 5      | 1     | TRAM3_ECOLI   |
| 27         | 2     | 20.0        | 6      | 1     | ASP2_LACSN    |
| 28         | 2     | 20.0        | 6      | 1     | E101_LITRU    |
| 29         | 2     | 20.0        | 7      | 1     | ASCL_ALTAS    |
| 30         | 2     | 20.0        | 7      | 1     | CAP6_CANAL    |
| 31         | 2     | 20.0        | 7      | 1     | CCP1_BMTFA    |

|     |   |      |   |   |                |                     |
|-----|---|------|---|---|----------------|---------------------|
| 32  | 2 | 20.0 | 7 | 1 | TPPY_PACDA     | P83455 pachymedusa  |
| 33  | 2 | 20.0 | 7 | 1 | UP03_MOUSE     | P38641 mus musculus |
| 34  | 2 | 20.0 | 7 | 1 | UH11_RAT       | P56576 rattus norv  |
| 35  | 2 | 20.0 | 7 | 2 | Q8NHH7_HUMAN   | Q8NHH7 homo sapien  |
| 36  | 2 | 20.0 | 7 | 2 | Q28742_RABIT   | Q28742 oryctolagus  |
| 37  | 2 | 20.0 | 7 | 2 | P93233_LYCES   | P93233 lycopersico  |
| 38  | 2 | 20.0 | 7 | 2 | Q9C5B3_ARATH   | Q9C5B3 arabidopsis  |
| 39  | 2 | 20.0 | 7 | 2 | Q8RMS9_ZENTR   | Q8RMS9 enterobacte  |
| 40  | 2 | 20.0 | 7 | 2 | Q07354_SYNP8   | Q07354 synechococc  |
| 41  | 2 | 20.0 | 7 | 2 | O54248_STRGR   | O54248 streptomyce  |
| 42  | 2 | 20.0 | 7 | 2 | Q8K3H6_RAT     | Q8K3H6 rattus norv  |
| 43  | 2 | 20.0 | 7 | 2 | Q9YQ10_GCCORO  | Q9YQ10 transmiesib  |
| 44  | 2 | 20.0 | 7 | 2 | O42564_FUGRU   | O42564 fugu rubrip  |
| 45  | 2 | 20.0 | 7 | 2 | Q8JEB1_9HIV1   | Q8JEB1 human immu   |
| 46  | 2 | 20.0 | 8 | 1 | CAD1_ENTFA     | P13368 enterococcu  |
| 47  | 2 | 20.0 | 8 | 1 | CAP4_CANAL     | P83781 candida alb  |
| 48  | 2 | 20.0 | 8 | 1 | CPD1_BMTFA     | P13369 enterococcu  |
| 49  | 2 | 20.0 | 8 | 1 | DY54_LAMSA     | P82082 limodryast   |
| 50  | 2 | 20.0 | 8 | 1 | FUSP_FUSSO     | P81010 fusarium bo  |
| 51  | 2 | 20.0 | 8 | 1 | LCK2_LEUMA     | P81010 leucophanea  |
| 52  | 2 | 20.0 | 8 | 1 | LCK3_LEUMA     | P19987 leucophanea  |
| 53  | 2 | 20.0 | 8 | 1 | NPM8_BOVIN     | P15507 bos taurus   |
| 54  | 2 | 20.0 | 8 | 1 | ORNY_ORCLT     | P82455 orconectes   |
| 55  | 2 | 20.0 | 8 | 1 | UPAT_HUMAN     | P30087 homo sapien  |
| 56  | 2 | 20.0 | 8 | 1 | VAM6L_MOUSE    | P83853 mus musculu  |
| 57  | 2 | 20.0 | 8 | 1 | VGLG_HIV2B     | P81780 human herpe  |
| 58  | 2 | 20.0 | 8 | 2 | P87225_YEAST   | P87225 saccharomyc  |
| 59  | 2 | 20.0 | 8 | 2 | Q9HDS4_ASPFL   | Q9HDS4 aspergillus  |
| 60  | 2 | 20.0 | 8 | 2 | Q15888_HUMAN   | Q15888 homo sapien  |
| 61  | 2 | 20.0 | 8 | 2 | Q15894_HUMAN   | Q15894 homo sapien  |
| 62  | 2 | 20.0 | 8 | 2 | Q15895_HUMAN   | Q15895 homo sapien  |
| 63  | 2 | 20.0 | 8 | 2 | Q29797_HUMAN   | Q29797 homo sapien  |
| 64  | 2 | 20.0 | 8 | 2 | Q29801_HUMAN   | Q29801 homo sapien  |
| 65  | 2 | 20.0 | 8 | 2 | Q29810_HUMAN   | Q29810 homo sapien  |
| 66  | 2 | 20.0 | 8 | 2 | Q29812_HUMAN   | Q29812 homo sapien  |
| 67  | 2 | 20.0 | 8 | 2 | Q59AB6_HUMAN   | Q59AB6 homo sapien  |
| 68  | 2 | 20.0 | 8 | 2 | Q52EY7_HUMAN   | Q52EY7 homo sapien  |
| 69  | 2 | 20.0 | 8 | 2 | Q6BCZ9_HUMAN   | Q6BCZ9 homo sapien  |
| 70  | 2 | 20.0 | 8 | 2 | Q583U9_HUMAN   | Q583U9 homo sapien  |
| 71  | 2 | 20.0 | 8 | 2 | Q9HCQ0_HUMAN   | Q9HCQ0 homo sapien  |
| 72  | 2 | 20.0 | 8 | 2 | Q15899_BABOV   | Q15899 babesia ovi  |
| 73  | 2 | 20.0 | 8 | 2 | Q6U0R5_PARKI   | Q6U0R5 patencitroc  |
| 74  | 2 | 20.0 | 8 | 2 | Q7M4C7_PSEMC   | Q7M4C7 pseudobole   |
| 75  | 2 | 20.0 | 8 | 2 | Q8W8G2_DIASA   | Q8W8G2 diadema pau  |
| 76  | 2 | 20.0 | 8 | 2 | Q8W8G3_9EICHN  | Q8W8G3 diadema mex  |
| 77  | 2 | 20.0 | 8 | 2 | Q8W8G4_9EICHN  | Q8W8G4 diadema ant  |
| 78  | 2 | 20.0 | 8 | 2 | Q8W8G5_9EICHN  | Q8W8G5 diadema mex  |
| 79  | 2 | 20.0 | 8 | 2 | Q8W8G6_9EICHN  | Q8W8G6 diadema mex  |
| 80  | 2 | 20.0 | 8 | 2 | Q8W8G7_9EICHN  | Q8W8G7 diadema mex  |
| 81  | 2 | 20.0 | 8 | 2 | Q8W8G8_9EICHN  | Q8W8G8 diadema mex  |
| 82  | 2 | 20.0 | 8 | 2 | Q8W8G9_9EICHN  | Q8W8G9 diadema mex  |
| 83  | 2 | 20.0 | 8 | 2 | Q8W8G10_9EICHN | Q8W8G10 diadema mex |
| 84  | 2 | 20.0 | 8 | 2 | Q8W8G11_9EICHN | Q8W8G11 diadema mex |
| 85  | 2 | 20.0 | 8 | 2 | Q8W8G12_9EICHN | Q8W8G12 diadema mex |
| 86  | 2 | 20.0 | 8 | 2 | Q8W8G13_9EICHN | Q8W8G13 diadema mex |
| 87  | 2 | 20.0 | 8 | 2 | Q8W8G14_9EICHN | Q8W8G14 diadema mex |
| 88  | 2 | 20.0 | 8 | 2 | Q8W8G15_9EICHN | Q8W8G15 diadema mex |
| 89  | 2 | 20.0 | 8 | 2 | Q8W8G16_9EICHN | Q8W8G16 diadema mex |
| 90  | 2 | 20.0 | 8 | 2 | Q8W8G17_9EICHN | Q8W8G17 diadema mex |
| 91  | 2 | 20.0 | 8 | 2 | Q8W8G18_9EICHN | Q8W8G18 diadema mex |
| 92  | 2 | 20.0 | 8 | 2 | Q8W8G19_9EICHN | Q8W8G19 diadema mex |
| 93  | 2 | 20.0 | 8 | 2 | Q8W8G20_9EICHN | Q8W8G20 diadema mex |
| 94  | 2 | 20.0 | 8 | 2 | Q8W8G21_9EICHN | Q8W8G21 diadema mex |
| 95  | 2 | 20.0 | 8 | 2 | Q8W8G22_9EICHN | Q8W8G22 diadema mex |
| 96  | 2 | 20.0 | 8 | 2 | Q8W8G23_9EICHN | Q8W8G23 diadema mex |
| 97  | 2 | 20.0 | 8 | 2 | Q8W8G24_9EICHN | Q8W8G24 diadema mex |
| 98  | 2 | 20.0 | 8 | 2 | Q8W8G25_9EICHN | Q8W8G25 diadema mex |
| 99  | 2 | 20.0 | 8 | 2 | Q8W8G26_9EICHN | Q8W8G26 diadema mex |
| 100 | 2 | 20.0 | 8 | 2 | Q8W8G27_9EICHN | Q8W8G27 diadema mex |
| 101 | 2 | 20.0 | 8 | 2 | Q8W8G28_9EICHN | Q8W8G28 diadema mex |
| 102 | 2 | 20.0 | 8 | 2 | Q8W8G29_9EICHN | Q8W8G29 diadema mex |
| 103 | 2 | 20.0 | 8 | 2 | Q8W8G30_9EICHN | Q8W8G30 diadema mex |
| 104 | 2 | 20.0 | 8 | 2 | Q8W8G31_9EICHN | Q8W8G31 diadema mex |

|     |   |      |   |   |              |                    |     |   |      |   |   |              |                    |
|-----|---|------|---|---|--------------|--------------------|-----|---|------|---|---|--------------|--------------------|
| 105 | 2 | 20.0 | 8 | 2 | 09T2Y3_9ROSI | 09E2Y3 begonia for | 178 | 2 | 20.0 | 9 | 2 | 071EB9_HUMAN | 071EB9 homo sapien |
| 106 | 2 | 20.0 | 8 | 2 | 09TMA4_9ROSI | 09E2M4 begonia for | 179 | 2 | 20.0 | 9 | 2 | 081U05_HUMAN | 081U05 homo sapien |
| 107 | 2 | 20.0 | 8 | 2 | 09XGL8_9ROSI | 09XGL8 begonia chi | 180 | 2 | 20.0 | 9 | 2 | 099887_HUMAN | 099887 homo sapien |
| 108 | 2 | 20.0 | 8 | 2 | 09XGL9_9ROSI | 09XGL9 begonia nan | 181 | 2 | 20.0 | 9 | 2 | 09UCN5_HUMAN | 09UCN5 homo sapien |
| 109 | 2 | 20.0 | 8 | 2 | 06Z201_SILCO | 06Z201 siene conti | 182 | 2 | 20.0 | 9 | 2 | 09UCQ9_HUMAN | 09UCQ9 homo sapien |
| 110 | 2 | 20.0 | 8 | 2 | 056140_STYTR | 056140 streptococc | 183 | 2 | 20.0 | 9 | 2 | 09UCS8_HUMAN | 09UCS8 homo sapien |
| 111 | 2 | 20.0 | 8 | 2 | P83532_LACSN | P83532 lactobacill | 184 | 2 | 20.0 | 9 | 2 | 09UK44_HUMAN | 09UK44 homo sapien |
| 112 | 2 | 20.0 | 8 | 2 | 079CX6_MYXSA | 079CX6 myxococcus  | 185 | 2 | 20.0 | 9 | 2 | 053VS2_HUMAN | 053VS2 homo sapien |
| 113 | 2 | 20.0 | 8 | 2 | 07X405_NODSP | 07X405 nodularia s | 186 | 2 | 20.0 | 9 | 2 | 04UMF3_HUMAN | 04UMF3 homo sapien |
| 114 | 2 | 20.0 | 8 | 2 | 09R4M3_ENTRA | 09R4M3 enterococcu | 187 | 2 | 20.0 | 9 | 2 | 04PIZ7_HUMAN | 04PIZ7 homo sapien |
| 115 | 2 | 20.0 | 8 | 2 | 09RQ49_9ENTR | 09RQ49 buchnera ap | 188 | 2 | 20.0 | 9 | 2 | P92072_PPUTM | P92072 euhadra her |
| 116 | 2 | 20.0 | 8 | 2 | 09RQ57_9ENTR | 09RQ57 buchnera ap | 189 | 2 | 20.0 | 9 | 2 | 07M3L3_PENVA | 07M3L3 penaeus van |
| 117 | 2 | 20.0 | 8 | 2 | 09X3K1_9PROC | 09X3K1 pichloroco  | 190 | 2 | 20.0 | 9 | 2 | 07M471_VESOR | 07M471 vespa orien |
| 118 | 2 | 20.0 | 8 | 2 | 056429_THETH | 056429 thermus the | 191 | 2 | 20.0 | 9 | 2 | 08WSS8_LEPDE | 08WSS8 lepidotars  |
| 119 | 2 | 20.0 | 8 | 2 | 076DX6_RAT   | 076DX6 rattus norv | 192 | 2 | 20.0 | 9 | 2 | 09TW06_LEPDE | 09TW06 lepidotars  |
| 120 | 2 | 20.0 | 8 | 2 | 07M032_RAT   | 07M032 rattus norv | 193 | 2 | 20.0 | 9 | 2 | 09TWX7_MANSE | 09TWX7 manduca sex |
| 121 | 2 | 20.0 | 8 | 2 | 07M039_RAT   | 07M039 rattus norv | 194 | 2 | 20.0 | 9 | 2 | 07RCI3_PLAYO | 07RCI3 plasmodium  |
| 122 | 2 | 20.0 | 8 | 2 | 07M041_RAT   | 07M041 rattus norv | 195 | 2 | 20.0 | 9 | 2 | 08W8W5_DIASZ | 08W8W5 didema set  |
| 123 | 2 | 20.0 | 8 | 2 | 08CJ03_MOUSE | 08CJ03 mus musculi | 196 | 2 | 20.0 | 9 | 2 | 08W8W6_9ECHN | 08W8W6 didema ant  |
| 124 | 2 | 20.0 | 8 | 2 | 099P40_MOUSE | 099P40 mus musculi | 197 | 2 | 20.0 | 9 | 2 | 08W8X4_9ECHN | 08W8X4 diadema mex |
| 125 | 2 | 20.0 | 8 | 2 | 09RT21_MOUSE | 09RT21 mus musculi | 198 | 2 | 20.0 | 9 | 2 | 08WFS4_9ECHN | 08WFS4 diadema mex |
| 126 | 2 | 20.0 | 8 | 2 | 09RTU6_MOUSE | 09RTU6 mus musculi | 199 | 2 | 20.0 | 9 | 2 | 08WFT4_9ECHN | 08WFT4 diadema ant |
| 127 | 2 | 20.0 | 8 | 2 | 06Z527_MOSSP | 06Z527 mus spretus | 200 | 2 | 20.0 | 9 | 2 | 04Y9N3_PLABE | 04Y9N3 plasmodium  |

## ALIGNMENTS

RESULT 1  
ID FAF2\_ASCSU STANDARD; PRT; 7 AA.  
FAF2\_ASCSU

AC P67879; P31890; PubMed=8332542; DOI=10.1016/0196-9781(93)90127-3;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-JUL-1993 (Rel. 26, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE FMRFamide-like neuropeptide AP2.  
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoideae).  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascarididae; Ascaridoidea;  
OC Ascarididae; Ascaridae.  
OX NCBI\_TaxID=6253;  
RN [1]

RP PROTEIN SEQUENCE.  
RX MEDLINE=93324431; PubMed=8332542; DOI=10.1016/0196-9781(93)90127-3;  
RA Cowden C., Stretton A.O.W.;  
RT "AP2, an Ascaris neuropeptide: isolation, sequence, and bioactivity.";  
RL Peptides 14:423-430(1993).  
CC -|- FUNCTION: Has effects on muscle tension.  
CC -|- SUBCELLULAR LOCATION: Secreted.  
CC -|- TISSUE SPECIFICITY: Found in the nerve cords and a variety of ganglia particularly in the anterior regions.  
CC -|- SIMILARITY: Belongs to the FAPF (FMRFamide related peptide) family.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

CC Amiation; Direct protein sequencing; Neuropeptide.  
KW MOD RES 7 Phenylalanine amide.  
SQ SEQUENCE 7 AA; 992 MW; 69D4073B5B1BE50 CRC64;

Query Match 30.0%; Score 3; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EYL 4  
|||  
Db 3 EYL 5

RESULT 2

|     |   |      |   |   |              |                     |
|-----|---|------|---|---|--------------|---------------------|
| 105 | 2 | 20.0 | 8 | 2 | 09T2Y3_9ROSI | 09E2Y3 begonia for  |
| 106 | 2 | 20.0 | 8 | 2 | 09TMA4_9ROSI | 09E2M4 begonia for  |
| 107 | 2 | 20.0 | 8 | 2 | 09XGL8_9ROSI | 09XGL8 begonia chi  |
| 108 | 2 | 20.0 | 8 | 2 | 09XGL9_9ROSI | 09XGL9 begonia nan  |
| 109 | 2 | 20.0 | 8 | 2 | 06Z201_SILCO | 06Z201 siene conti  |
| 110 | 2 | 20.0 | 8 | 2 | 056140_STYTR | 056140 streptococc  |
| 111 | 2 | 20.0 | 8 | 2 | P83532_LACSN | P83532 lactobacill  |
| 112 | 2 | 20.0 | 8 | 2 | 079CX6_MYXSA | 079CX6 myxococcus   |
| 113 | 2 | 20.0 | 8 | 2 | 07X405_NODSP | 07X405 nodularia s  |
| 114 | 2 | 20.0 | 8 | 2 | 09R4M3_ENTRA | 09R4M3 enterococcu  |
| 115 | 2 | 20.0 | 8 | 2 | 09RQ49_9ENTR | 09RQ49 buchnera ap  |
| 116 | 2 | 20.0 | 8 | 2 | 09RQ57_9ENTR | 09RQ57 buchnera ap  |
| 117 | 2 | 20.0 | 8 | 2 | 09X3K1_9PROC | 09X3K1 pichloroco   |
| 118 | 2 | 20.0 | 8 | 2 | 056429_THETH | 056429 thermus the  |
| 119 | 2 | 20.0 | 8 | 2 | 076DX6_RAT   | 076DX6 rattus norv  |
| 120 | 2 | 20.0 | 8 | 2 | 07M032_RAT   | 07M032 rattus norv  |
| 121 | 2 | 20.0 | 8 | 2 | 07M039_RAT   | 07M039 rattus norv  |
| 122 | 2 | 20.0 | 8 | 2 | 07M041_RAT   | 07M041 rattus norv  |
| 123 | 2 | 20.0 | 8 | 2 | 08CJ03_MOUSE | 08CJ03 mus musculi  |
| 124 | 2 | 20.0 | 8 | 2 | 099P40_MOUSE | 099P40 mus musculi  |
| 125 | 2 | 20.0 | 8 | 2 | 09RT21_MOUSE | 09RT21 mus musculi  |
| 126 | 2 | 20.0 | 8 | 2 | 09RTU6_MOUSE | 09RTU6 mus musculi  |
| 127 | 2 | 20.0 | 8 | 2 | 06Z527_MOSSP | 06Z527 mus spretus  |
| 128 | 2 | 20.0 | 8 | 2 | 083977_9INFA | 083977 influenza a  |
| 129 | 2 | 20.0 | 8 | 2 | 083349_9COCO | 083349 murine hepa  |
| 130 | 2 | 20.0 | 8 | 2 | 089498_9COCO | 089498 murine hepa  |
| 131 | 2 | 20.0 | 8 | 2 | 05Y8D4_ONCMY | 05Y8D4 oncorhynch   |
| 132 | 2 | 20.0 | 8 | 2 | 068LFL_9PASS | 068LFL mymocheuti   |
| 133 | 2 | 20.0 | 8 | 2 | 068LGL_9PASS | 068LGL sakesphorus  |
| 134 | 2 | 20.0 | 8 | 2 | 06R7U6_9SAUR | 06R7U6 gnyptococin  |
| 135 | 2 | 20.0 | 8 | 2 | 08UJ35_9PASS | 08UJ35 flicedula hy |
| 136 | 2 | 20.0 | 8 | 2 | 090ZV5_9GRUI | 090ZV5 fulica leuc  |
| 137 | 2 | 20.0 | 8 | 2 | 094V82_9SAUR | 094V82 varanus yuw  |
| 138 | 2 | 20.0 | 8 | 2 | 094VA7_9SAUR | 094VA7 varanus sal  |
| 139 | 2 | 20.0 | 8 | 2 | 094VB2_9SAUR | 094VB2 varanus sal  |
| 140 | 2 | 20.0 | 8 | 2 | 094VB5_9SAUR | 094VB5 varanus sal  |
| 141 | 2 | 20.0 | 9 | 1 | ALU10_CARMA  | P81813 carcinus ma  |
| 142 | 2 | 20.0 | 9 | 1 | BRK1_RANMI   | Q71254 rana nigrom  |
| 143 | 2 | 20.0 | 9 | 1 | CABR_PHYSA   | Q71AC4 phyllomedus  |
| 144 | 2 | 20.0 | 9 | 1 | CB22_SPIOI   | 09C2K9 spinacia ol  |
| 145 | 2 | 20.0 | 9 | 1 | CK6AI_THUOB  | P80975 thunnus obe  |
| 146 | 2 | 20.0 | 9 | 1 | FARS_PANRE   | P82661 panagrellus  |
| 147 | 2 | 20.0 | 9 | 1 | FARD_CALVO   | P41868 calliphora   |
| 148 | 2 | 20.0 | 9 | 1 | FIBB_EERYA   | P19346 erythrocebu  |
| 149 | 2 | 20.0 | 9 | 1 | FIBB_MACFU   | P19345 macaca fusc  |
| 150 | 2 | 20.0 | 9 | 1 | FLAA2_TREHY  | P80159 trepomena h  |
| 151 | 2 | 20.0 | 9 | 1 | KMT3_BOMVA   | P83058 bombina var  |
| 152 | 2 | 20.0 | 9 | 1 | KMT3_CYPDO   | P83659 cyphononyx   |
| 153 | 2 | 20.0 | 9 | 1 | LITO_LITAO   | P08945 litorea aur  |
| 154 | 2 | 20.0 | 9 | 1 | LMT3_LOCM1   | P41489 locusta mig  |
| 155 | 2 | 20.0 | 9 | 1 | OXYT_RAJICL  | P42994 raja clavata |
| 156 | 2 | 20.0 | 9 | 1 | PKK1_PERAM   | P82691 periplaneta  |
| 157 | 2 | 20.0 | 9 | 1 | PKY2_SARBU   | P84353 sarcophaga   |
| 158 | 2 | 20.0 | 9 | 1 | RHG_RAT      | P84107 rattus norv  |
| 159 | 2 | 20.0 | 9 | 1 | SAMF_MOSCA   | P19095 muscelus ca  |
| 160 | 2 | 20.0 | 9 | 1 | THYF_PIG     | P01255 sus scrofa   |
| 161 | 2 | 20.0 | 9 | 1 | TKL1_LOCM1   | P16223 locusta mig  |
| 162 | 2 | 20.0 | 9 | 1 | TRP4_LEUMA   | P81736 leucophaea   |
| 163 | 2 | 20.0 | 9 | 1 | UHA2_HUMAN   | P40929 homo sapien  |
| 164 | 2 | 20.0 | 9 | 1 | ULAD_HUMAN   | P31929 homo sapien  |
| 165 | 2 | 20.0 | 9 | 1 | ULAD_HUMAN   | P31934 homo sapien  |
| 166 | 2 | 20.0 | 9 | 2 | Q7RYB9_NEUCR | Q7RYB9 neurospora   |
| 167 | 2 | 20.0 | 9 | 2 | Q7S182_NEUCR | Q7S182 neurospora   |
| 168 | 2 | 20.0 | 9 | 2 | Q9P8E5_KLULA | Q9P8E5 kluyveromyc  |
| 169 | 2 | 20.0 | 9 | 2 | Q9S9S3_HUMAN | Q9S9S3 homo sapien  |
| 170 | 2 | 20.0 | 9 | 2 | Q16220_HUMAN | Q16220 homo sapien  |
| 171 | 2 | 20.0 | 9 | 2 | Q5QEX9_HUMAN | Q5QEX9 homo sapien  |
| 172 | 2 | 20.0 | 9 | 2 | Q67A07_HUMAN | Q67A07 homo sapien  |
| 173 | 2 | 20.0 | 9 | 2 | Q67AR4_HUMAN | Q67AR4 homo sapien  |
| 174 | 2 | 20.0 | 9 | 2 | Q67AR6_HUMAN | Q67AR6 homo sapien  |
| 175 | 2 | 20.0 | 9 | 2 | Q67AR7_HUMAN | Q67AR7 homo sapien  |
| 176 | 2 | 20.0 | 9 | 2 | Q67AT1_HUMAN | Q67AT1 homo sapien  |
| 177 | 2 | 20.0 | 9 | 2 | Q67AT2_HUMAN | Q67AT2 homo sapien  |

FAF2\_PANRE STANDARD; PRT; 7 AA.

AC P67880; P31890; (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE FMRamide-like neuropeptide Af2.

OS Pangrelus redivivus.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;

OC Pangrolaimidae; Pangrolaimidae; Pangrelus.

OX NCBI\_TaxId=6233;

RN [1]

RP PROTEIN SEQUENCE.

RX MEDLINE=95060998; PubMed=7970891;

RA Maule A.G., Shaw C., Bowman J.W.;

RT "The FMRamide-like neuropeptide Af2 (*Ascaris suum*) is present in the free-living nematode, *Pangrelus redivivus* (Nematoda, Rhabditida).";

RL Parasitology 109:351-356(1994).

CC -1- FUNCTION: Has effects on muscle tension.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: Found in the nerve cords and a variety of ganglia particularly in the anterior regions.

CC -1- SIMILARITY: Belongs to the FAPR (FMRamide related peptide) family.

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CC

KM Amidation; Direct protein sequencing; Neuropeptide.

FT MOD RES 7 Phenylalanine amide.

FT SEQUENCE 7 AA; 992 MW; 69D4073B5B11E350 CRC64;

SO

Query Match 30.0%; Score 3; DB 1; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.2e+06;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 EYL 4

DB 3 EYL 5

-----

RESULT 3

LCK3\_LEUMA STANDARD; PRT; 8 AA.

ID LCK3 LEUMA (Rel. 18, Created)

DT 01-MAY-1991 (Rel. 18, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Leucokinin-3 (leucokinin III) (L-III).

OS Leucophaea maderae (Maderia cockroach).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberodea;

OC Blaberidae; Leucophaea.

OX NCBI\_TaxId=6988;

RN [1]

RP PROTEIN SEQUENCE, AND SYNTHESIS.

RC TISSUE=Head;

RA Holman G.M., Cook B.J., Nachman R.J.;

RT "Primary structure and synthesis of two additional neuropeptides from *Leucophaea maderae*: members of a new family of Cephalomyotopsins.";

RL Comp. Biochem. Physiol. 84C:271-276(1986).

CC -1- FUNCTION: This cephalomyotopic peptide stimulates contractile activity of cockroach proodeum (hindgut).

CC -1- SUBCELLULAR LOCATION: Secreted.

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CC

KM Amidation; Direct protein sequencing; Neuropeptide.

FT MOD RES 8 Glycine amide.

FT SEQUENCE 8 AA; 910 MW; DC6365B449C866DA CRC64;

SO

Query Match 30.0%; Score 3; DB 1; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.2e+06;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 OGF 10

DB 2 OGF 4

-----

RESULT 4

PPK3\_PPRAM STANDARD; PRT; 8 AA.

ID PPK3\_PPRAM (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Pyrokinin-3 (Pea-PK-3) (PXPL-amide).

OS Periplaneta americana (American cockroach).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;

OC Blattidae; Blattinae; Periplaneta.

OX NCBI\_TaxId=6978;

RN [1]

RP PROTEIN SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.

RC TISSUE=Retrocerebral complex;

RX MEDLINE=99212469; PubMed=10196736; DOI=10.1016/S0965-1748(98)00117-9;

RA Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede G.;

RT "Differential distribution of pyrokinin-isoforms in cerebral and abdominal neuromal organs of the American cockroach.";

RL Insect Biochem. Mol. Biol. 29:139-144(1999).

RN [2]

RP TISSUE SPECIFICITY.

RX MEDLINE=20189894; PubMed=10723010;

RA Predel R., Eckert M.;

RT "Tagma-specific distribution of FxPRlamides in the nervous system of the American cockroach.";

RL J. Comp. Neurol. 419:352-363(2000).

CC -1- FUNCTION: Mediates visceral muscle contractile activity (myotrophic activity).

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: Corpora cardiaca.

CC -1- MASS SPECTROMETRY: MW=996.5; METHOD=MALDI; RANGE=1-8; NOTE=Ref.1.

CC -1- SIMILARITY: Belongs to the pyrokinin family.

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CC

DR InterPro: IPR001484; Pyrokinin.

DR PROSITE: PS00539; PYROKININ; FALSE NEG.

KM Amidation; Direct protein sequencing; Neuropeptide; Pyrokinin.

FT MOD RES 8 Leucine amide.

FT SEQUENCE 8 AA; 997 MW; 0B34177409D772C7 CRC64;

SO

Query Match 30.0%; Score 3; DB 1; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.2e+06;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 LVP 6

DB 1 LVP 3

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RESULT 5

Q83332\_9CORO PRELIMINARY; PRT; 8 AA.

ID Q83332\_9CORO PRELIMINARY;

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AC 083332;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE HE (Fragment).
OS Murine hepatitis virus.
CC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
CC Coronaviridae; Coronavirus; Group 2 species.
CX NCBI_TaxID=11138;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=JHM;
RX MEDLINE=95191005; PubMed=7884877;
RA Kim K.H., Makino S.;
RT "Two murine coronavirus genes suffice for viral RNA synthesis.";
RL J. Virol. 69:2313-2321(1995).
DR EMBL; U19933; AAA69002.1; -; Genomic_RNA.
FT NON_TER
FT NON_TER
SQ SEQUENCE 8 AA; 907 MW; 922735B1735A2CD CRC64;

Query Match 30.0%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EYL 4
DB 5 EYL 7

RESULT 6
FBI1 CALVO STANDARD; PRT; 9 AA.
ID P41856;
AC 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE CallifMRamide 1.
OS Calliphora vomitoria (Blue blowfly).
CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
CC Calliphoridae; Calliphora.
CX NCBI_TaxID=27454;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated callifMRamides) from the blowfly Calliphora
RT vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -1- FUNCTION: Able to induce fluid secretion from the isolated
CC salivary gland of Calliphora.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the PARP (FMRamide related peptide)
CC family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; A41978; A41978.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RES 9 Phenylalanine amide.
FT SEQUENCE 9 AA; 1169 MW; 29D00699CAB6C6C7 CRC64;

Query Match 30.0%; Score 3; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 6 PQQ 8
DB 2 PQQ 4

RESULT 7
UPA7 HUMAN STANDARD; PRT; 9 AA.
ID P30093;
AC P30093;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Unknown protein from 2D-PAGE of plasma (Spot 18) (Fragment).
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
CC Homo.
CX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasqualli C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 5.05, its MW is: 37 kDa.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC SWISS-2DPAGE; P30093; HUMAN.
DR Direct protein sequencing.
FT UNSURE 5
FT NON_TER 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 1043 MW; SC14477AEB0772C7 CRC64;

Query Match 30.0%; Score 3; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LVP 6
DB 2 LVP 4

RESULT 8
P78484 HUMAN PRELIMINARY; PRT; 9 AA.
ID P78484;
AC P78484;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE FYN protein (Fragment).
GN Name=FYN;
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
CC Homo.
CX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=88234523; PubMed=3287380;
RA Kawakami T., Kawakami Y., Aaronson S.A., Robbins K.C.;
RT "Acquisition of transforming properties by FYN, a normal SRC-related
RT human gene.";

```

RL Proc. Natl. Acad. Sci. U.S.A. 85:3870-3874 (1988).  
 DR EMBL; M20284; AAA52491.1; -; Genomic\_DNA.  
 RT NON\_TER 1 1143 MW; 12BA1179D5A6D73B CRC64;  
 SQ SEQUENCE 9 AA; 1143 MW; 12BA1179D5A6D73B CRC64;

Query Match 30.0%; Score 3; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EYL 4  
 |||  
 Db 1 EYL 3

## RESULT 9

GPCR\_MOUSE  
 ID GPCR\_MOUSE STANDARD; PRT; 10 AA.  
 AC P8354;  
 DT 05-JUL-2004 (Rel. 44, Created)  
 DT 05-JUL-2004 (Rel. 44, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Putative G-protein coupled receptor (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Theria; Eumarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN (1)  
 RP PROTEIN SEQUENCE.  
 RC TISSUE=Testis;  
 RA Laloraya M., Kumar G.P.;  
 RT "Identification of a G-protein coupled receptor (GPCR) on mouse  
 spermatozoa";  
 RL Submitted (MAR-2004) to Swiss-Prot.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

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 CC removed.

CC InterPro: IPR000276; GPCR\_Rhodopn.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1, PARTIAL.  
 DR PROSITE; PS0262; G\_PROTEIN\_RECEP\_F1\_2, PARTIAL.  
 KW Direct protein sequencing; G-protein coupled receptor; Receptor;  
 KW Transducer; Transmembrane.  
 FT NON\_TER 10  
 SQ SEQUENCE 10 AA; 1192 MW; DBSC8D96944B06C6 CRC64;

Query Match 30.0%; Score 3; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PQQ 8  
 |||  
 Db 2 PQQ 4

## RESULT 10

Q8WGD2\_9EUCA PRELIMINARY; PRT; 10 AA.  
 ID Q8WGD2\_9EUCA PRELIMINARY; PRT; 10 AA.  
 AC Q8WGD2;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE NADH dehydrogenase subunit 1 (Fragment).  
 OS Hepaticus epheliticus (Calico box crab).  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 OC Brachyura; Leucostoidae; Calappidae; Hepatus.

OX NCBI\_TaxID=6799;

RN (1)  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=21884466; PubMed=11886621; DOI=10.1098/rspb.2001.1886;  
 RA Morrison C.L., Harvey A.W., Lavery S., Tieu K., Huang Y.,  
 RA Cunningham C.W.;  
 RT "Mitochondrial gene rearrangements confirm the parallel evolution of  
 RT the crab-like form";  
 RL Proc. R. Soc. Lond., B, Biol. Sci. 269:345-350 (2002).  
 DR EMBL; AF36043; AF361618.1; -; Genomic\_DNA.  
 DR GO; GO:0005733; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON\_TER 10  
 SQ SEQUENCE 10 AA; 1178 MW; DB16025452C05B02 CRC64;

Query Match 30.0%; Score 3; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YLV 5  
 |||  
 Db 8 YLV 10

## RESULT 11

Q7M1F6\_9POAL PRELIMINARY; PRT; 10 AA.  
 ID Q7M1F6\_9POAL PRELIMINARY; PRT; 10 AA.  
 AC Q7M1F6;  
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Alpha-glucanase 6Ha (Fragment).  
 OS Haynaldia villosa.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticeae; Haynaldia.  
 OX NCBI\_TaxID=40247;

RN (1)  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=91315394; PubMed=1859356;  
 RA Shewry P.R., Sabeelli P.A., Farmer S., Lafandra D.;  
 RT "alpha-type prolamin are encoded by genes on chromosomes 4Ha and 6Ha  
 RT of Haynaldia villosa Schur (syn. Dasypyrum villosum L.).";  
 RL Biochem. Genet. 29:207-211 (1991).  
 DR PIR; B61218; B61218.  
 FT NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 10 AA; 1132 MW; DEAE5936C772D772 CRC64;

Query Match 30.0%; Score 3; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VPQ 7  
 |||  
 Db 5 VPQ 7

## RESULT 12

Q7M1F7\_9POAL PRELIMINARY; PRT; 10 AA.  
 ID Q7M1F7\_9POAL PRELIMINARY; PRT; 10 AA.  
 AC Q7M1F7;  
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Alpha-glucanase 4Ha (Fragment).  
 OS Haynaldia villosa.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticeae; Haynaldia.  
 OX NCBI\_TaxID=40247;  
 RN (1)  
 RP PROTEIN SEQUENCE.

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RX MEDLINE=91315394; PubMed=1859356;
RA Shewry P.R., Sabelli P.A., Parnar S., Iatfandra D.;
RT "alpha-typa prolamin are encoded by genes on chromosomes 4th and 6th
RT of Haynaldia villosa Schur (syn. Dasypyrum villosum L.).",
RL Biochem. Genet. 29:207-211(1991).
DR PIR; A61218; A61218.
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 10 AA; 1162 MW; 72F11BC772D772D4 CRC64;

Query Match 30.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPQ 7
DB 6 VPQ 8

RESULT 13
Q8L7F5 HEVR PRELIMINARY; PRT; 10 AA.
ID Q8L7F5;
AC Q8L7F5;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 24, Last annotation update)
DE Rubber elongation factor (Fragment).
GN Name=ref;
OS Hevea brasiliensis (Para rubber tree).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spemacophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eumecopsida I; Malpighiales; Euphorbiaceae; Crotonoideae; Mitrandrae;
OC Hevea.
OX NCBI_Taxid=3981;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Arcotaj P., Jones H.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY134670; AA095706.1; -; Genomic DNA.
DR GO; GO:0003746; Translation elongation factor activity; IEA.
KW Elongation factor.
FT NON TER 10
FT NON TER 10
SQ SEQUENCE 10 AA; 1136 MW; 793CFPD44AAB1AAB CRC64;

Query Match 30.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 QOG 9
DB 8 QOG 10

RESULT 14
Q53VQ3 MOUSE PRELIMINARY; PRT; 10 AA.
ID Q53VQ3;
AC Q53VQ3;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE D region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86136012; PubMed=3937730;
RA Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
RT "The idotypic network and the internal image: possible regulation of
RT a germ-line network by paucigene encoded Ab2 (anti-idotypic)
RT antibodies in the GAT system.";

```

```

RL EMO J. 4:3681-3688(1985).
DR EMBL; X03378; CAA27099.1; -; mRNA.
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 10 AA; 1410 MW; 08620B1AB841B4B CRC64;

Query Match 30.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 BEY 3
DB 8 BEY 10

RESULT 15
Q53VQ7 MOUSE PRELIMINARY; PRT; 10 AA.
ID Q53VQ7;
AC Q53VQ7;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE D region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86136012; PubMed=3937730;
RA Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
RT "The idotypic network and the internal image: possible regulation of
RT a germ-line network by paucigene encoded Ab2 (anti-idotypic)
RT antibodies in the GAT system.";
RL EMO J. 4:3681-3688(1985).
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 10 AA; 1394 MW; 08620B1A9D41B4B CRC64;

Query Match 30.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 BEY 3
DB 8 BEY 10

RESULT 16
Q53VRI MOUSE PRELIMINARY; PRT; 10 AA.
ID Q53VRI;
AC Q53VRI;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE D region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86136012; PubMed=3937730;
RA Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
RT "The idotypic network and the internal image: possible regulation of
RT a germ-line network by paucigene encoded Ab2 (anti-idotypic)
RT antibodies in the GAT system.";
RL EMO J. 4:3681-3688(1985).
DR EMBL; X03376; CAA27087.1; -; mRNA.
FT NON TER 1

```

FT NON TER 10 10  
 SQ SEQUENCE 10 AA; 1368 MW; 08620B1AA1F409DB CRC64;  
 Query Match 30.0%; Score 3; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 BEY 3  
 |||  
 DB 8 BEY 10  
 RESULT 17  
 083978\_9INFA PRELIMINARY; PRT; 10 AA.  
 ID 083978\_9INFA  
 AC 083978;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE Influenza A/udorn/72 (h3n2), nucleoprotein (seg 5), 3' cDNA.  
 DE (Fragment).  
 OS Influenza A virus.  
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
 OC Influenzavirus A.  
 OX NCBI\_TaxId=11320;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=83112211; PubMed=6296449;  
 RA Lin B.-C., Lai C.-J.;  
 RT "The influenza virus nucleoprotein synthesized from cloned DNA in a  
 RT simian virus 40 vector is detected in the nucleus."  
 RL J. Virol. 45:434-438(1983).  
 DR EMBL: J02171; AAA43468.1; -; Genomic\_RNA.  
 KW GO:0030529; C:ribonucleoprotein complex; IEA.  
 DR Ribonucleoprotein; Viral nucleoprotein.  
 FT NON TER 1 1  
 SQ SEQUENCE 10 AA; 1173 MW; 8787655B1B1DD4A CRC64;  
 Query Match 30.0%; Score 3; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 BEY 3  
 |||  
 DB 6 BEY 8  
 RESULT 18  
 ACH1\_ACHFU STANDARD; PRT; 4 AA.  
 ID ACH1\_ACHFU  
 AC P35974;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Achatina-I.  
 OS Achatina fulica (Giant African snail).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;  
 OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.  
 OX NCBI\_TaxId=6530;  
 RN [1]  
 RP PROTEIN SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.  
 RC STRAIN=Perussac; TISSUE=Ganglion;  
 RX MEDLINE=89273551; PubMed=2597281;  
 RA Kametani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K.,  
 RA Navales E.T., Sun X.P., Yongsiri A., Kim K.H., Navales-Li P.,  
 RA Navales E.T., Kanadi C.G., Takeuchi H., Nomoto K.;  
 RT "Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina  
 RT fulica. Perussac containing a D-amino acid residue."  
 RL Biochem. Biophys. Res. Commun. 160:1015-1020(1989).  
 RN [2]  
 RP CHARACTERIZATION.  
 RC STRAIN=Perussac; TISSUE=Heart atrium;  
 RX MEDLINE=91264856; PubMed=1675568;

RA Fujimoto K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nomoto K.,  
 RA Yoshida M., Harada A., Muneoka Y., Kobayashi M.;  
 RT "Purification of achatin-I from the atria of the African giant snail,  
 RT Achatina fulica, and its possible function."  
 RL Biochem. Biophys. Res. Commun. 177:847-853(1991).  
 RN [3]  
 RP CRYSTALLIZATION.  
 RX MEDLINE=93014529; PubMed=1399265;  
 RA Iwashita T., Inoue M., Yasuda-Kamatani Y., Minakata H.,  
 RA Iwashita T., Nomoto K.;  
 RT "Crystal structure and molecular conformation of achatin-I (H-Gly-D-  
 RT phe-Ala-Asp-OH), an endogenous neuropeptide containing a D-amino acid  
 RT residue."  
 RL Int. J. Pept. Protein Res. 39:258-264(1992).  
 CC -1- FUNCTION: Neuroexcitatory peptide; increases the impulse frequency  
 CC and produces a spike broadening of the identified heart excitatory  
 CC neuron (PON); also enhances the amplitude and frequency of the  
 CC heart beat. Has also an effect on several other muscles.  
 CC -----  
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 CC removed.  
 CC -----  
 DR PIR: A32480; A32480.  
 KW D-amino acid; Direct protein sequencing; Hormone.  
 FT MOD RES 2 2 D-phenylalanine.  
 SQ SEQUENCE 4 AA; 408 MW; 6AADD9C810000000 CRC64;  
 Query Match 20.0%; Score 2; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 9 GF 10  
 |||  
 DB 1 GF 2  
 RESULT 19  
 PAR3\_HIRME STANDARD; PRT; 4 AA.  
 ID PAR3\_HIRME  
 AC P42562;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE FMRFamide-like neuropeptide YLRP-amide.  
 OS Hirudo medicinalis (Medicinal leech).  
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea; Hirudinea;  
 OC Arhynchobdellida; Hirudiniiformes; Hirudindae; Hirudo.  
 OX NCBI\_TaxId=6421;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=92195954; PubMed=1686933; DOI=10.1016/0196-9781(91)90035-N;  
 RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;  
 RT "Identification of RPeptide neuropeptides in the medicinal leech."  
 RL Peptides 12:897-908(1991).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: Belongs to the PARP (FMRFamide related peptide)  
 CC family.  
 CC -----  
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 CC removed.  
 CC -----  
 KM Annotation: Direct protein sequencing; Neuropeptide.  
 FT MOD RES 4 4 Phenylalanine amide.  
 SQ SEQUENCE 4 AA; 598 MW; 69D4073B30000000 CRC64;  
 Query Match 20.0%; Score 2; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 YL 4  
DB 1 YL 2

## RESULT 20

OCPL\_OCTMT STANDARD; PRT; 4 AA.  
AC P58648;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Octopod active peptides Ocp-1/Ocp-2.  
OS Octopus minor (Octopus).  
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Colecoidea; Neocolecoidea;  
OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.  
OX NCBI\_TaxId=89766;

PROTEIN SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.  
[1]  
RT TISSUE=Brain;  
RX MEDLINE=20336815; PubMed=10876044; DOI=10.1016/S0196-9781(00)00201-1;  
RA Iwakoshi E., Hisada M., Minakata H.;  
RT "Cardioactive peptides isolated from the brain of a Japanese octopus,  
Octopus minor.";  
RT Octopus minor.";  
RT Peptides 21:623-630(2000).  
CC -1- FUNCTION: Cardioactive; has both positive chronotropic and  
inotropic effects on the heart. Ocp-2 is a 1000 time less active  
than Ocp-1.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- PTM: Ocp-2 has L-Phe instead of D-Phe.  
CC -1- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI; RANGE=1-4; NOTE=Ref.1.

-----  
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removed.  
CC -----  
CC D-amino acid; Direct protein sequencing; Hormone.  
KW MOD RES 2 D-phenylalanine (in form Ocp-1).  
FT SEQUENCE 4 AA; 394 MW; 6AA879C810000000 CRC64;  
SQ

Query Match 20.0%; Score 2; DB 1; Length 4;

Best Local Similarity 100.0%; Pred. No. 2.2e+06;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 GF 10  
DB 1 GF 2

## RESULT 21

PAP2\_PAPMA STANDARD; PRT; 5 AA.  
AC P8164;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Pardaxin II (PXII) (Fragment).  
OS Pardachirus marmoratus (Red sea moose sole).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;  
OC Soleioidi; Soleidae; Pardachirus.  
OX NCBI\_TaxId=31087;  
RN [1]

PROTEIN SEQUENCE.  
RP TISSUE=Skin secretion;  
RX MEDLINE=87057369; PubMed=3782138;  
RA Lazarovici P., Primor N., Loew L.M.;  
RT "Purification and pore-forming activity of two hydrophobic  
polypeptides from the secretion of the Red sea moose sole (Pardachirus  
marmoratus).";  
RT J. Biol. Chem. 261:16704-16713(1986).  
CC -1- FUNCTION: Exhibits unusual shark repellent and surfactant  
properties. Forms voltage-dependent, ion-permeable channels in  
membranes. At high concentration causes cell membrane lysis.  
CC -1- SUBUNIT: Monomer. In aqueous solution exists as a tetramer.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: Belongs to the pardaxin family.  
-----  
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use as long as its content is in no way modified and this statement is not  
removed.  
CC -----  
CC Direct protein sequencing; Neuropeptide.  
KW SEQUENCE 5 AA; 649 MW; 71B7673B44600000 CRC64;  
SQ

Query Match 20.0%; Score 2; DB 1; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.2e+06;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 YL 4  
DB 2 YL 3

## RESULT 22

PROTEIN SEQUENCE.  
RP MEDLINE=86232789; PubMed=2872661; DOI=10.1016/0196-9781(86)90063-X;  
RX Stangier J., Dirksen H., Keller R.;  
RT "Identification and immunocytochemical localization of proctolin in  
pericardial organs of the shore crab, Carcinus maenas.";  
RT Peptides 7:67-72(1986).  
CC -1- FUNCTION: Stimulates cardiac output and hindgut motility,  
modulates visceral and skeletal muscle in many arthropods.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Found in the crab pericardial organs.  
-----  
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removed.  
CC -----  
CC Direct protein sequencing; Toxin.  
KW NON TER 5  
FT SEQUENCE 5 AA; 614 MW; 7769C9C9C8100000 CRC64;  
SQ

Query Match 20.0%; Score 2; DB 1; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.2e+06;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 GF 10  
DB 1 GF 2

## RESULT 23

PCT\_CARMA STANDARD; PRT; 5 AA.  
AC P67857; P01373;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Proctolin.  
OS Carcinus maenas (Common shore crab) (Green crab).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Decapoda; Pleocyemata; Brachyura;  
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.  
OX NCBI\_TaxId=6759;  
RN [1]

PROTEIN SEQUENCE.  
RP MEDLINE=86232789; PubMed=2872661; DOI=10.1016/0196-9781(86)90063-X;  
RX Stangier J., Dirksen H., Keller R.;  
RT "Identification and immunocytochemical localization of proctolin in  
pericardial organs of the shore crab, Carcinus maenas.";  
RT Peptides 7:67-72(1986).  
CC -1- FUNCTION: Stimulates cardiac output and hindgut motility,  
modulates visceral and skeletal muscle in many arthropods.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Found in the crab pericardial organs.  
-----  
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use as long as its content is in no way modified and this statement is not  
removed.  
CC -----  
CC Direct protein sequencing; Neuropeptide.  
KW SEQUENCE 5 AA; 649 MW; 71B7673B44600000 CRC64;  
SQ

Query Match 20.0%; Score 2; DB 1; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.2e+06;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 YL 4  
DB 2 YL 3



```

PRCT LIMPO
ID PRCT LIMPO STANDARD; PRT; 5 AA.
AC P67858; P01373;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Procollin.
OS Limulus polyphemus (Atlantic horseshoe crab).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
OC Limulidae; Limulus.
NCBI_TaxID=6850;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=90287800; PubMed=2356151; DOI=10.1016/0196-9781(90)90072-D;
RA Groome J.R., Tillinghast E.K., Townley M.A., Vetrove A.,
RA Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.B.,
RA Shabanowitz J.;
RT "Identification of procollin in the central nervous system of the
RT horseshoe crab, Limulus polyphemus.";
RL Peptides 11:205-211(1990).
CC -1- FUNCTION: Stimulates cardiac output and hindgut motility,
CC modulates visceral and skeletal muscle in many arthropods.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Found in the crab pericardial organs.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PIR; A60411; A60411.
KW Direct protein sequencing; Neuropeptide.
SQ SEQUENCE 5 AA; 649 MW; 71B7673B460000 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YL 4
DB 2 YL 3

RESULT 24
PRCT PERAM STANDARD; PRT; 5 AA.
ID PRCT PERAM STANDARD; PRT; 5 AA.
AC P67859; P01373;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Procollin.
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattellidae;
OC Blattellidae; Blattellae; Periplaneta.
NCBI_TaxID=6978;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=6074708; PubMed=576; DOI=10.1016/0024-3205(75)90134-4;
RA Starratt A.N., Brown B.E.;
RT "Structure of the pentapeptide procollin, a proposed neurotransmitter
RT in insects.";
RL Life Sci. 17:1253-1256(1975).
RN [2]
RP BIOLOGICAL SOURCE.
RX MEDLINE=8122865; PubMed=6113690;
RA O'Shea M., Adams M.E.;
RA "Pentapeptide (procollin) associated with an identified neuron.";
RT Science 213:567-569(1981).
CC -1- FUNCTION: Stimulates cardiac output and hindgut motility,
CC modulates visceral and skeletal muscle in many arthropods.
CC -1- SUBCELLULAR LOCATION: Secreted.

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CC -1- TISSUE SPECIFICITY: Found in the lateral white neurons.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
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CC -----
DR PIR; A01644; HOROHA.
KW Direct protein sequencing; Neuropeptide.
SQ SEQUENCE 5 AA; 649 MW; 71B7673B460000 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YL 4
DB 2 YL 3

RESULT 25
RBB32_LITRU STANDARD; PRT; 5 AA.
ID RBB32_LITRU STANDARD; PRT; 5 AA.
AC P82073;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 01-FEB-2005 (Rel. 46, Last annotation update)
DE Rubellidin-3.2.
OS Litorea rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hyllidae;
OC Pelodyadinae; Litorea.
NCBI_TaxID=104695;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litorea electrica. Comparison with the skin peptides from Litorea
RT rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -1- FUNCTION: Shows neither neuropeptide activity nor antibiotic
CC activity.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
KW Amphibian defense peptide; Direct protein sequencing.
SQ SEQUENCE 5 AA; 570 MW; 71A9C9C862A00000 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GF 10
DB 2 GF 3

RESULT 26
TRAM3_ECOLI STANDARD; PRT; 5 AA.
ID TRAM3_ECOLI STANDARD; PRT; 5 AA.
AC P13973;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Tram protein (Fragment).

```

GN Name=tram;  
 OS Escherichia coli.  
 CC Plasmid IncFIR R100 (NR1).  
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 CC Enterobacteriaceae; Escherichia.  
 OK NCBI\_TaxId=562;  
 RN NUCLEOTIDE SEQUENCE (GENOMIC DNA).  
 RP MEDLINE=88227859; PubMed=2836369;  
 RA Inamoto S., Yoshioaka Y., Ohtsubo E.;  
 RT Identification and characterization of the products from the tram and  
 RT tram genes of plasmid R100." (1988).  
 CC J. Bacteriol. 170:2749-2757(1988).  
 CC -1- FUNCTION: Transfer gene protein. Is involved in the conjugation  
 CC process of bacterial cells for the exchange of plasmid DNA.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- SIMILARITY: Belongs to the tram family.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
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 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC EMBL; M20941; -; NOT ANNOTATED; CDS; Genomic DNA.  
 DR PIR; A32014; A32014.  
 DR Conjugation; DNA-binding; Plasmid.  
 KW NON TER  
 FT SEQUENCE 5 AA; 634 MW; 6B1B1AA43500000 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EE 2  
 DB 4 EE 5

RESULT 27  
 AS22\_LACSN STANDARD; PRT; 6 AA.  
 ID AS22\_LACSN  
 AC P82655;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Acid shock protein 2 (Fragment).  
 OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).  
 CC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;  
 CC Lactobacillus.  
 OK NCBI\_TaxId=1625;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RC STRAIN=CBL;  
 RA MEDLINE=21322712; PubMed=1129463;  
 RA De Angelis M., Bhil L., Pallini V., Cocconcelli P.S., Gobberti M.;  
 RT "The acid-stress response in Lactobacillus sanfranciscensis CBL.";  
 RT Microbiology 147:1863-1873(2001).  
 CC -1- INDUCTION: Overexpressed in acid environments.  
 CC -----  
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC Direct protein sequencing.  
 KW NON TER  
 FT SEQUENCE 6 AA; 779 MW; 6AA45B5B132A8000 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EX 3  
 DB 3 EX 4

RESULT 28  
 E101\_LITRU STANDARD; PRT; 6 AA.  
 ID E101\_LITRU  
 AC P82056;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Electricin-1.  
 OS Litoria rubella (Desert tree frog).  
 CC Amphibia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Anura; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;  
 CC Pelodyadinae; Litoria.  
 OK NCBI\_TaxId=104895;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RA Mahnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
 RT "Peptides from the skin glands of the Australian buzzing tree frog  
 RT Litoria electrica. Comparison with the skin peptides from Litoria  
 RT rubella.";  
 RT Aust. J. Chem. 52:639-645(1999).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Expressed by the skin glands.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC Amidation; Amphibian defense peptide; Direct protein sequencing.  
 KW MOD RES  
 FT MOD RES  
 SQ SEQUENCE 6 AA; 792 MW; 6683704772C9A000 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VP 6  
 DB 2 VP 3

RESULT 29  
 ASCL\_ALIAS STANDARD; PRT; 7 AA.  
 ID ASCL\_ALIAS  
 AC P84071;  
 DT 25-OCT-2004 (Rel. 45, Created)  
 DT 25-OCT-2004 (Rel. 45, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Ascalin (Fragment).  
 OS Allium ascalonicum (Shallot) (Allium cepa var. aggregatum).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Alliaceae;  
 CC Allium.  
 OK NCBI\_TaxId=28911;  
 RN [1]  
 RP PROTEIN SEQUENCE, AND FUNCTION.  
 RC TISSUE=Bud;  
 RX PubMed=12126728; DOI=10.1016/S0196-9781(02)00032-3;  
 RA Wang H.X., Ng T.B.;  
 RT "Ascalin, a new anti-fungal peptide with human immunodeficiency virus  
 RT type 1 reverse transcriptase-inhibiting activity from shallot bulbs.";  
 RT Peptides 23:1025-1029(2002).  
 CC -1- FUNCTION: Has antifungal activity against B.ciherea. Inhibits HIV-  
 CC 1 reverse transcriptase.  
 CC -1- MISCELLANEOUS: Inhibits HIV-1 reverse transcriptase with an IC(50)

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CC of 10 uM.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC Anticribial; Direct protein sequencing; Fungicide.
CC NON TER
CC SEQUENCE 7 AA; 712 MW; 687866D87EA6CB30 CRC64;
CC
CC Query Match 20.0%; Score 2; DB 1; Length 7;
CC Best Local Similarity 100.0%; Pred. No. 2.2e+06;
CC Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
QY 8 QG 9
DB 5 QG 6
DB

```

RESULT 30

CAP6 CANAL STANDARD; PRT; 7 AA.

AC P83784;

DT 01-FEB-2005 (Rel. 46, Created)

DT 01-FEB-2005 (Rel. 46, Last sequence update)

DE 01-FEB-2005 (Rel. 46, Last annotation update)

DE Cytoplasmic antigenic protein 6 (Fragment).

OS Candida albicans (Yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Microsporid Saccharomycetales; Candida.

OX NCBI\_TaxID=5476;

RN [1]

RP PROTEIN SEQUENCE, SUBCELLULAR LOCATION, AND ANTIGENICITY.

RC STRAIN=SC5314; TISSUE=Protoplast;

RX PubMed=15378761; DOI=10.1002/pmic.200400903;

RA Pitarach A., Abian J., Carrascal M., Sanchez M., Nombela C., Gil C.;

RT "Proteomics-based identification of novel Candida albicans antigens

RT for diagnosis of systemic candidiasis in patients with underlying

RT hematological malignancies.";

RL Proteomics 4:3084-3106(2004).

CC -1- SUBCELLULAR LOCATION: Cytoplasmic.

CC -1- MISCELLANEOUS: Has antigenic properties. Elicits a specific immune

CC response in systemic candidiasis human patients undergoing

CC malignant hematological disorders.

CC -----

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

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CC use as long as its content is in no way modified and this statement is not

CC removed.

CC Antigen; Direct protein sequencing.

CC NON TER

CC SEQUENCE 7 AA; 900 MW; 740736C6D046DAC0 CRC64;

CC

CC Query Match 20.0%; Score 2; DB 1; Length 7;

CC Best Local Similarity 100.0%; Pred. No. 2.2e+06;

CC Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC

QY 7 QG 8

DB 4 QG 5

DB

```

DT 05-JUL-2004 (Rel. 44, Last annotation update)
DB Sex pheromone cCp10.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=89008313; PubMed=3139658;
RA Mori M., Sakagami Y., Ishii Y., Isogai A., Kitada C., Fujino M.,
RA Adair J.C., Dunn G.M., Suzuki A.;
RT "Structure of cCp10, a peptide sex pheromone which induces conjugative
RT transfer of the Streptococcus faecalis tetracycline resistance
RT plasmid, pCp10.";
RL J. Biol. Chem. 263:14574-14578(1988).
CC -1- FUNCTION: cCp10 is involved in the conjugative transfer of the
CC hemolysin plasmid pCp10.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; A30812; A30812.
DR Direct protein sequencing; Pheromone.
KM SEQUENCE 7 AA; 790 MW; 72C9D2C731B2C740 CRC64;
KM
SQ

```

Query Match 20.0%; Score 2; DB 1; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.2e+06;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LV 5

DB 1 LV 2

DB

RESULT 32

TPPY\_PACDA STANDARD; PRT; 7 AA.

AC P8345;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Trypophyllin-1 (Pdt-1).

OS Pachymedusa daenicolour (Giant mexican leaf frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eureleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;

OC Phyllomedusinae; Pachymedusa.

OX NCBI\_TaxID=75988;

RN [1]

RP PROTEIN SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND

RP AMIDATION.

RA TISSUE=Skin secretion;

RA Chen T.B., Orr D.F., Shaw C.;

RT "Pachymedusa daenicolour tryptophyllin-1 (Pdt-1): structural

RT characterization, pharmacological activity and cloning of precursor

RT cDNA.";

RL Submitted (SEP-2002) to Swiss-Prot.

CC -1- FUNCTION: Myoactive. Has selective relaxing activity on vascular

CC smooth muscle.

CC -1- TISSUE SPECIFICITY: Expressed by the skin glands.

CC -1- MASS SPECTROMETRY: MW=809.2; METHOD=MALDI; RANGE=1-7; NOTE=Ref.1.

CC -----

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CC removed.

CC GO: GO:0005576; C:extracellular; region; NMS.

DR GO: GO:0045986; P:negative regulation of smooth muscle contra. . .; NMS.

AMidation; Amphibian defense peptide; Direct protein sequencing;

```

KW Hydroxylation.
FT MOD RES 3 3 Hydroxyproline.
FT MOD RES 7 7 Proline amide.
SQ SEQUENCE 7 AA; 794 MW; 7772D37DC776350 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VP 6
DB 6 VP 7

RESULT 33
ID UP03 MOUSE STANDARD; PRT; 7 AA.
AC P38641;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Unknown protein from 2D-PAGE of fibroblasts (P36) (Fragment).
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Fibroblast;
RA MEDLINE=9500907; PubMed=7523108;
RA Merrick B.A., Paterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins using
RT preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 5.1, its MW is: 36 kDa.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC Direct protein sequencing.
KW NON TER
FT SEQUENCE 7 AA; 842 MW; 6AA72B1DB1B180 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EE 2
DB 2 EE 3

RESULT 34
ID UP11 RAT STANDARD; PRT; 7 AA.
AC P56576;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Unknown protein from 2D-PAGE of heart tissue (Spot P11) (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP PROTEIN SEQUENCE.
RC STRAIN=Wistar; TISSUE=Heart;

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RA Li X.-P., Pleisner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,
RA Jungblut P.R.;
RL Submitted (SEP-1998) to Swiss-Prot.
CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 8.5, its MW is: 42 kDa.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC Direct protein sequencing.
KW UNSURE
FT NON TER
FT SEQUENCE 7 AA; 775 MW; 6866DB040DC5A6B0 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 QG 9
DB 6 QG 7

RESULT 35
ID O8NH7 HUMAN PRELIMINARY; PRT; 7 AA.
AC O8NH7;
DT 01-OCT-2002 (TRENBLREL. 22, Created)
DT 01-OCT-2002 (TRENBLREL. 22, Last sequence update)
DT 01-OCT-2002 (TRENBLREL. 22, Last annotation update)
DE Min-cistron.
OS Name=NEH3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Malkooti J., Ramaswamy K.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF282824; AAMS3436.1; -; Genomic DNA.
SQ SEQUENCE 7 AA; 842 MW; 74072DC772D406F0 CRC64;

Query Match 20.0%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VP 6
DB 3 VP 4

RESULT 36
ID Q28742 RABIT PRELIMINARY; PRT; 7 AA.
AC Q28742;
DT 01-NOV-1996 (TRENBLREL. 01, Created)
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
DE Alpha-myosin heavy chain (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=84221901; PubMed=6328491;
RA Friedmann D.J., Umeda P.K., Sinha A.M., Heu H.J., Jokovic S.,

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RA Rabinowitz M.;  
RT "Characterization of genomic clones specifying rabbit alpha- and beta-  
RT ventricular myosin heavy chains.";  
RL Proc. Natl. Acad. Sci. U.S.A. 81:3044-3048 (1984).  
DR EMBL; K01698; AAA31415.1; -; Genomic\_DNA.  
DR PIR; I46868; I46868.  
FT NON\_TER  
SQ SEQUENCE 7 AA; 916 MW; 6B1B1A1E69326B0 CRC64;  
  
Query Match 20.0%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 EE 2  
DB 6 EE 7  
  
RESULT 37  
P93233\_LYCES PRELIMINARY; PRT; 7 AA.  
AC P93233;  
DT 01-MAY-1997 (TEMBLrel. 03, Created)  
DT 01-MAY-1997 (TEMBLrel. 03, Last sequence update)  
DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)  
DE 1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14)  
DE (Fragment).  
GN Name=LC-ACS1B;  
OS Lycopersicon esculentum (Tomato).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
OC Lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.  
OX NCBI\_TaxId=4081;  
RN (1)  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=97351561; PubMed=9207843; DOI=10.1023/A:1005800511372;  
RA Oelker J.H., Olson D.C., Shu O.Y., Yang S.F.;  
RT "Differential induction of seven 1-aminocyclopropane-1-carboxylate  
RT synthase genes by elicitor in suspension cultures of tomato  
RT (Lycopersicon esculentum).";  
RT EMBL; U75692; AAC49682.1; -; mRNA.  
DR GO; GO:0016647; P:1-aminocyclopropane-1-carboxylate synthase . . .; IEA.  
DR CO; CO:0016629; P:lyase activity; IEA.  
KW Lyase.  
FT NON\_TER  
SQ SEQUENCE 7 AA; 828 MW; 71B412C7377415D0 CRC64;  
  
Query Match 20.0%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 4 LV 5  
DB 4 LV 5  
  
RESULT 38  
Q9CSB3\_ARATH PRELIMINARY; PRT; 7 AA.  
ID Q9CSB3\_ARATH  
AC Q9CSB3;  
DT 01-JUN-2001 (TEMBLrel. 17, Created)  
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)  
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)  
DE Hypothetical protein D1D1 10A-2b (Fragment).  
GN Name=D1D1 10A-2b;  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsid.  
OX NCBI\_TaxId=3702;  
RN (1)  
RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Roots;  
RX MEDLINE=21171025; PubMed=11277426;  
RA Vercauteren I., Van Der Schueren E., Van Montagu M., Gheysen G.;  
RT "Arabidopsis thaliana genes expressed in the early compatible  
RT interaction with root-knot nematodes.";  
RL Mol. Plant Microbe Interact. 14:288-299 (2001).  
RN (2)  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Roots;  
RA Vercauteren I., J.R.;  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ286350; CAB71014.2; -; mRNA.  
KW Hypothetical protein.  
FT NON\_TER  
FT NON\_TER  
SQ SEQUENCE 7 AA; 719 MW; 6732C7287BB325D0 CRC64;  
  
Query Match 20.0%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 4 LV 5  
DB 5 LV 6  
  
RESULT 39  
Q8KMS9\_GENTR PRELIMINARY; PRT; 7 AA.  
ID Q8KMS9\_GENTR  
AC Q8KMS9;  
DT 01-OCT-2002 (TEMBLrel. 22, Created)  
DT 01-OCT-2002 (TEMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TEMBLrel. 22, Last annotation update)  
DE Putative transposase (Fragment).  
GN Name=tNA;  
OS Enterobacter sp. CH2-4.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Enterobacter.  
OX NCBI\_TaxId=143777;  
RN (1)  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=CH2-4;  
RX MEDLINE=21604134; PubMed=11763242; DOI=10.1016/S0923-2508(01)01265-7;  
RA Mindlin S.Z., Kholodii G.Y., Gorlenko Z.M., Minakhina S.V.,  
RA Minakhin L.S., Kalyaeva B.S., Kopleva A.V., Petrova M.A.,  
RA Yurleva O.V., Nikiforov V.G.;  
RT "Mercury resistance transposons of gram-negative environmental  
RT bacteria and their classification.";  
RL Res. Microbiol. 152:811-822 (2001).  
DR EMBL; AJ302778; CAC83058.1; -; Genomic\_DNA.  
FT NON\_TER  
SQ SEQUENCE 7 AA; 966 MW; 737B1B1046DAA9A0 CRC64;  
  
Query Match 20.0%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 EE 2  
DB 5 EE 6  
  
RESULT 40  
O07354\_SYNP8 PRELIMINARY; PRT; 7 AA.  
ID O07354\_SYNP8  
AC O07354;  
DT 01-JUL-1997 (TEMBLrel. 04, Created)  
DT 01-JUL-1997 (TEMBLrel. 04, Last sequence update)  
DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)  
DE Nifk (Fragment).  
GN Name=nifk;  
OS Synechococcus sp. (strain PCC 8801 / RP-1) (Cyanothace PCC 8801).  
OC Bacteria; Cyanobacteria; Chroococcales; Cyanothecae.

OK NCBI\_TaxID=41431;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=RF-1;  
 RA MEDLINE=99231861; PubMed=10217509;  
 RX Huang T.-C., Lin R.-F., Chu M.-K., Chen H.-M.,  
 RT "Organization and expression of nitrogen-fixation genes in the aerobic  
 RT nitrogen-fixing unicellular cyanobacterium *Synechococcus* sp. strain  
 RT RF-1."  
 RL Microbiology 145:743-753(1999).  
 DR EMBL; AF003700; AAC35193.1; -, Genomic\_DNA.  
 FT NON TER  
 SQ SEQUENCE 7 AA; 849 MW; 7412C72AA9D5B030 CRC64;

Query Match 20.0%; Score 2; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LV 5  
 DB 5 LV 6

RESULT 41  
 ID 054248 STRGR PRELIMINARY; PRT; 7 AA.  
 AC 054248;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE RplO protein (Fragment).  
 GN Name=rplO;  
 OS Streptomyces griseus.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Streptomyces; Streptomycetaceae; Streptomyces.  
 RX NCBI\_TaxID=1911;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=N2-3-11;  
 RA MEDLINE=20011291; PubMed=10542330;  
 RX Poehling S., Piepersberg W., Wehmeyer U.F.,  
 RT "Analysis and regulation of the secY gene from *Streptomyces griseus*  
 RT N2-3-11 and interaction of the secY protein with the SecA protein."  
 RL Biochim. Biophys. Acta 1447:298-302(1999).  
 DR EMBL; X95915; CA65160.1; -, Genomic\_DNA.  
 FT NON TER  
 SQ SEQUENCE 7 AA; 760 MW; 72C72B01B2D1B2A0 CRC64;

Query Match 20.0%; Score 2; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LV 5  
 DB 6 LV 7

RESULT 42  
 ID 08K3H6 RAT PRELIMINARY; PRT; 7 AA.  
 AC 08K3H6;  
 DT 01-OCT-2002 (TREMBlrel. 22, Created)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
 DE Collagenase-3 (Fragment).  
 GN Name=Mmp13;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Eumarchontoglires; Glires; Rodentia; Sciurognathu;  
 OC Muridae; Murinae; Rattus.  
 RX NCBI\_TaxID=10116;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=Sprague-Dawley;  
 RA Prietco S.M., Lyons J.G.,  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY101357; AAM51172.1; -, Genomic\_DNA.  
 KW Collagen.  
 FT NON TER  
 FT NON TER  
 SQ SEQUENCE 7 AA; 907 MW; 63373B51B1DD9A0 CRC64;

Query Match 20.0%; Score 2; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YL 4  
 DB 5 YL 6

RESULT 43  
 ID 09Y010 SCORO PRELIMINARY; PRT; 7 AA.  
 AC 09Y010;  
 DT 01-MAY-1999 (TREMBlrel. 10, Created)  
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE Hypothetical fusion protein.  
 OS Transmissible gastroenteritis virus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
 OC Coronaviridae; Coronavirus; Group 1 species.  
 RX NCBI\_TaxID=11149;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.

RA MEDLINE=88078100; PubMed=2825819; DOI=10.1016/0300-9084(87)90178-7;  
 RX Rascheert D., Gelfi J., Laude H.,  
 RT "Enteric coronavirus TGEV: partial sequence of the genomic RNA, its  
 RT organization and expression."  
 RL Biochimie 69:591-600(1987).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=95159435; PubMed=7856095;  
 RA Eleuter J., Rascheert D., Lambert P., Levy L., Vende P., Laude H.,  
 RT "Complete sequence (20 kilobases) of the polyprotein-encoding gene 1  
 RT of transmissible gastroenteritis virus."  
 RL Virology 206:817-822(1995).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=99099045; PubMed=9882359;  
 RA Izeta A., Smerdou C., Alonso S., Penzes Z., Mendez A., Plana-Duran J.,  
 RA Enjuanes L.,  
 RT "Replication and packaging of transmissible gastroenteritis  
 RT coronavirus-derived synthetic minigenomes."  
 RL J. Virol. 73:1535-1545(1999).  
 DR EMBL; AJ011482; CA09625.1; -, Genomic\_RNA.  
 KW Hypothetical protein.  
 SQ SEQUENCE 7 AA; 927 MW; 69D6D7273B5726F0 CRC64;

Query Match 20.0%; Score 2; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YL 4  
 DB 3 YL 4

RESULT 44  
 ID 042564\_FUGRU PRELIMINARY; PRT; 7 AA.  
 AC 042564;  
 DT 01-JAN-1998 (TREMBlrel. 05, Created)  
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE Truncated voltage-gated sodium channel alpha subunit (Fragment).  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.

GN Name=Scn8a;  
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Perciformes; Tetraodontiformes;  
 OC Tetraodontidae; Tetraodontidae; Takifugu.  
 NCBI\_TaxID=31033;  
 RX NUCLEOTIDE SEQUENCE.  
 RA PubMed=97442476; PubMed=9295353; DOI=10.1074/jbc.272.38.24008;  
 RA Plummer N.W., McBurney M.W., Meisler M.H.;  
 RT "Alternative splicing of the sodium channel SCN8A predicts a truncated  
 two-domain protein in fetal brain and non-neuronal cells."  
 RL J. Biol. Chem. 272:24008-24015(1997).  
 DR EMBL; U97673; AAB80916.1; -, Genomic DNA.  
 DR GO; GO:0005216; P1 ion channel activity; IEA.  
 KW Ionic channel.  
 KM NON TER  
 SQ SEQUENCE 7 AA; 730 MW; 75B72EA2C73772A0 CRC64;  
 Query Match 20.0%; Score 2; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 5 VP 6  
 Db 1 VP 2  
 RESULT 45  
 ID OGBE81\_9HIV1 PRELIMINARY; PRT; 7 AA.  
 AC OGBE81;  
 DT 01-OCT-2002 (TREMBlrel. 22, Created)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
 DE Truncated pol protein (Fragment).  
 GN Name=pol;  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus;  
 OC Primate lentivirus group.  
 OC NCBI\_TaxID=11676;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=22056123; PubMed=12060770; DOI=10.1073/pnas.112177799;  
 RA Beerwinkler N., Schmidt B., Walter H., Kaiser R., Lengauer T.,  
 RA Hoffmann D., Korn K., Selbig J.;  
 RT "Diversity and complexity of HIV-1 drug resistance: a bioinformatics  
 approach to predicting phenotype from genotype."  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:8271-8276(2002).  
 RL EMBL; AF347267; AAK32344.1; -, Genomic RNA.  
 DR NON TER  
 FT NON TER  
 SQ SEQUENCE 7 AA; 885 MW; 76C37731A046C700 CRC64;  
 Query Match 20.0%; Score 2; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 6 PQ 7  
 Db 1 PQ 2  
 RESULT 46  
 ID CAD1\_ENTFA STANDARD; PRT; 8 AA.  
 AC P13268;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Sex pheromone CAD1.  
 OS Enterococcus faecalis (Streptococcus faecalis).  
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.

OX NCBI\_TaxID=1351;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=85051889; PubMed=6437872; DOI=10.1016/0014-5793(84)81248-X;  
 RA Mori M., Sagakami Y., Narita M., Isogai A., Fujino M., Kitada C.,  
 RA Craig R.A., Clewell D.B., Suzuki A.;  
 RT "Isolation and structure of the bacteriacal sex pheromone, CAD1, that  
 induces plasmid transfer in Streptococcus faecalis."  
 RL FEBS Lett. 178:97-100(1984).  
 CC -1- FUNCTION: Involved in the conjugative transfer of the hemolysin  
 plasmid pAD1.  
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC Direct protein sequencing: Pheromone.  
 KM SEQUENCE 8 AA; 819 MW; 047DD732C735B9C7 CRC64;  
 Query Match 20.0%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 4 LV 5  
 Db 4 LV 5  
 RESULT 47  
 ID CAP4\_CANAL STANDARD; PRT; 8 AA.  
 AC P83781;  
 DT 01-FEB-2005 (Rel. 46, Created)  
 DT 01-FEB-2005 (Rel. 46, Last sequence update)  
 DT 01-FEB-2005 (Rel. 46, Last annotation update)  
 DE Cytoplasmic antigenic protein 4 (Fragment).  
 GN Candida albicans (Yeast).  
 OS Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; mtosporic Saccharomycetales; Candida.  
 OC NCBI\_TaxID=5476;  
 RN [1]  
 RP PROTEIN SEQUENCE, SUBCELLULAR LOCATION, AND ANTIGENICITY.  
 RC STRAIN=SC5314; TISSUE=Protoplast;  
 RX PubMed=15378761; DOI=10.1002/pmic.200400903;  
 RA Pitarich A., Abian O., Carrascal M., Sanchez M., Nombela C., Gil C.;  
 RT "Proteomics-based identification of novel Candida albicans antigens  
 RT for diagnosis of systemic candidiasis in patients with underlying  
 RT hematological malignancies."  
 RL Proteomics 4:3084-3106(2004).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- MISCELLANEOUS: Has antigenic properties. Elicits a specific immune  
 CC response in systemic candidiasis human patients undergoing  
 CC malignant hematological disorders.  
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 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC Antigen, direct protein sequencing.  
 KM NON TER  
 FT NON TER  
 SQ SEQUENCE 8 AA; 844 MW; 085772D2D5A1AA7 CRC64;  
 Query Match 20.0%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 5 VP 6  
 Db 1 VP 2

Db 6 VP 7

## RESULT 48

CPD1\_ENTFA STANDARD; PRT; 8 AA.

AC P13269;

DT 01-JAN-1990 (Rel. 13, Created)

DT 01-JAN-1990 (Rel. 13, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Sex pheromone CPD1.

OS Enterococcus faecalis (Streptococcus faecalis).

OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.

OX NCBI\_TaxID=1351;

RN [1]

RP PROTEIN SEQUENCE.

RA MEDLINE=85040388; PubMed=6436978;

RA Suzuki A., Mori M., Sugakami Y., Isogai A., Fujino M., Kltada C.,

RA Craig R.A., Clewell D.B.;

RT "Isolation and structure of bacterial sex pheromone, CPD1.;"

RL Science 226:849-850(1984).

CC -1- FUNCTION: CPD1 is involved in the conjugative transfer of the

CC bacteriocin plasmid pPDI.

CC -----

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

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CC removed.

CC Direct protein sequencing; Pheromone.

KW SEQUENCE 8 AA; 913 MW; 865B729C682C729 CRC64;

SQ

Query Match 20.0%; Score 2; DB 1; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.2e+06; Indels 0; Gaps 0;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 LV 5

Db 2 LV 3

## RESULT 49

DYS4\_LIMSA STANDARD; PRT; 8 AA.

AC P82082;

DT 29-MAR-2004 (Rel. 43, Created)

DT 29-MAR-2004 (Rel. 43, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Dynastin-4.

OS Limodynastes salmuni (Salmon-striped frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;

OC Limodynastinae; Limodynastes.

OX NCBI\_TaxID=39404;

RN [1]

RP PROTEIN SEQUENCE AND MASS SPECTROMETRY.

RA Bradford A.M., Rattery M.J., Bowie J.H., Wallace J.C., Tyler M.J.;

RT "Peptides from Australian frogs. The structure of the dynastins from

RT Limodynastes salmuni and fletcherin from Limodynastes fletcheri.;"

RL Aust. J. Chem. 46:1235-1244(1993).

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: Expressed by the skin glands.

CC -1- MASS SPECTROMETRY: MW=772; METHOD=FA/MS; RANGE=1-8; NOTE=Ref.1.

CC -----

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CC use as long as its content is in no way modified and this statement is not

CC removed.

CC Direct protein sequencing.

SQ SEQUENCE 8 AA; 772 MW; 7B58772455A2C728 CRC64;

## Query Match

Best Local Similarity 100.0%; Score 2; DB 1; Length 8;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 LV 5

Db 2 LV 3

## RESULT 50

FUS5\_FUSO

ID FUS5\_FUSO STANDARD; PRT; 8 AA.

AC P81010;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Allergen Fus s 13596\* (Fragment).

OS Fusarium solani subsp. pisi (Nectria haematococca).

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

OC Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.

OX NCBI\_TaxID=70791;

RN [1]

RP PROTEIN SEQUENCE.

RA STRAIN=IARI 3596; TISSUE=Mycelium;

RA Verma J., Gangal S.V.;

RT Submitted (JUL-1997) to Swiss-Prot.

CC -1- ALLERGEN: Causes an allergic reaction in human.

CC -----

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use as long as its content is in no way modified and this statement is not

CC removed.

KW Allergen; Direct protein sequencing.

FT NON TER 8

SQ SEQUENCE 8 AA; 898 MW; C372C441F5B69041 CRC64;

## Query Match

Best Local Similarity 100.0%; Score 2; DB 1; Length 8;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 VP 6

Db 7 VP 8

Search completed: January 18, 2006, 21:05:30

Job time : 165 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 18, 2006, 20:57:58 ; Search time 39 Seconds  
(without alignments)  
24.671 Million cell updates/sec

Title: US-09-930-125-3  
Perfect score: 10  
Sequence: 1 BEVLVPOQGF 10

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1102

Minimum DB seq length: 0  
Maximum DB seq length: 10

Post-processing: Listing first 200 summaries

Database :  
1: PIR 80:\*  
2: PIR1:\*  
3: PIR2:\*  
4: PIR3:\*  
5: PIR4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description        |
|------------|-------|-------------|--------|-------|--------------------|
| 1          | 3     | 30.0        | 7      | 2     | ICL2 protein - Par |
| 2          | 3     | 30.0        | 9      | 2     | late G1-69 protein |
| 3          | 3     | 30.0        | 9      | 2     | callifmrfamide 1 - |
| 4          | 3     | 30.0        | 10     | 2     | alpha-gliadin 4Ha  |
| 5          | 3     | 30.0        | 10     | 2     | B61218             |
| 6          | 3     | 30.0        | 3      | 3     | PQ0010             |
| 7          | 3     | 30.0        | 3      | 3     | E37196             |
| 8          | 3     | 30.0        | 3      | 3     | A23751             |
| 9          | 3     | 30.0        | 4      | 1     | ECXNA              |
| 10         | 3     | 30.0        | 4      | 2     | B43848             |
| 11         | 3     | 30.0        | 4      | 2     | T46627             |
| 12         | 3     | 30.0        | 4      | 2     | A25844             |
| 13         | 3     | 30.0        | 4      | 2     | I54357             |
| 14         | 3     | 30.0        | 4      | 2     | S55238             |
| 15         | 3     | 30.0        | 4      | 2     | S09478             |
| 16         | 3     | 30.0        | 4      | 2     | A32480             |
| 17         | 3     | 30.0        | 5      | 1     | HOROMA             |
| 18         | 3     | 30.0        | 5      | 2     | C41225             |
| 19         | 3     | 30.0        | 5      | 2     | B37325             |
| 20         | 3     | 30.0        | 5      | 2     | B22565             |
| 21         | 3     | 30.0        | 5      | 2     | B61445             |
| 22         | 3     | 30.0        | 5      | 2     | A61445             |
| 23         | 3     | 30.0        | 5      | 2     | JH0253             |
| 24         | 3     | 30.0        | 5      | 2     | A60521             |
| 25         | 3     | 30.0        | 5      | 2     | A32014             |
| 26         | 3     | 30.0        | 5      | 2     | A60411             |
| 27         | 3     | 30.0        | 6      | 2     | S11556             |
| 28         | 3     | 30.0        | 6      | 2     | A37765             |

|     |   |      |   |   |        |                     |
|-----|---|------|---|---|--------|---------------------|
| 30  | 2 | 20.0 | 6 | 2 | B44510 | hypothetical prote  |
| 31  | 2 | 20.0 | 6 | 2 | I65546 | MHC H2-L antigen -  |
| 32  | 2 | 20.0 | 6 | 2 | PT0514 | T-cell receptor be  |
| 33  | 2 | 20.0 | 6 | 2 | A41946 | T-cell receptor ga  |
| 34  | 2 | 20.0 | 7 | 2 | A60224 | Met-enkephalin-Arg  |
| 35  | 2 | 20.0 | 7 | 2 | PQ0663 | membrane protein -  |
| 36  | 2 | 20.0 | 7 | 2 | A44428 | platelet aggregati  |
| 37  | 2 | 20.0 | 7 | 2 | PT0087 | ribulose-bisphosph  |
| 38  | 2 | 20.0 | 7 | 2 | B61491 | seed protein wa-5   |
| 39  | 2 | 20.0 | 7 | 2 | PQ0728 | unidentified 5.0/1  |
| 40  | 2 | 20.0 | 7 | 2 | S78024 | ribosomal protein   |
| 41  | 2 | 20.0 | 7 | 2 | H33098 | 180k exoantigen     |
| 42  | 2 | 20.0 | 7 | 2 | PT0283 | Ig heavy chain CRD  |
| 43  | 2 | 20.0 | 7 | 2 | B39040 | calsequestrin, fas  |
| 44  | 2 | 20.0 | 7 | 2 | PT0543 | T-cell receptor be  |
| 45  | 2 | 20.0 | 7 | 2 | PT0579 | T-cell receptor be  |
| 46  | 2 | 20.0 | 7 | 2 | PT0581 | T-cell receptor be  |
| 47  | 2 | 20.0 | 7 | 2 | PT0671 | T-cell receptor be  |
| 48  | 2 | 20.0 | 7 | 2 | PX0008 | glucuronosyltransf  |
| 49  | 2 | 20.0 | 7 | 2 | A38081 | amine oxidase (cop  |
| 50  | 2 | 20.0 | 7 | 2 | S45648 | Na+-transporting A  |
| 51  | 2 | 20.0 | 7 | 2 | PQ0777 | NADH2 dehydrogenas  |
| 52  | 2 | 20.0 | 7 | 2 | A30812 | sex pheromone cCp1  |
| 53  | 2 | 20.0 | 7 | 2 | I46868 | alpha-myosin heavy  |
| 54  | 2 | 20.0 | 8 | 2 | S16324 | hypothetical prote  |
| 55  | 2 | 20.0 | 8 | 2 | TI0952 | hypothetical prote  |
| 56  | 2 | 20.0 | 8 | 2 | B33099 | 158k exoantigen -   |
| 57  | 2 | 20.0 | 8 | 2 | G33098 | 205k exoantigen -   |
| 58  | 2 | 20.0 | 8 | 2 | PT0368 | Ig gamma chain C r  |
| 59  | 2 | 20.0 | 8 | 2 | PT0311 | Ig heavy chain CRD  |
| 60  | 2 | 20.0 | 8 | 2 | A38887 | T-cell receptor ga  |
| 61  | 2 | 20.0 | 8 | 2 | C39690 | neural cell adhesi  |
| 62  | 2 | 20.0 | 8 | 2 | S29272 | locopherol-binding  |
| 63  | 2 | 20.0 | 8 | 2 | B47594 | aspartate kinase (  |
| 64  | 2 | 20.0 | 8 | 2 | S45651 | probable Na+-trans  |
| 65  | 2 | 20.0 | 8 | 2 | A59495 | Vesicle associated  |
| 66  | 2 | 20.0 | 8 | 2 | PQ0726 | unidentified 4.5/4  |
| 67  | 2 | 20.0 | 8 | 2 | US0315 | leucokinin V - Mad  |
| 68  | 2 | 20.0 | 8 | 2 | I49404 | prealbumin - weste  |
| 69  | 2 | 20.0 | 8 | 2 | A42689 | major postnaptic    |
| 70  | 2 | 20.0 | 8 | 2 | A5180  | neural proteinase   |
| 71  | 2 | 20.0 | 8 | 2 | PC4373 | telomeric and tetr  |
| 72  | 2 | 20.0 | 8 | 2 | T13818 | cytochrome oxidase  |
| 73  | 2 | 20.0 | 8 | 2 | S69165 | ferredoxin a2 - Ja  |
| 74  | 2 | 20.0 | 8 | 2 | S20162 | leghemoglobin III   |
| 75  | 2 | 20.0 | 8 | 2 | P60588 | sperm-activating p  |
| 76  | 2 | 20.0 | 8 | 2 | B60588 | sperm-activating p  |
| 77  | 2 | 20.0 | 8 | 2 | G60588 | neuropeptide B - b  |
| 78  | 2 | 20.0 | 8 | 2 | B24749 | thymic factor - pi  |
| 79  | 2 | 20.0 | 9 | 1 | YPRG   | thymocyte growth p  |
| 80  | 2 | 20.0 | 9 | 2 | A60957 | litorin I - Austr   |
| 81  | 2 | 20.0 | 9 | 2 | S07204 | phyllotoxinlele     |
| 82  | 2 | 20.0 | 9 | 2 | A61357 | caldesmon - rabbit  |
| 83  | 2 | 20.0 | 9 | 2 | A44873 | calsequestrin, car  |
| 84  | 2 | 20.0 | 9 | 2 | A61230 | fibrinogen beta ch  |
| 85  | 2 | 20.0 | 9 | 2 | D24180 | fibrinogen beta ch  |
| 86  | 2 | 20.0 | 9 | 2 | C24180 | translation elonga  |
| 87  | 2 | 20.0 | 9 | 2 | D58503 | endospem protein,   |
| 88  | 2 | 20.0 | 9 | 2 | S70332 | amine oxidase (cop  |
| 89  | 2 | 20.0 | 9 | 2 | S65433 | bradykinin - horn   |
| 90  | 2 | 20.0 | 9 | 2 | S65433 | Ig heavy chain CRD  |
| 91  | 2 | 20.0 | 9 | 2 | PT0324 | gasterin - domestic |
| 92  | 2 | 20.0 | 9 | 2 | C60070 | T-cell receptor ga  |
| 93  | 2 | 20.0 | 9 | 2 | G41946 | peptidylglycine mo  |
| 94  | 2 | 20.0 | 9 | 2 | A42266 | T-cell receptor be  |
| 95  | 2 | 20.0 | 9 | 2 | PH0942 | locustamycitropin I |
| 96  | 2 | 20.0 | 9 | 2 | A61620 | venom protein HR-3  |
| 97  | 2 | 20.0 | 9 | 2 | D44787 | serum amyloid P-co  |
| 98  | 2 | 20.0 | 9 | 2 | S10920 | cytochrome-c oxida  |
| 99  | 2 | 20.0 | 9 | 2 | B20569 | 60k Ca binding pro  |
| 100 | 2 | 20.0 | 9 | 2 | S77984 | enamelin I - bovin  |
| 101 | 2 | 20.0 | 9 | 2 | PT0080 |                     |
| 102 | 2 | 20.0 | 9 | 2 | S10784 |                     |

|     |   |      |    |   |        |                     |
|-----|---|------|----|---|--------|---------------------|
| 103 | 2 | 20.0 | 9  | 2 | A28924 | fructose-bisphosph  |
| 104 | 2 | 20.0 | 9  | 2 | PC7074 | translation elonga  |
| 105 | 2 | 20.0 | 9  | 2 | A43065 | hydroxyproline-3-b  |
| 106 | 2 | 20.0 | 9  | 2 | PD0027 | pev-tachykinin - p  |
| 107 | 2 | 20.0 | 9  | 2 | B60246 | ornitho-kinin - ch  |
| 108 | 2 | 20.0 | 9  | 2 | S15850 | vitamin D3 26-mono  |
| 109 | 2 | 20.0 | 9  | 2 | A26744 | bradykinin-like pe  |
| 110 | 2 | 20.0 | 9  | 2 | A61057 | Thr-6 bradykinin -  |
| 111 | 2 | 20.0 | 9  | 2 | A60579 | bradykinin-like pe  |
| 112 | 2 | 20.0 | 9  | 2 | A61363 | bradykinin - commo  |
| 113 | 2 | 20.0 | 9  | 2 | A61358 | bradykinin-like pe  |
| 114 | 2 | 20.0 | 10 | 1 | XASNPC | angiotensin-conver  |
| 115 | 2 | 20.0 | 10 | 1 | XAVI68 | angiotensin-conver  |
| 116 | 2 | 20.0 | 10 | 1 | ECLQIM | tachykinin I - mig  |
| 117 | 2 | 20.0 | 10 | 1 | ECLQIM | tachykinin III - m  |
| 118 | 2 | 20.0 | 10 | 1 | ECLQIM | tachykinin IV - m   |
| 119 | 2 | 20.0 | 10 | 2 | S65388 | cytochrome-c oxida  |
| 120 | 2 | 20.0 | 10 | 2 | A43405 | 6-phosphofructo-2-  |
| 121 | 2 | 20.0 | 10 | 2 | S39392 | calpain (EC 3.4.22  |
| 122 | 2 | 20.0 | 10 | 2 | S33844 | alpha-2-macroglobu  |
| 123 | 2 | 20.0 | 10 | 2 | A46491 | C3 homolog HX - in  |
| 124 | 2 | 20.0 | 10 | 2 | A60410 | beta-neoendorphin   |
| 125 | 2 | 20.0 | 10 | 2 | A61337 | caerulein - frog (  |
| 126 | 2 | 20.0 | 10 | 2 | A13687 | caerulein-like pep  |
| 127 | 2 | 20.0 | 10 | 2 | B43590 | pillin type A6 - A  |
| 128 | 2 | 20.0 | 10 | 2 | S65728 | hemoglobin, extrac  |
| 129 | 2 | 20.0 | 10 | 2 | S70721 | heat shock protein  |
| 130 | 2 | 20.0 | 10 | 2 | JP0072 | ribosomal protein   |
| 131 | 2 | 20.0 | 10 | 2 | C38925 | seed storage prote  |
| 132 | 2 | 20.0 | 10 | 2 | PC0753 | beta-fructofuranos  |
| 133 | 2 | 20.0 | 10 | 2 | PS0209 | 24K protein 4407 -  |
| 134 | 2 | 20.0 | 10 | 2 | A61622 | vitellogenin. 190k  |
| 135 | 2 | 20.0 | 10 | 2 | C39111 | Ig heavy chain C r  |
| 136 | 2 | 20.0 | 10 | 2 | PT0243 | Ig heavy chain CRD  |
| 137 | 2 | 20.0 | 10 | 2 | PT0284 | Ig heavy chain CRD  |
| 138 | 2 | 20.0 | 10 | 2 | PT0310 | Ig heavy chain CRD  |
| 139 | 2 | 20.0 | 10 | 2 | PH1344 | Ig heavy chain DJ   |
| 140 | 2 | 20.0 | 10 | 2 | B45482 | platelet activatin  |
| 141 | 2 | 20.0 | 10 | 2 | S66214 | cartilage oligomer  |
| 142 | 2 | 20.0 | 10 | 2 | C39398 | Fc mu (1gM) recept  |
| 143 | 2 | 20.0 | 10 | 2 | E48778 | small nuclear ribo  |
| 144 | 2 | 20.0 | 10 | 2 | E41946 | T-cell receptor ga  |
| 145 | 2 | 20.0 | 10 | 2 | C41946 | T-cell receptor ga  |
| 146 | 2 | 20.0 | 10 | 2 | B18887 | T-cell receptor ga  |
| 147 | 2 | 20.0 | 10 | 2 | S65715 | aryl hydrocarbon (  |
| 148 | 2 | 20.0 | 10 | 2 | S65385 | cytochrome-c oxida  |
| 149 | 2 | 20.0 | 10 | 2 | S13224 | vite protein - Agr  |
| 150 | 2 | 20.0 | 10 | 2 | S06964 | hypothetical prote  |
| 151 | 2 | 20.0 | 10 | 2 | A43590 | pillin type Ael - A |
| 152 | 2 | 20.0 | 10 | 2 | D28027 | protein P7 - curle  |
| 153 | 2 | 20.0 | 10 | 2 | PH0113 | alpha-amylase (EC   |
| 154 | 2 | 20.0 | 10 | 2 | S30348 | clotting protein -  |
| 155 | 2 | 20.0 | 10 | 2 | S43625 | cytochrome-c oxida  |
| 156 | 2 | 20.0 | 10 | 2 | S43630 | cytochrome-c oxida  |
| 157 | 2 | 20.0 | 10 | 2 | S43631 | cytochrome-c oxida  |
| 158 | 2 | 20.0 | 10 | 2 | B37196 | bradykinin-potent   |
| 159 | 2 | 20.0 | 10 | 2 | S66638 | acetylcholinestera  |
| 160 | 2 | 20.0 | 10 | 2 | F33932 | Ig mu chain J regi  |
| 161 | 2 | 20.0 | 10 | 2 | C54226 | light-harvesting p  |
| 162 | 2 | 20.0 | 10 | 2 | PC0785 | NADH2 dehydrogenas  |
| 163 | 2 | 20.0 | 10 | 2 | S74147 | glyceraldehyde-3-P  |
| 164 | 2 | 20.0 | 10 | 2 | H60787 | sperm-activating p  |
| 165 | 2 | 20.0 | 10 | 2 | G60787 | sperm-activating p  |
| 166 | 2 | 20.0 | 10 | 2 | G60787 | sperm-activating p  |
| 167 | 2 | 20.0 | 10 | 2 | E60787 | sperm-activating p  |
| 168 | 2 | 20.0 | 10 | 2 | G60787 | sperm-activating p  |
| 169 | 2 | 20.0 | 10 | 2 | B60787 | sperm-activating p  |
| 170 | 2 | 20.0 | 10 | 2 | D60588 | sperm-activating p  |
| 171 | 2 | 20.0 | 10 | 2 | B60588 | sperm-activating p  |
| 172 | 2 | 20.0 | 10 | 2 | G60588 | sperm-activating p  |
| 173 | 2 | 20.0 | 10 | 2 | I60527 | sperm-activating p  |
| 174 | 2 | 20.0 | 10 | 2 | D60527 | sperm-activating p  |
| 175 | 2 | 20.0 | 10 | 2 | C39572 | sperm-activating p  |

|     |   |      |    |   |        |                    |
|-----|---|------|----|---|--------|--------------------|
| 176 | 2 | 20.0 | 10 | 2 | F60527 | sperm-activating p |
| 177 | 2 | 20.0 | 10 | 2 | G60527 | sperm-activating p |
| 178 | 2 | 20.0 | 10 | 2 | E60527 | sperm-activating p |
| 179 | 2 | 20.0 | 10 | 2 | G60527 | sperm-activating p |
| 180 | 2 | 20.0 | 10 | 2 | E39572 | sperm-activating p |
| 181 | 2 | 20.0 | 10 | 2 | D60788 | sperm-activating p |
| 182 | 2 | 20.0 | 10 | 2 | E60788 | sperm-activating p |
| 183 | 2 | 20.0 | 10 | 2 | G60788 | sperm-activating p |
| 184 | 2 | 20.0 | 10 | 2 | F60589 | sperm-activating p |
| 185 | 2 | 20.0 | 10 | 2 | G60589 | sperm-activating p |
| 186 | 2 | 20.0 | 10 | 2 | D60589 | sperm-activating p |
| 187 | 2 | 20.0 | 10 | 2 | E60589 | sperm-activating p |
| 188 | 2 | 20.0 | 10 | 2 | B60589 | sperm-activating p |
| 189 | 2 | 20.0 | 10 | 2 | A60527 | sperm-activating p |
| 190 | 2 | 20.0 | 10 | 2 | A60787 | sperm-activating p |
| 191 | 2 | 20.0 | 10 | 2 | A60588 | sperm-activating p |
| 192 | 2 | 20.0 | 10 | 2 | A60788 | sperm-activating p |
| 193 | 2 | 20.0 | 10 | 2 | PC2172 | triacylglycerol 11 |
| 194 | 2 | 20.0 | 3  | 3 | A22565 | R-phycoerythrin al |
| 195 | 1 | 10.0 | 3  | 3 | A43391 | TRH-like tripeptid |
| 196 | 1 | 10.0 | 3  | 3 | F37196 | bradykinin-potent  |
| 197 | 1 | 10.0 | 3  | 3 | PT0636 | T-cell receptor be |
| 198 | 1 | 10.0 | 3  | 3 | PT0571 | tyrosine protein k |
| 199 | 1 | 10.0 | 3  | 3 | I78890 | blood cell protein |
| 200 | 1 | 10.0 | 3  | 3 | S68328 |                    |

## ALIGNMENTS

## RESULT 1

S71299 ICL2 protein - Parametium tetraurelia (fragment)

C:Species: Parametium tetraurelia

C&gt;Date: 11-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 07-Dec-1999

R:Accession: S71299

R:Madeddu, L.; Klotz, C.; le Caer, J.P.; Beilsen, J.

Eur. J. Biochem. 238, 121-128, 1996

A&gt;Title: Characterization of centrin genes in Parametium.

A:Reference number: S71298; MUID:96248429; PMID:8665928

A:Accession: S71299

A:Molecule type: protein

A:Residues: 1-7 &lt;MAD&gt;

A:Cross-references: UNIPARC:UPI000017B66B

A:Experimental source: strain d4-2

A:Genetic code: SGC5

Query Match 30.0%; Score 3; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;

QY 6 PQQ 8  
 |||  
 Db 5 PQQ 7

## RESULT 2

PH0108 late G1-69 protein - mouse (fragment)

C:Species: Mus musculus (house mouse)

C&gt;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999

C:Accession: PH0108

R:Nikaido, T.; Bradley, D.W.; Pardee, A.B.

Exp. Cell Res. 192, 102-109, 1991

A&gt;Title: Molecular cloning of transcripts that accumulate during the late G1 phase in cul

A:Reference number: PH0108; MUID:91078351; PMID:1984406

A:Accession: PH0108

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-9 &lt;NIK&gt;

A:Cross-references: UNIPARC:UPI000017C6E9

Query Match 30.0%; Score 3; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEY 3  
|||  
DB 7 EEY 9

## RESULT 3

A41978  
callitricarpamide 1 - bluebottle fly (Calliphora vomitoria)  
C/Species: Calliphora vomitoria  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
C/Accession: A41978  
R/Duve, H.; Johnsen, A.H.; Sewell, J.C.; Scott, A.G.; Orchard, I.; Rehfeld, J.F.; Thorpe  
Proc. Natl. Acad. Sci. U.S.A. 89, 2326-2330, 1992  
A/Title: Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH-2 neuropeptides (desi  
A/Reference number: A41978; MUID:92196111; PMID:1549595  
A/Accession: A41978  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-9 <DUV>  
A/Cross-references: UNIPROT:P41856; UNIPARC:UPI000012A50D  
C/Keywords: amidated carboxyl end; neuropeptide  
P/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 30.0%; Score 3; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PQQ 8  
|||  
DB 2 PQQ 4

## RESULT 4

A61218  
alpha-glucan 4Ha - grass (Haynaldia villosa) (fragment)  
C/Species: Haynaldia villosa, Daasyrium villosum  
C/Date: 19-Mar-1997 #sequence\_revision 19-Dec-1997 #text\_change 09-Jul-2004  
C/Accession: A61218  
R/Shewry, P.R.; Sabelli, P.A.; Parmar, S.; Lafandra, D.  
Biochem. Genet. 29, 207-211, 1991  
A/Title: alpha-type prolamins are encoded by genes on chromosomes 4Ha and 6Ha of Haynald  
A/Reference number: A61218; MUID:91315394; PMID:1859356  
A/Accession: A61218  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-10 <SHR>  
A/Cross-references: UNIPROT:Q7M1F7; UNIPARC:UPI000017CA45  
C/Keywords: seed; storage protein

Query Match 30.0%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPQ 7  
|||  
DB 6 VPQ 8

## RESULT 5

B61218  
alpha-glucan 6Ha - grass (Haynaldia villosa) (fragment)  
C/Species: Haynaldia villosa, Daasyrium villosum  
C/Date: 19-Mar-1997 #sequence\_revision 19-Dec-1997 #text\_change 09-Jul-2004  
C/Accession: B61218  
R/Shewry, P.R.; Sabelli, P.A.; Parmar, S.; Lafandra, D.  
Biochem. Genet. 29, 207-211, 1991  
A/Title: alpha-type prolamins are encoded by genes on chromosomes 4Ha and 6Ha of Haynald  
A/Reference number: A61218; MUID:91315394; PMID:1859356  
A/Accession: B61218

A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-10 <SHR>  
A/Cross-references: UNIPROT:Q7M1F6; UNIPARC:UPI000017B85  
C/Keywords: seed; storage protein

Query Match 30.0%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPQ 7  
|||  
DB 5 VPQ 7

## RESULT 6

PQ0010  
angiotensin-converting enzyme inhibitor (FIP-3) - common fig  
N/Alternate names: ficus latex peptide 3  
C/Species: Ficus carica (common fig)  
C/Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
C/Accession: PQ0010  
R/Maryama, S.; Miyoshi, S.; Tanaka, H.  
Agric. Biol. Chem. 53, 2763-2767, 1989  
A/Title: Angiotensin I-converting enzyme inhibitors derived from Ficus carica.  
A/Reference number: PQ0008  
A/Accession: PQ0010  
A/Molecule type: protein  
A/Residues: 1-3 <MAR>  
A/Cross-references: UNIPARC:UPI000011E971  
A/Experimental source: latex  
C/Keywords: angiotensin-converting enzyme inhibitor

Query Match 20.0%; Score 2; DB 3; Length 3;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LV 5  
|||  
DB 1 LV 2

## RESULT 7

E37196  
bradykinin-potentiating peptide 5 - island jararaca  
C/Species: Bothrops insularis (island jararaca)  
C/Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 30-Jun-2001  
C/Accession: E37196  
R/Cintre, A.C.O.; Vieira, C.A.; Giglio, J.R.  
J. Protein Chem. 9, 221-227, 1990  
A/Title: Primary structure and biological activity of bradykinin potentiating peptides fr  
A/Reference number: A37196; MUID:90351557; PMID:2286615  
A/Accession: E37196  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-3 <GIN>  
A/Cross-references: UNIPARC:UPI0000158403  
C/Keywords: pyroglutamic acid  
P/Modified site: pyroglutamic carboxylic acid (Gln) #status experimental

Query Match 20.0%; Score 2; DB 3; Length 3;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 QQ 8  
|||  
DB 1 QQ 2

## RESULT 8

A23751  
spinal cord peptide SCP-4 - pig  
C/Species: Sus scrofa domestica (domestic pig)

CjDate: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Mar-2004  
CjAccession: A23751  
RjHst, K.L.; Chen, R.L.; Chen, Z.G.; Zhang, H.L.; Lu, Y.A.; Guo, S.Y.; Wu, S.X.; Tsou, K.  
Arch. Biochem. Biophys. 240, 178-183, 1985  
AjReference number: A23751; MUID:85250425; PMID:4015098  
AjAccession: A23751  
AjStatus: preliminary  
AjMolecule type: protein  
AjResidues: 1-3 <HST>  
AjCross-References: UNIPARC:UPI000017CE97

Query Match 20.0%; Score 2; DB 3; Length 3;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 QG 9  
||  
DB 1 QG 2

RESULT 9  
EXXAA  
antho-RFamide neuropeptide - sea anemone (Anthopleura elegantissima)  
CjSpecies: Anthopleura elegantissima  
CjDate: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 09-Jul-2004  
CjAccession: A26666  
RjGrimmelikhuizen, C.J.P.; Graff, D.  
Proc. Natl. Acad. Sci. U.S.A. 83, 9817-9821, 1986  
AjTitle: Isolation of <Glu-Gly-Arg-Phe-NH2 (Antho-RFamide), a neuropeptide from sea anem  
AjReference number: A26666; MUID:87092339; PMID:2879288  
AjAccession: A26666  
AjMolecule type: protein  
AjResidues: 1-4 <GRI>  
AjCross-References: UNIPROT:P10419; UNIPARC:UPI00001733AF  
CjComment: The function of this peptide is not known but it could act as a transmitter a  
CjSuperfamily: RFamide neuropeptide  
CjKeywords: amidated carboxyl end; neuropeptide; pyroglutamic acid  
F1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F14/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 20.0%; Score 2; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 QG 9  
||  
DB 1 QG 2

RESULT 10  
B43848  
cell surface adhesin for heparan sulfate, 60K - Staphylococcus aureus (fragment)  
CjSpecies: Staphylococcus aureus  
CjDate: 10-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 24-Feb-1995  
CjAccession: B43848  
RjLiang, O.D.; Accencio, F.; Fransson, L.A.; Wadstrom, T.  
Infect. Immun. 60, 899-906, 1992  
AjTitle: Binding of heparan sulfate to Staphylococcus aureus.  
AjReference number: A43848; MUID:92176005; PMID:1541563  
AjAccession: B43848  
AjStatus: preliminary  
AjMolecule type: protein  
AjResidues: 1-4 <LHA>  
AjCross-References: UNIPARC:UPI000017ABF7  
AjNote: sequence extracted from NCBI backbone (NCBIP:85444)

Query Match 20.0%; Score 2; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LV 5  
||

DB 2 LV 3

RESULT 11  
T46627  
hypothetical protein c4 - loblolly pine  
CjSpecies: Pinus taeda (loblolly pine)  
CjDate: 18-Feb-2000 #sequence\_revision 18-Feb-2000 #text\_change 18-Feb-2000  
CjAccession: T46627  
RjChang, S.; Purya, J.; Funkhouser, B.A.; Newton, R.J.; Cairney, J.  
submitted to the EMBL Data Library, July 1995  
AjDescription: Cloning of a chitinase homolog which lacks chitin binding sites and is do  
AjReference number: 223105  
AjAccession: T46627  
AjStatus: preliminary; translated from GB/EMBL/DBJ  
AjMolecule type: mRNA  
AjResidues: 1-4 <CHA>  
AjCross-References: UNIPARC:UPI000011B913; EMBL:U31309; MUID:9974285; PID:9974292  
AjExperimental source: strain 66P7x86FT3; 8 month seedlings

Query Match 20.0%; Score 2; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LV 5  
||  
DB 3 LV 4

RESULT 12  
A25844  
antho-RF amide neuropeptide - sea pansy (Renilla koellikeri)  
CjSpecies: Renilla koellikeri (Koelliker's sea pansy)  
CjDate: 21-May-1998 #sequence\_revision 30-Sep-1993 #text\_change 11-Jul-1997  
CjAccession: A25844  
RjGrimmelikhuizen, C.J.P.; Groeger, A.  
RFS Lett. 211, 105-108, 1987  
AjTitle: Isolation of the neuropeptide pGlu-Gly-Arg-Phe-amide from the pennatulid Renilla  
AjReference number: A25844  
AjAccession: A25844  
AjMolecule type: protein  
AjResidues: 1-4 <GRI>  
AjCross-References: UNIPARC:UPI00001733AF  
CjKeywords: amidated carboxyl end; neuropeptide; pyroglutamic acid  
F1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F14/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 20.0%; Score 2; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 QG 9  
||  
DB 1 QG 2

RESULT 13  
I54357  
schwannomin - mouse (fragment)  
CjSpecies: Mus musculus (house mouse)  
CjDate: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 05-Nov-1999  
CjAccession: I54357  
RjHuynh, D.P.; Nechiporuk, T.; Puls, S.  
Hum. Mol. Genet. 3, 1075-1079, 1994  
AjTitle: Alternative transcripts in the mouse neurofibromatosis type 2 (NF2) gene are cor  
AjReference number: I54357; MUID:95072570; PMID:7981675  
AjAccession: I54357  
AjStatus: preliminary; translated from GB/EMBL/DBJ  
AjMolecule type: mRNA  
AjResidues: 1-4 <RSS>  
AjCross-References: UNIPARC:UPI000011B801; GB:I28838; MUID:9454836; PIDN:AAA57150.1; PID:9  
AjGene: NF2

Query Match 20.0%; Score 2; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VP 6  
 ||  
 1 VP 2

## RESULT 14

S55238  
 pallidipin - assassin bug (fragment)  
 C/Species: Triatoma pallidipennis (assassin bug)  
 C/Date: 19-Mar-1997 #sequence\_revision 18-Jul-1997 #text\_change 19-May-2000  
 C/Accession: S55238  
 R/Handler: B.; Becker, A.; Noeske-Dunplut, C.; Kraetzschmar, J.; Donner, P.; Schleunin  
 Biochem. J. 307, 465-470, 1995  
 A/Title: Expression of active recombinant pallidipin, a novel platelet aggregation inhib  
 A/Reference number: S55238; PMID:95251610; PMID:7733884  
 A/Accession: S55238  
 A/Molecule type: protein  
 A/Residues: 1-4 <HAE>  
 A/Cross-references: UNIPARC:UPI000017CB07

Query Match 20.0%; Score 2; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EE 2  
 ||  
 1 EE 2

## RESULT 15

S09478  
 globulin IV alpha subunit gamma chain, seed - cucurbit (fragment)  
 N/Alternate names: 11S globulin alpha subunit gamma chain  
 C/Species: Cucurbita sp. (cucurbit)  
 C/Date: 21-Nov-1993 #sequence\_revision 08-Nov-1996 #text\_change 08-Nov-1996  
 C/Accession: S09478  
 R/Ohmly, M.; Hara, I.; Matsubara, H.  
 Plant Cell Physiol. 21, 157-167, 1980  
 A/Title: Pumpkin (Cucurbita sp.) seed globulin IV. Terminal sequences of the acidic and  
 A/Reference number: S09066  
 A/Accession: S09478  
 A/Molecule type: protein  
 A/Residues: 1-4 <OHM>  
 A/Cross-references: UNIPARC:UPI000017CB16

Query Match 20.0%; Score 2; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 OG 9  
 ||  
 2 OG 3

## RESULT 16

A33480  
 achatin-I - giant African snail  
 N/Contains: achatin-II  
 C/Species: Achatina fulica (giant African snail)  
 C/Date: 12-Oct-1989 #sequence\_revision 12-Oct-1989 #text\_change 09-Jul-2004  
 C/Accession: A33480  
 R/Kametani, Y.; Minakata, H.; Kenny, P.T.M.; Iwashita, T.; Watanabe, K.; Funase, K.; Sut  
 Biochem. Biophys. Res. Commun. 160, 1015-1020, 1989  
 A/Title: Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina fulica feru  
 A/Reference number: A33480; PMID:9273551; PMID:2597281  
 A/Accession: A33480  
 A/Molecule type: protein  
 A/Residues: 1-4 <KAM>

A/Cross-references: UNIPROT:P35904; UNIPARC:UPI0000125223  
 A/Note: stereochemistry of the active form confirmed by chemical synthesis  
 R/ishida, T.; In, Y.; Inoue, M.; Yasuda-Kamatani, Y.; Minakata, H.; Iwashita, T.; Nomoto,  
 FEBS Lett. 307, 253-256, 1992  
 A/Title: Effect of the D-Phe(2) residue on molecular conformation of an endogenous neuro  
 (H-Gly-Phe-Ala-Asp-OH).  
 A/Reference number: A44691; PMID:92354723; PMID:1644179  
 A/Contents: annotation; X-ray crystallography, 0.85 angstroms  
 A/Note: achatin-II has L-phenylalanine  
 C/Keywords: D-amino acid  
 F/2/Modified site: D-phenylalanine (Phe) #status experimental

Query Match 20.0%; Score 2; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GP 10  
 ||  
 1 GP 2

## RESULT 17

HOKOHA  
 proctolin - American cockroach  
 C/Species: Periplaneta americana (American cockroach)  
 C/Date: 29-Jul-1981 #sequence\_revision 29-Jul-1981 #text\_change 09-Jul-2004  
 C/Accession: A01644  
 R/Starratt, A.N.; Brown, B.E.  
 Life Sci. 17, 1253-1256, 1975  
 A/Title: Structure of the pentapeptide proctolin, a proposed neurotransmitter in insects.  
 A/Reference number: A93048; PMID:76074708; PMID:576  
 A/Accession: A01644  
 A/Molecule type: protein  
 A/Residues: 1-5 <STR>  
 A/Cross-references: UNIPROT:P01373; UNIPARC:UPI0000132177  
 A/Note: the synthetic peptide had the same chromatographic, electrophoretic, and pharmac  
 R/O'Shea, M.; Adams, M.E.  
 Science 213, 567-569, 1981  
 A/Title: Pentapeptide (proctolin) associated with an identified neuron.  
 A/Reference number: A94260; PMID:8122585; PMID:6113690  
 A/Contents: annotation; biological source  
 C/Comment: This peptide is found in the lateral white neurons, which occur (in the cockr  
 innervate the striated hindgut muscles in insects and stimulate contraction of these musc  
 C/Superfamily: proctolin  
 C/Keywords: neuropeptide

Query Match 20.0%; Score 2; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YL 4  
 ||  
 2 YL 3

## RESULT 18

C41225  
 copper resistance protein - Pseudomonas syringae pv. tomato (fragment)  
 C/Species: Pseudomonas syringae pv. tomato  
 C/Date: 19-Jun-1992 #sequence\_revision 19-Jun-1992 #text\_change 24-Jun-1993  
 C/Accession: C41225  
 R/Cha, J.S.; Cooksey, D.A.  
 Proc. Natl. Acad. Sci. U.S.A. 88, 8915-8919, 1991  
 A/Title: Copper resistance in Pseudomonas syringae mediated by periplasmic and outer mem  
 A/Reference number: A41225; PMID:92020961; PMID:1924351  
 A/Accession: C41225  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-5 <CHA>  
 A/Cross-references: UNIPARC:UPI000017A984

Query Match 20.0%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 LV 5  
 DB 4 LV 5

## RESULT 19

B37325  
 pap fimbrial regulatory protein papI - Escherichia coli (fragment)  
 C:Species: Escherichia coli  
 C:Date: 11-Sep-1992 #sequence\_revision 11-Sep-1992 #text\_change 23-Mar-1993  
 C:Accession: B37325  
 R:Bratton, B.A.; Blym, L.B.; Skinner, B.S.; Low, D.A.  
 J:Biomet. 173, 1769-1800, 1991  
 A:Title: Evidence for a methylation-blocking factor (mbf) locus involved in pap pilus ex  
 A:Reference number: A37325; MUID:91154136; PMID:1671857  
 A:Accession: B37325  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-5 <BR>  
 A:Cross-references: UNIPARC:UPI000011B98D; GB:M63747

Query Match 20.0%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 BY 3  
 DB 3 BY 4

## RESULT 20

B22565  
 R-phycoerythrin alpha-2 chain - red alga (Gastrocionium coulteri) (fragment)  
 C:Species: Gastrocionium coulteri  
 C:Date: 07-Mar-1988 #sequence\_revision 07-Mar-1988 #text\_change 23-Mar-1993  
 C:Accession: B22565  
 R:Klotz, A.V.; Glazer, A.N.  
 J:Biol. Chem. 260, 4656-4663, 1985  
 A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.  
 A:Reference number: A22565; MUID:85182601; PMID:3886644  
 A:Accession: B22565  
 A:Molecule type: protein  
 A:Residues: 1-5 <KLO>  
 A:Cross-references: UNIPARC:UPI000017ABE3

Query Match 20.0%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VP 6  
 DB 3 VP 4

## RESULT 21

B61445  
 Leu-enkephalin - blue mussel  
 C:Species: Mytilus edulis (blue mussel)  
 C:Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 21-Jan-2000  
 C:Accession: B61445  
 R:Leung, M.K.; Stefano, G.B.  
 Proc. Natl. Acad. Sci. U.S.A. 81, 955-958, 1984  
 A:Title: Isolation and identification of enkephalins in pedal ganglia of Mytilus edulis  
 A:Reference number: A61445; MUID:84144823; PMID:6583690  
 A:Accession: B61445  
 A:Molecule type: protein  
 A:Residues: 1-5 <LEU>  
 A:Cross-references: UNIPARC:UPI000002D557  
 A:Experimental source: pedal ganglia  
 C:Keywords: neuropeptide; opioid peptide

Query Match 20.0%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 9 GF 10  
 DB 3 GF 4

## RESULT 22

A61445  
 Met-enkephalin - blue mussel  
 C:Species: Mytilus edulis (blue mussel)  
 C:Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 21-Jan-2000  
 C:Accession: A61445  
 R:Leung, M.K.; Stefano, G.B.  
 Proc. Natl. Acad. Sci. U.S.A. 81, 955-958, 1984  
 A:Title: Isolation and identification of enkephalins in pedal ganglia of Mytilus edulis  
 A:Reference number: A61445; MUID:84144823; PMID:6583690  
 A:Accession: A61445  
 A:Molecule type: protein  
 A:Residues: 1-5 <LEU>  
 A:Cross-references: UNIPARC:UPI000002CF9B  
 A:Experimental source: pedal ganglia  
 C:Keywords: neuropeptide; opioid peptide

Query Match 20.0%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GF 10  
 DB 3 GF 4

## RESULT 23

B61168  
 cocoonase (BC 3.4.21.-) - Chinese oak silkworm (fragment)  
 C:Species: Antheraea pernyi (Chinese oak silkworm)  
 C:Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 07-May-1999  
 C:Accession: B61168  
 R:Kramer, K.J.; Felsted, R.L.; Law, J.H.  
 J: Biol. Chem. 248, 3021-3028, 1973  
 A:Title: Cocoonase, V. Structural studies on an insect serine protease.  
 A:Reference number: A61168; MUID:7316540; PMID:4735570  
 A:Accession: B61168  
 A:Molecule type: protein  
 A:Residues: 1-5 <KRA>  
 A:Cross-references: UNIPARC:UPI000017BB47  
 A:Keywords: hydrolase; serine proteinase; zymogen  
 F:1-5/Product: cocoonase (fragment) #status experimental <MAT>

Query Match 20.0%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GF 10  
 DB 4 GF 5

## RESULT 24

JH0253  
 gut pentapeptide - Japanese eel  
 C:Species: Anguilla japonica (Japanese eel)  
 C:Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 11-Apr-1995  
 C:Accession: JH0253  
 R:Uesaka, T.; Ikeda, T.; Kubota, I.; Muneoka, Y.; Ando, M.  
 Biochem. Biophys. Res. Commun. 180, 828-832, 1991  
 A:Title: Structure and function of a pentapeptide isolated from the gut of the eel.  
 A:Reference number: JH0253; MUID:92062113; PMID:1953755  
 A:Accession: JH0253  
 A:Molecule type: protein

A:Residues: 1-5 <UES>  
A:Cross-references: UNIPARC:UPI000017BF42  
C:Date: 03-Feb-1993 #sequence\_revision 03-Feb-1993 #text\_change 09-Jul-2004  
C:Accession: A60411  
R:Groome, J.R.; Tillinghast, E.K.; Townley, M.A.; Vetrovs, A.; Watson III, W.H.; Hunt, D.  
Peptides 11, 205-211, 1990  
A:Title: Identification of proctolin in the central nervous system of the horseshoe crab,  
and of the circular muscle of the gastro-intestinal junction.

Query Match 20.0%; Score 2; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GF 10  
DB 1 GF 2

RESULT 25  
A60521  
glycogen phosphorylase (EC 2.4.1.1), muscle - mullet (Liza ramada) (fragment)  
N:Alternate names: glycogen phosphorylase b  
C:Species: Liza ramada  
C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 15-Mar-2004  
C:Accession: A60521  
R:Bonamura, L.; Baanante, I.V.  
Comp. Biochem. Physiol. B 95, 295-301, 1990  
A:Title: Purification and characterization of glycogen phosphorylase B from skeletal mus  
A:Reference number: A60521; PMID:90227907; PMID:2109669  
A:Accession: A60521  
A:Molecule type: protein  
A:Residues: 1-5 <BON>  
A:Cross-references: UNIPARC:UPI00001753C3  
C:Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein  
P/3/Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase) #status experim

Query Match 20.0%; Score 2; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VP 6  
DB 4 VP 5

RESULT 26  
A32014  
tram protein - Escherichia coli plasmid R100 (fragment)  
C:Species: Escherichia coli  
C:Date: 22-Jun-1989 #sequence\_revision 22-Jun-1989 #text\_change 09-Jul-2004  
C:Accession: A32014  
R:Imamoto, S.; Yoshioke, Y.; Ohtsubo, E.  
J. Bacteriol. 170, 2749-2757, 1988  
A:Title: Identification and characterization of the products from the trau and tray gene  
A:Reference number: A32014; PMID:88227859; PMID:2836369  
A:Accession: A32014  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-5 <INA>  
A:Cross-references: UNIPROT:P13973; UNIPARC:UPI000011ECA2  
C:Genetics:  
A:Genome: plasmid  
C:Keywords: DNA binding

Query Match 20.0%; Score 2; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EB 2  
DB 4 EB 5

RESULT 27  
A60411  
proctolin - Atlantic horseshoe crab

C:Species: Limulus polyphemus (Atlantic horseshoe crab)  
C:Date: 03-Feb-1993 #sequence\_revision 03-Feb-1993 #text\_change 09-Jul-2004  
C:Accession: A60411  
R:Groome, J.R.; Tillinghast, E.K.; Townley, M.A.; Vetrovs, A.; Watson III, W.H.; Hunt, D.  
Peptides 11, 205-211, 1990  
A:Title: Identification of proctolin in the central nervous system of the horseshoe crab,  
and of the circular muscle of the gastro-intestinal junction.  
A:Reference number: A60411; PMID:90287800; PMID:2356151  
A:Accession: A60411  
A:Molecule type: protein  
A:Residues: 1-5 <GRO>  
A:Cross-references: UNIPROT:P01373; UNIPARC:UPI0000132177  
C:Comment: This neuropeptide stimulates cardiac output and hindgut motility in the horse  
C:Keywords: neuropeptide

Query Match 20.0%; Score 2; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YL 4  
DB 2 YL 3

RESULT 28  
S11556  
hydrogenulfite reductase (EC 1.8.99.3) chain 2 - Desulfovibrio thermophilus (fragment)  
N:Alternate names: bisulfite reductase; desulfofuscidin  
C:Species: Desulfovibrio thermophilus  
C:Date: 19-Mar-1997 #sequence\_revision 12-Dec-1997 #text\_change 30-Jan-1998  
C:Accession: S11556  
R:Fauque, G.; Lino, A.R.; Czechowski, M.; Kang, L.; DerVartanian, D.V.; Moura, J.J.G.; Le  
Bichlm. Biophys. Acta 1040, 112-118, 1990  
A:Title: Purification and characterization of bisulfite reductase (desulfofuscidin) from  
A:Reference number: S11024; PMID:90335276; PMID:2165817  
A:Accession: S11556  
A:Molecule type: protein  
A:Residues: 1-6 <FAU>  
A:Cross-references: UNIPARC:UPI000017AB75  
C:Keywords: oxidoreductase

Query Match 20.0%; Score 2; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EB 2  
DB 2 EB 3

RESULT 29  
A37765  
hypothetical protein (cema 5' region) - Chloroflexus aurantiacus (fragment)  
C:Species: Chloroflexus aurantiacus  
C:Date: 31-May-1991 #sequence\_revision 31-May-1991 #text\_change 30-Sep-1993  
C:Accession: A37765  
R:Theroux, S.J.; Redlinger, T.E.; Fuller, R.C.; Robinson, S.J.  
J. Bacteriol. 172, 4497-4504, 1990  
A:Title: Gene encoding the 5.7-kilodalton chlorosome protein of Chloroflexus aurantiacus:  
A:Reference number: A37765; PMID:90330558; PMID:2376566  
A:Accession: A37765  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-6 <THE>  
A:Cross-references: UNIPARC:UPI000017ABA1; GB:M33964

Query Match 20.0%; Score 2; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PQ 7  
DB 1 PQ 2

```

RESULT 30
B44510
hypothetical protein C (mler 3' region) - Lactococcus lactis (fragment)
C:Species: Lactococcus lactis
C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 30-Sep-1993
C:Accession: B44510
R:Renault, P.; Gallardin, C.; Heeslot, H.
J. Bacteriol. 171, 3108-3114, 1989
A:Title: Product of the Lactococcus lactis gene required for malolactic fermentation is
A:Reference number: A44510; MUID:89255069; PMID:2498286
A:Accession: B44510
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-6 <REN>
A:Cross-references: UNIPARC:UPI000017AC46; EMBL:W90762

Query Match
Best Local Similarity 20.0%; Score 2; DB 2; Length 6;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YL 4
||
Db 5 YL 6

RESULT 31
I65546
MHC H2-L antigen - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C:Accession: I65546
R:Kimura, A.; Israel, A.; Le Bail, O.; Kourilsky, P.
Cell 44, 261-272, 1986
A:Title: Detailed analysis of the mouse H-2Kb promoter: Enhancer-like sequences and their
A:Reference number: I52778; MUID:86106202; PMID:3510743
A:Accession: I65546
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-6 <RES>
A:Cross-references: UNIPARC:UPI000011B8A9; GB:M12483; NID:9199565; PIDD:AAA39663.1; PID:

Query Match
Best Local Similarity 20.0%; Score 2; DB 2; Length 6;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VP 6
||
Db 2 VP 3

RESULT 32
PT0514
T-cell receptor beta chain V-D-J region (100-4AC) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0514
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0514
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-6 <FE>
A:Cross-references: UNIPARC:UPI000017C7B4
A:Experimental source: adult thymus, strain BALB/c
A:Keywords: T-cell receptor

Query Match
Best Local Similarity 20.0%; Score 2; DB 2; Length 6;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 8 QG 9
||
Db 5 QG 6

RESULT 33
A1946
T-cell receptor gamma chain (1c.22) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C:Accession: A1946
R:Whitwell, M.; Mosley, R.L.; Whetzel, L.; Scheffer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A:Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma ger
A:Reference number: A1946; MUID:92049316; PMID:1658619
A:Accession: A1946
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-6 <WHE>
A:Cross-references: UNIPARC:UPI000017C865
C:Keywords: T-cell receptor

Query Match
Best Local Similarity 20.0%; Score 2; DB 2; Length 6;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GF 10
||
Db 5 GF 6

RESULT 34
A60224
Met-enkephalin-Arg-Phe - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 21-Oct-1992 #sequence_revision 21-Oct-1992 #text_change 02-Sep-2000
C:Accession: A60224
R:Madden IV, J.; Evans, C.J.; Tyler, A.N.; Esch, F.S.; Boehlen, P.; Makr, G.; Weber, E.
J. Neurochem. 56, 1914-1920, 1991
A:Title: Isolation and characterization of opiod peptides from rabbit cerebellum.
A:Reference number: A60224; MUID:91225680; PMID:2027006
A:Accession: A60224
A:Status: preliminary
A:Molecule type: Protein
A:Residues: 1-7 <MAD>
A:Cross-references: UNIPARC:UPI00000352EB
C:Superfamily: proenkephalin
C:Keywords: neuropeptide; opiod peptide

Query Match
Best Local Similarity 20.0%; Score 2; DB 2; Length 7;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GF 10
||
Db 3 GF 4

RESULT 35
P00663
membrane protein - porcine epidemic diarrhea virus (isolate Belgian CV777) (fragment)
C:Species: porcine epidemic diarrhea virus
C:Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 08-Oct-1999
C:Accession: P00663
R:Bridgen, A.; Duarte, M.; Tobler, K.; Laude, H.; Ackermann, M.
J. Gen. Virol. 74, 1785-1804, 1993
A:Title: Sequence determination of the nucleocapsid protein gene of the porcine epidemic
isole gasastroenteritis virus.
A:Reference number: J02191; MUID:93389433; PMID:8397280
A:Accession: P00663
A:Molecule type: mRNA
A:Residues: 1-7 <BRI>
A:Cross-references: UNIPARC:UPI0000170FAC; GB:Z14976; NID:9311650; PIDD:CAA78699.1; PID:

```



C/Comment: This virus is coronavirus related to human coronavirus 229E.  
C/Keywords: membrane protein

Query Match 20.0%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LV 5  
DB 6 LV 7

## RESULT 36

A44428  
platelet aggregation-associated protein - Streptococcus sanguis (fragment)  
C/Species: Streptococcus sanguis  
C/Date: 11-Nov-1994 #sequence\_revision 11-Nov-1994 #text\_change 11-Nov-1994  
C/Accession: A44428  
R.Brickson, P.R.; Herzberg, M.C.  
J. Biol. Chem. 268, 1646-1649, 1993  
A/Title: The Streptococcus sanguis platelet aggregation-associated protein. Identification  
A/Reference number: A44428; MUID:93131902; PMID:8420939  
A/Accession: A44428  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-7 <ERL>  
A/Cross-references: UNIPARC:UPI000017AC2A  
C/Keywords: cell wall

Query Match 20.0%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 QG 9  
DB 4 QG 5

## RESULT 37

PT0087  
ribulose-bisphosphate carboxylase (EC 4.1.1.39) large chain - Arabidopsis thaliana (frag  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 10-Apr-1996 #sequence\_revision 24-May-1996 #text\_change 24-Nov-1999  
C/Accession: PT0087  
R.Yagita, A.; Kamo, M.; Kawakami, M.; Ohki, Y.  
Submitted to JIPD, December 1995  
A/Description: Two dimensional electrophoresis of plant proteins and standardization of  
A/Reference number: PN0173  
A/Accession: PT0087  
A/Molecule type: protein  
A/Residues: 1-7 <TSU>  
A/Cross-references: UNIPARC:UPI000017B001  
A/Experimental source: leaf  
C/Keywords: acetylated amino end; carbon-carbon lyase; carboxy-lyase  
P.1/Modified site: acetylated amino end (Ser) #status experimental

Query Match 20.0%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PQ 7  
DB 2 PQ 3

## RESULT 38

B61491  
seed protein w8-5 - winged bean (fragment)  
C/Species: Psophocarpus tetragonolobus (winged bean)  
C/Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 07-Oct-1994  
C/Accession: B61491  
R.Hirano, H.  
J. Protein Chem. 8, 115-130, 1989

A/Title: Microsequence analysis of winged bean seed proteins electrophoretically separated from two-dim

A/Reference number: A61491; MUID:89351606; PMID:2765119  
A/Accession: B61491  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-7 <HIR>  
A/Cross-references: UNIPARC:UPI000017B074  
C/Keywords: glycoprotein; seed

Query Match 20.0%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VP 6  
DB 3 VP 4

## RESULT 39

PQ0728  
unidentified 5.0/16k protein [imported] - rice (fragment)  
C/Species: Oryza sativa (rice)  
C/Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000  
C/Accession: PQ0728  
R.Komatsu, S.; Kajiwara, H.; Hirano, H.  
Theor. Appl. Genet. 86, 935-942, 1993  
A/Title: A rice protein library; a data-file of rice proteins separated by two-dimension  
A/Reference number: PQ0696  
A/Accession: PQ0728  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-7 <KOM>  
A/Cross-references: UNIPARC:UPI000017B123

Query Match 20.0%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LV 5  
DB 5 LV 6

## RESULT 40

S78024  
ribosomal protein Yml21, mitochondrial - yeast (Saccharomyces cerevisiae) (fragment)  
C/Species: Saccharomyces cerevisiae  
C/Date: 09-Oct-1997 #sequence\_revision 24-Oct-1997 #text\_change 14-Nov-1997  
C/Accession: S78024  
R.Kitakawa, M.; Grack, H.R.; Grobmann, L.; Goldschmidt-Reisin, S.; Herfurth, E.; Wiltmar  
Bur. J. Biochem. 245, 449-456, 1997  
A/Title: Identification and characterization of the genes for mitochondrial ribosomal pr  
A/Reference number: S78018; MUID:97296414; PMID:9151978  
A/Accession: S78024  
A/Molecule type: protein  
A/Residues: 1-7 <KIT>  
A/Cross-references: UNIPARC:UPI000017B33C  
C/Genetics: nuclear  
A/Genome: nuclear  
C/Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 20.0%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YL 4  
DB 1 YL 2

## RESULT 41

H33098  
180K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)

C:Species: Plasmodium falciparum  
 C:Date: 24-Aug-1990 #sequence\_revision 24-Aug-1990 #text\_change 09-Jun-2000  
 C:Accession: H33098  
 R:Nichols, J.H.; Hager, L.P.  
 Submitted to the Protein Sequence Database, May 1990  
 A:Reference number: A33098  
 A:Accession: H33098  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-7 <NIC>  
 A:Cross-references: UNIPARC:UPI000017B5R2

Query Match 20.0%; Score 2; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 QG 10  
 ||  
 DB 2 QG 3

## RESULT 42

PT0283  
 Ig heavy chain CRD3 region (clone 4-94B) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
 C:Accession: PT0283  
 R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caeon, A.J.; Rovera, G.  
 J. Exp. Med. 173, 395-407, 1991  
 A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J  
 A:Reference number: PT0222; MUID:91108337; PMID:1899102  
 A:Accession: PT0283  
 A:Molecule type: DNA  
 A:Residues: 1-7 <YAM>  
 A:Cross-references: UNIPARC:UPI000017C206  
 A:Experimental source: B lymphocyte  
 C:Keywords: heterotrimer; immunoglobulin

Query Match 20.0%; Score 2; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 QG 8  
 ||  
 DB 4 QG 5

## RESULT 43

B39040  
 calsequestrin, fast skeletal muscle - rabbit (fragment)  
 C:Species: Oryctolagus cuniculus (domestic rabbit)  
 C:Date: 23-Aug-1991 #sequence\_revision 23-Aug-1991 #text\_change 23-Feb-1997  
 C:Accession: B39040  
 R:Gale, S.E.; Jones, L.R.  
 J. Biol. Chem. 266, 391-398, 1991  
 A:Title: Phosphorylation of cardiac and skeletal muscle calsequestrin isoforms by casein  
 A:Reference number: A39040; MUID:91093153; PMID:1985907  
 A:Accession: B39040  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-7 <CAL>  
 A:Cross-references: UNIPARC:UPI000017C5BC  
 C:Keywords: phosphoprotein; skeletal muscle

Query Match 20.0%; Score 2; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EE 2  
 ||  
 DB 3 EE 4

## RESULT 44

PT0543  
 T-cell receptor beta chain V-D-J region (126-18B) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
 C:Accession: PT0543  
 R:Feeney, A.J.  
 J. Exp. Med. 174, 115-124, 1991  
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
 A:Reference number: PT0509; MUID:91277601; PMID:1711558  
 A:Accession: PT0543  
 A:Status: translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-7 <FEE>  
 A:Cross-references: UNIPARC:UPI000017C80B  
 A:Experimental source: day 18 fetal thymus, strain BALB/c  
 C:Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 QG 9  
 ||  
 DB 6 QG 7

## RESULT 45

PT0579  
 T-cell receptor beta chain V-D-J region (141-1N) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
 C:Accession: PT0579  
 R:Feeney, A.J.  
 J. Exp. Med. 174, 115-124, 1991  
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
 A:Reference number: PT0509; MUID:91277601; PMID:1711558  
 A:Accession: PT0579  
 A:Status: translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-7 <FEE>  
 A:Cross-references: UNIPARC:UPI000017C83B  
 A:Experimental source: day 19 fetal thymus, strain BALB/c  
 C:Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 QG 9  
 ||  
 DB 6 QG 7

## RESULT 46

PT0581  
 T-cell receptor beta chain V-D-J region (159-1A) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
 C:Accession: PT0581  
 R:Feeney, A.J.  
 J. Exp. Med. 174, 115-124, 1991  
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
 A:Reference number: PT0509; MUID:91277601; PMID:1711558  
 A:Accession: PT0581  
 A:Status: translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-7 <FEE>  
 A:Cross-references: UNIPARC:UPI000017C83B  
 A:Experimental source: day 19 fetal thymus, strain BALB/c  
 C:Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 QG 9  
Db 6 QG 7

## RESULT 47

T-cell receptor beta chain V-D-J region - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 04-Mar-2000

C/Accession: PT0671; PT0564; PT0537; PT0536; PT0682

R/Feeney, A.J. 174, 115-124, 1991

A/Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A/Reference number: PT0509; MUID:91277601; PMID:1711558

A/Accession: PT0671

A/Status: translation not shown

A/Molecule type: DNA

A/Residues: 1-7 <PEB>

A/Cross-references: UNIPARC:UPI000017C84A

A/Accession: PT0564

A/Status: translation not shown

A/Molecule type: mRNA

A/Residues: 1-6 <FE1>

A/Cross-references: UNIPARC:UPI000017C84B

A/Experimental source: day 19 fetal thymus, strain BALB/c, clone 141-1CE

A/Accession: PT0537

A/Status: translation not shown

A/Molecule type: mRNA

A/Residues: 1-6 <FE2>

A/Cross-references: UNIPARC:UPI000017C84B

A/Experimental source: adult thymus, strain BALB/c, clone 126-1CH

A/Accession: PT0536

A/Status: translation not shown

A/Molecule type: mRNA

A/Residues: 1-3 <FE3>

A/Cross-references: UNIPARC:UPI000017C84C

A/Experimental source: adult thymus, strain BALB/c, clone 126-1CC

A/Accession: PT0682

A/Status: translation not shown

A/Molecule type: DNA

A/Residues: 1-3 <FE4>

A/Cross-references: UNIPARC:UPI000017C84C

A/Experimental source: day 18 fetal thymus, strain BALB/c, clone 140-1B

C/Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 QG 9  
Db 5 QG 6

## RESULT 48

glucuronosyltransferase (EC 2.4.1.17), hepatic - rat (fragment)

N/Alternate names: UDP-glucuronosyltransferase

C/Species: Rattus norvegicus (Norway rat)

C/Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 07-Feb-1997

C/Accession: PX0008

R/Yokota, H.; Yuasa, A.; Sato, R.

J. Biochem. 104, 531-536, 1988

A/Title: Purification and properties of a form of UDP-glucuronosyltransferase from liver

A/Reference number: PX0008; MUID:9197852; PMID:3149280

A/Accession: PX0008

A/Molecule type: protein

A/Residues: 1-7 <YOK>

A/Cross-references: UNIPARC:UPI000017C913  
C/Keywords: glycosyltransferase; hexosyltransferase; liver

Query Match 20.0%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LV 5  
Db 4 LV 5

## RESULT 49

amine oxidase (copper-containing) (EC 1.4.3.6) - Yeast (*Pichia angusta*) (fragment)

A/Accession: A38081

C/Species: *Pichia angusta*

C/Date: 31-Dec-1993 #sequence\_revision 03-Feb-1994 #text\_change 20-Apr-2000

C/Accession: A38081

R/Mu, D.; Jones, S.M.; Smith, A.J.; Brown, D.E.; Dooley, D.M.; Kliman, J.P.

J. Biol. Chem. 267, 7979-7982, 1992

A/Title: Tyrosine codon corresponds to topa quinone at the active site of copper amine

A/Reference number: A38081; MUID:92235001; PMID:1569055

A/Accession: A38081

A/Molecule type: protein

A/Residues: 1-7 <MDA>

A/Cross-references: UNIPARC:UPI000017CA48

C/Keywords: copper; oxidoreductase; quinoprotein; topaquinone

P/4/Modified site: topaquinone (Tyr) #status experimental

Query Match 20.0%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EV 3  
Db 5 EV 6

## RESULT 50

Na+-transporting ATP synthase (EC 3.6.1.-) alpha chain - *Acetobacterium woodii* (fragment)

N/Alternate names: ATPase alpha chain

C/Species: *Acetobacterium woodii*

C/Date: 19-Mar-1997 #sequence\_revision 06-Jun-1997 #text\_change 07-May-1999

C/Accession: S45648

R/Reidinger, J.J.; Mueller, V.

Eur. J. Biochem. 223, 275-283, 1994

A/Title: Purification of ATP synthase from *Acetobacterium woodii* and identification as a

A/Reference number: S45648; MUID:94307271; PMID:8033902

A/Accession: S45648

A/Molecule type: protein

A/Residues: 1-34-7 <REI>

A/Cross-references: UNIPARC:UPI000017CA71; UNIPARC:UPI000017CA72

A/Experimental source: DSM 1030

C/Keywords: hydrolase

Query Match 20.0%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EE 2  
Db 5 EE 6

Search completed: January 18, 2006, 21:06:35  
Job time : 42 sec

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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 18, 2006, 20:49:16 : Search time 112 Seconds  
(without alignments)  
876.695 Million cell updates/sec

Title: US-09-930-125-2\_COPY\_975\_1209

Perfect score: 235  
Sequence: 1 EESRRARBPQRVYQINBDL.....AVENPEYLPGGAAPQHP 235

Scoring table:  
Gapop 60.0, Gapext 60.0

Searched: 1867569 seqs, 417829326 residues

Word size: 0  
Total number of hits satisfying chosen parameters: 1241939

Minimum DB seq length: 0  
Maximum DB seq length: 235

Post-Processing: Listing first 200 summaries

Database:

Published Applications AA Main:  
1: /cgn2\_6/prodata/1/pubppa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/prodata/1/pubppa/US08\_PUBCOMB.pep:\*  
3: /cgn2\_6/prodata/1/pubppa/US09\_PUBCOMB.pep:\*  
4: /cgn2\_6/prodata/1/pubppa/US10A\_PUBCOMB.pep:\*  
5: /cgn2\_6/prodata/1/pubppa/US10B\_PUBCOMB.pep:\*  
6: /cgn2\_6/prodata/1/pubppa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description          |
|------------|-------|-------------|--------|----|----------------------|
| 1          | 178   | 75.7        | 224    | 5  | US-10-149-138-3713   |
| 2          | 132   | 56.2        | 217    | 3  | US-09-821-883-25     |
| 3          | 132   | 56.2        | 217    | 6  | US-11-144-912-25     |
| 4          | 84    | 35.7        | 88     | 4  | US-10-029-186-29225  |
| 5          | 59    | 25.1        | 59     | 3  | US-09-854-356-5      |
| 6          | 45    | 19.1        | 79     | 4  | US-10-425-115-217661 |
| 7          | 39    | 16.6        | 135    | 3  | US-09-925-301-1232   |
| 8          | 37    | 15.7        | 221    | 5  | US-10-484-067-7      |
| 9          | 15    | 6.4         | 15     | 3  | US-09-354-533-51     |
| 10         | 15    | 6.4         | 15     | 3  | US-09-354-533-52     |
| 11         | 15    | 6.4         | 15     | 3  | US-09-354-533-53     |
| 12         | 15    | 6.4         | 15     | 3  | US-09-354-533-54     |
| 13         | 15    | 6.4         | 15     | 3  | US-09-354-533-55     |
| 14         | 15    | 6.4         | 15     | 4  | US-10-245-871-581    |
| 15         | 15    | 6.4         | 15     | 4  | US-10-149-138-3722   |
| 16         | 15    | 6.4         | 15     | 4  | US-10-149-138-3738   |
| 17         | 15    | 6.4         | 15     | 4  | US-10-149-138-3739   |
| 18         | 15    | 6.4         | 15     | 4  | US-10-149-138-3740   |
| 19         | 15    | 6.4         | 15     | 4  | US-10-149-138-3743   |
| 20         | 15    | 6.4         | 15     | 4  | US-10-149-138-3748   |
| 21         | 15    | 6.4         | 15     | 4  | US-10-149-138-3755   |
| 22         | 15    | 6.4         | 15     | 4  | US-10-149-138-3756   |
| 23         | 15    | 6.4         | 15     | 4  | US-10-149-138-3769   |
| 24         | 15    | 6.4         | 15     | 4  | US-10-149-138-3793   |
| 25         | 15    | 6.4         | 15     | 4  | US-10-149-138-3812   |
| 26         | 15    | 6.4         | 15     | 4  | US-10-149-138-3813   |
| 27         | 15    | 6.4         | 15     | 4  | US-10-149-138-3832   |

|     |    |     |    |   |                    |                   |
|-----|----|-----|----|---|--------------------|-------------------|
| 28  | 15 | 6.4 | 15 | 4 | US-10-149-138-3834 | Sequence 3834, Ap |
| 29  | 15 | 6.4 | 15 | 4 | US-10-149-138-3845 | Sequence 3845, Ap |
| 30  | 15 | 6.4 | 15 | 4 | US-10-149-138-3854 | Sequence 3854, Ap |
| 31  | 15 | 6.4 | 15 | 4 | US-10-149-138-3858 | Sequence 3858, Ap |
| 32  | 15 | 6.4 | 15 | 4 | US-10-149-138-3860 | Sequence 3860, Ap |
| 33  | 15 | 6.4 | 15 | 4 | US-10-149-138-3870 | Sequence 3870, Ap |
| 34  | 15 | 6.4 | 15 | 4 | US-10-149-138-3882 | Sequence 3882, Ap |
| 35  | 15 | 6.4 | 15 | 4 | US-10-149-138-3911 | Sequence 3911, Ap |
| 36  | 15 | 6.4 | 15 | 4 | US-10-149-138-3916 | Sequence 3916, Ap |
| 37  | 15 | 6.4 | 15 | 4 | US-10-149-138-3917 | Sequence 3917, Ap |
| 38  | 15 | 6.4 | 15 | 4 | US-10-149-138-3918 | Sequence 3918, Ap |
| 39  | 15 | 6.4 | 15 | 4 | US-10-149-138-3923 | Sequence 3923, Ap |
| 40  | 15 | 6.4 | 15 | 4 | US-10-149-138-3925 | Sequence 3925, Ap |
| 41  | 15 | 6.4 | 15 | 4 | US-10-149-138-3932 | Sequence 3932, Ap |
| 42  | 15 | 6.4 | 15 | 4 | US-10-149-138-3934 | Sequence 3934, Ap |
| 43  | 15 | 6.4 | 15 | 4 | US-10-149-138-3935 | Sequence 3935, Ap |
| 44  | 15 | 6.4 | 15 | 4 | US-10-149-138-3939 | Sequence 3939, Ap |
| 45  | 15 | 6.4 | 15 | 4 | US-10-149-138-3943 | Sequence 3943, Ap |
| 46  | 15 | 6.4 | 15 | 4 | US-10-149-138-3946 | Sequence 3946, Ap |
| 47  | 15 | 6.4 | 15 | 4 | US-10-149-138-4487 | Sequence 4487, Ap |
| 48  | 15 | 6.4 | 15 | 4 | US-10-149-138-4488 | Sequence 4488, Ap |
| 49  | 15 | 6.4 | 15 | 4 | US-10-149-138-4541 | Sequence 4541, Ap |
| 50  | 15 | 6.4 | 15 | 4 | US-10-149-138-4542 | Sequence 4542, Ap |
| 51  | 15 | 6.4 | 15 | 4 | US-10-149-138-4543 | Sequence 4543, Ap |
| 52  | 15 | 6.4 | 15 | 4 | US-10-149-138-4544 | Sequence 4544, Ap |
| 53  | 15 | 6.4 | 15 | 4 | US-10-149-138-4545 | Sequence 4545, Ap |
| 54  | 15 | 6.4 | 15 | 4 | US-10-149-138-4546 | Sequence 4546, Ap |
| 55  | 15 | 6.4 | 15 | 4 | US-10-149-138-4547 | Sequence 4547, Ap |
| 56  | 15 | 6.4 | 15 | 4 | US-10-149-138-4548 | Sequence 4548, Ap |
| 57  | 15 | 6.4 | 15 | 4 | US-10-149-138-4549 | Sequence 4549, Ap |
| 58  | 15 | 6.4 | 15 | 4 | US-10-149-138-4550 | Sequence 4550, Ap |
| 59  | 15 | 6.4 | 15 | 4 | US-10-149-138-4551 | Sequence 4551, Ap |
| 60  | 15 | 6.4 | 15 | 4 | US-10-253-286-581  | Sequence 581, Ap  |
| 61  | 15 | 6.4 | 15 | 4 | US-10-647-005-581  | Sequence 581, Ap  |
| 62  | 15 | 6.4 | 15 | 4 | US-10-647-005-582  | Sequence 582, Ap  |
| 63  | 15 | 6.4 | 15 | 4 | US-10-647-005-583  | Sequence 583, Ap  |
| 64  | 15 | 6.4 | 15 | 4 | US-10-647-005-584  | Sequence 584, Ap  |
| 65  | 15 | 6.4 | 15 | 4 | US-10-647-005-585  | Sequence 585, Ap  |
| 66  | 15 | 6.4 | 15 | 4 | US-10-149-138-3722 | Sequence 3722, Ap |
| 67  | 15 | 6.4 | 15 | 4 | US-10-149-138-3729 | Sequence 3729, Ap |
| 68  | 15 | 6.4 | 15 | 4 | US-10-149-138-3730 | Sequence 3730, Ap |
| 69  | 15 | 6.4 | 15 | 4 | US-10-149-138-3743 | Sequence 3743, Ap |
| 70  | 15 | 6.4 | 15 | 4 | US-10-149-138-3748 | Sequence 3748, Ap |
| 71  | 15 | 6.4 | 15 | 4 | US-10-149-138-3755 | Sequence 3755, Ap |
| 72  | 15 | 6.4 | 15 | 4 | US-10-149-138-3756 | Sequence 3756, Ap |
| 73  | 15 | 6.4 | 15 | 4 | US-10-149-138-3769 | Sequence 3769, Ap |
| 74  | 15 | 6.4 | 15 | 4 | US-10-149-138-3812 | Sequence 3812, Ap |
| 75  | 15 | 6.4 | 15 | 4 | US-10-149-138-3813 | Sequence 3813, Ap |
| 76  | 15 | 6.4 | 15 | 4 | US-10-149-138-3814 | Sequence 3814, Ap |
| 77  | 15 | 6.4 | 15 | 4 | US-10-149-138-3824 | Sequence 3824, Ap |
| 78  | 15 | 6.4 | 15 | 4 | US-10-149-138-3832 | Sequence 3832, Ap |
| 79  | 15 | 6.4 | 15 | 4 | US-10-149-138-3845 | Sequence 3845, Ap |
| 80  | 15 | 6.4 | 15 | 4 | US-10-149-138-3854 | Sequence 3854, Ap |
| 81  | 15 | 6.4 | 15 | 4 | US-10-149-138-3858 | Sequence 3858, Ap |
| 82  | 15 | 6.4 | 15 | 4 | US-10-149-138-3860 | Sequence 3860, Ap |
| 83  | 15 | 6.4 | 15 | 4 | US-10-149-138-3870 | Sequence 3870, Ap |
| 84  | 15 | 6.4 | 15 | 4 | US-10-149-138-3882 | Sequence 3882, Ap |
| 85  | 15 | 6.4 | 15 | 4 | US-10-149-138-3911 | Sequence 3911, Ap |
| 86  | 15 | 6.4 | 15 | 4 | US-10-149-138-3916 | Sequence 3916, Ap |
| 87  | 15 | 6.4 | 15 | 4 | US-10-149-138-3917 | Sequence 3917, Ap |
| 88  | 15 | 6.4 | 15 | 4 | US-10-149-138-3918 | Sequence 3918, Ap |
| 89  | 15 | 6.4 | 15 | 4 | US-10-149-138-3923 | Sequence 3923, Ap |
| 90  | 15 | 6.4 | 15 | 4 | US-10-149-138-3925 | Sequence 3925, Ap |
| 91  | 15 | 6.4 | 15 | 4 | US-10-149-138-3932 | Sequence 3932, Ap |
| 92  | 15 | 6.4 | 15 | 4 | US-10-149-138-3934 | Sequence 3934, Ap |
| 93  | 15 | 6.4 | 15 | 4 | US-10-149-138-3935 | Sequence 3935, Ap |
| 94  | 15 | 6.4 | 15 | 4 | US-10-149-138-3939 | Sequence 3939, Ap |
| 95  | 15 | 6.4 | 15 | 4 | US-10-149-138-3943 | Sequence 3943, Ap |
| 96  | 15 | 6.4 | 15 | 4 | US-10-149-138-3946 | Sequence 3946, Ap |
| 97  | 15 | 6.4 | 15 | 4 | US-10-149-138-4487 | Sequence 4487, Ap |
| 98  | 15 | 6.4 | 15 | 4 | US-10-149-138-4488 | Sequence 4488, Ap |
| 99  | 15 | 6.4 | 15 | 4 | US-10-149-138-4541 | Sequence 4541, Ap |
| 100 | 15 | 6.4 | 15 | 4 | US-10-149-138-4542 | Sequence 4542, Ap |

|     |    |     |    |   |                    |                   |     |    |     |    |   |                    |                   |
|-----|----|-----|----|---|--------------------|-------------------|-----|----|-----|----|---|--------------------|-------------------|
| 101 | 15 | 6.4 | 15 | 4 | US-10-149-138-4542 | Sequence 4542, Ap | 174 | 11 | 4.7 | 11 | 4 | US-10-149-138-1581 | Sequence 1581, Ap |
| 102 | 15 | 6.4 | 15 | 4 | US-10-149-138-4543 | Sequence 4543, Ap | 175 | 11 | 4.7 | 11 | 4 | US-10-149-138-1598 | Sequence 1598, Ap |
| 103 | 15 | 6.4 | 15 | 4 | US-10-149-138-4544 | Sequence 4544, Ap | 176 | 11 | 4.7 | 11 | 4 | US-10-149-138-1689 | Sequence 1689, Ap |
| 104 | 15 | 6.4 | 15 | 4 | US-10-149-138-4545 | Sequence 4545, Ap | 177 | 11 | 4.7 | 11 | 4 | US-10-149-138-1692 | Sequence 1692, Ap |
| 105 | 15 | 6.4 | 15 | 4 | US-10-149-138-4546 | Sequence 4546, Ap | 178 | 11 | 4.7 | 11 | 4 | US-10-149-138-1798 | Sequence 1798, Ap |
| 106 | 15 | 6.4 | 15 | 4 | US-10-149-138-4547 | Sequence 4547, Ap | 179 | 11 | 4.7 | 11 | 4 | US-10-149-138-1805 | Sequence 1805, Ap |
| 107 | 15 | 6.4 | 15 | 4 | US-10-149-138-4548 | Sequence 4548, Ap | 180 | 11 | 4.7 | 11 | 4 | US-10-149-138-1817 | Sequence 1817, Ap |
| 108 | 15 | 6.4 | 15 | 4 | US-10-149-138-4549 | Sequence 4549, Ap | 181 | 11 | 4.7 | 11 | 4 | US-10-149-138-1858 | Sequence 1858, Ap |
| 109 | 15 | 6.4 | 15 | 4 | US-10-149-138-4550 | Sequence 4550, Ap | 182 | 11 | 4.7 | 11 | 4 | US-10-149-138-1866 | Sequence 1866, Ap |
| 110 | 15 | 6.4 | 15 | 4 | US-10-149-138-4551 | Sequence 4551, Ap | 183 | 11 | 4.7 | 11 | 4 | US-10-149-138-1896 | Sequence 1896, Ap |
| 111 | 15 | 6.4 | 15 | 6 | US-11-121-347-51   | Sequence 51, Appl | 184 | 11 | 4.7 | 11 | 4 | US-10-149-138-1928 | Sequence 1928, Ap |
| 112 | 15 | 6.4 | 15 | 6 | US-11-121-347-52   | Sequence 52, Appl | 185 | 11 | 4.7 | 11 | 4 | US-10-149-138-1938 | Sequence 1938, Ap |
| 113 | 15 | 6.4 | 15 | 6 | US-11-121-347-53   | Sequence 53, Appl | 186 | 11 | 4.7 | 11 | 4 | US-10-149-138-1938 | Sequence 1938, Ap |
| 114 | 15 | 6.4 | 15 | 6 | US-11-121-347-54   | Sequence 54, Appl | 187 | 11 | 4.7 | 11 | 4 | US-10-149-138-1945 | Sequence 1945, Ap |
| 115 | 15 | 6.4 | 15 | 6 | US-11-121-347-55   | Sequence 55, Appl | 188 | 11 | 4.7 | 11 | 4 | US-10-149-138-1952 | Sequence 1952, Ap |
| 116 | 13 | 5.5 | 13 | 4 | US-10-001-546-45   | Sequence 45, Appl | 189 | 11 | 4.7 | 11 | 4 | US-10-149-138-1963 | Sequence 1963, Ap |
| 117 | 13 | 5.5 | 13 | 5 | US-10-948-707-1219 | Sequence 1219, Ap | 190 | 11 | 4.7 | 11 | 4 | US-10-149-138-1970 | Sequence 1970, Ap |
| 118 | 12 | 5.1 | 12 | 4 | US-10-245-871-574  | Sequence 574, Ap  | 191 | 11 | 4.7 | 11 | 4 | US-10-149-138-2014 | Sequence 2014, Ap |
| 119 | 12 | 5.1 | 12 | 4 | US-10-253-286-574  | Sequence 574, Ap  | 192 | 11 | 4.7 | 11 | 4 | US-10-149-138-2017 | Sequence 2017, Ap |
| 120 | 11 | 4.7 | 11 | 3 | US-09-017-743C-118 | Sequence 118, Ap  | 193 | 11 | 4.7 | 11 | 4 | US-10-149-138-2026 | Sequence 2026, Ap |
| 121 | 11 | 4.7 | 11 | 3 | US-09-017-743C-119 | Sequence 119, Ap  | 194 | 11 | 4.7 | 11 | 4 | US-10-149-138-2047 | Sequence 2047, Ap |
| 122 | 11 | 4.7 | 11 | 4 | US-10-149-138-108  | Sequence 108, Ap  | 195 | 11 | 4.7 | 11 | 4 | US-10-149-138-2097 | Sequence 2097, Ap |
| 123 | 11 | 4.7 | 11 | 4 | US-10-149-138-120  | Sequence 120, Ap  | 196 | 11 | 4.7 | 11 | 4 | US-10-149-138-2154 | Sequence 2154, Ap |
| 124 | 11 | 4.7 | 11 | 4 | US-10-149-138-123  | Sequence 123, Ap  | 197 | 11 | 4.7 | 11 | 4 | US-10-149-138-2226 | Sequence 2226, Ap |
| 125 | 11 | 4.7 | 11 | 4 | US-10-149-138-125  | Sequence 125, Ap  | 198 | 11 | 4.7 | 11 | 4 | US-10-149-138-2228 | Sequence 2228, Ap |
| 126 | 11 | 4.7 | 11 | 4 | US-10-149-138-212  | Sequence 212, Ap  | 199 | 11 | 4.7 | 11 | 4 | US-10-149-138-2244 | Sequence 2244, Ap |
| 127 | 11 | 4.7 | 11 | 4 | US-10-149-138-230  | Sequence 230, Ap  | 200 | 11 | 4.7 | 11 | 4 | US-10-149-138-2281 | Sequence 2281, Ap |
| 128 | 11 | 4.7 | 11 | 4 | US-10-149-138-292  | Sequence 292, Ap  |     |    |     |    |   |                    |                   |
| 129 | 11 | 4.7 | 11 | 4 | US-10-149-138-299  | Sequence 299, Ap  |     |    |     |    |   |                    |                   |
| 130 | 11 | 4.7 | 11 | 4 | US-10-149-138-342  | Sequence 342, Ap  |     |    |     |    |   |                    |                   |
| 131 | 11 | 4.7 | 11 | 4 | US-10-149-138-419  | Sequence 419, Ap  |     |    |     |    |   |                    |                   |
| 132 | 11 | 4.7 | 11 | 4 | US-10-149-138-438  | Sequence 438, Ap  |     |    |     |    |   |                    |                   |
| 133 | 11 | 4.7 | 11 | 4 | US-10-149-138-451  | Sequence 451, Ap  |     |    |     |    |   |                    |                   |
| 134 | 11 | 4.7 | 11 | 4 | US-10-149-138-523  | Sequence 523, Ap  |     |    |     |    |   |                    |                   |
| 135 | 11 | 4.7 | 11 | 4 | US-10-149-138-529  | Sequence 529, Ap  |     |    |     |    |   |                    |                   |
| 136 | 11 | 4.7 | 11 | 4 | US-10-149-138-560  | Sequence 560, Ap  |     |    |     |    |   |                    |                   |
| 137 | 11 | 4.7 | 11 | 4 | US-10-149-138-582  | Sequence 582, Ap  |     |    |     |    |   |                    |                   |
| 138 | 11 | 4.7 | 11 | 4 | US-10-149-138-590  | Sequence 590, Ap  |     |    |     |    |   |                    |                   |
| 139 | 11 | 4.7 | 11 | 4 | US-10-149-138-592  | Sequence 592, Ap  |     |    |     |    |   |                    |                   |
| 140 | 11 | 4.7 | 11 | 4 | US-10-149-138-597  | Sequence 597, Ap  |     |    |     |    |   |                    |                   |
| 141 | 11 | 4.7 | 11 | 4 | US-10-149-138-606  | Sequence 606, Ap  |     |    |     |    |   |                    |                   |
| 142 | 11 | 4.7 | 11 | 4 | US-10-149-138-610  | Sequence 610, Ap  |     |    |     |    |   |                    |                   |
| 143 | 11 | 4.7 | 11 | 4 | US-10-149-138-611  | Sequence 611, Ap  |     |    |     |    |   |                    |                   |
| 144 | 11 | 4.7 | 11 | 4 | US-10-149-138-681  | Sequence 681, Ap  |     |    |     |    |   |                    |                   |
| 145 | 11 | 4.7 | 11 | 4 | US-10-149-138-682  | Sequence 682, Ap  |     |    |     |    |   |                    |                   |
| 146 | 11 | 4.7 | 11 | 4 | US-10-149-138-702  | Sequence 702, Ap  |     |    |     |    |   |                    |                   |
| 147 | 11 | 4.7 | 11 | 4 | US-10-149-138-728  | Sequence 728, Ap  |     |    |     |    |   |                    |                   |
| 148 | 11 | 4.7 | 11 | 4 | US-10-149-138-746  | Sequence 746, Ap  |     |    |     |    |   |                    |                   |
| 149 | 11 | 4.7 | 11 | 4 | US-10-149-138-805  | Sequence 805, Ap  |     |    |     |    |   |                    |                   |
| 150 | 11 | 4.7 | 11 | 4 | US-10-149-138-806  | Sequence 806, Ap  |     |    |     |    |   |                    |                   |
| 151 | 11 | 4.7 | 11 | 4 | US-10-149-138-845  | Sequence 845, Ap  |     |    |     |    |   |                    |                   |
| 152 | 11 | 4.7 | 11 | 4 | US-10-149-138-888  | Sequence 888, Ap  |     |    |     |    |   |                    |                   |
| 153 | 11 | 4.7 | 11 | 4 | US-10-149-138-899  | Sequence 899, Ap  |     |    |     |    |   |                    |                   |
| 154 | 11 | 4.7 | 11 | 4 | US-10-149-138-968  | Sequence 968, Ap  |     |    |     |    |   |                    |                   |
| 155 | 11 | 4.7 | 11 | 4 | US-10-149-138-1005 | Sequence 1005, Ap |     |    |     |    |   |                    |                   |
| 156 | 11 | 4.7 | 11 | 4 | US-10-149-138-1032 | Sequence 1032, Ap |     |    |     |    |   |                    |                   |
| 157 | 11 | 4.7 | 11 | 4 | US-10-149-138-1099 | Sequence 1099, Ap |     |    |     |    |   |                    |                   |
| 158 | 11 | 4.7 | 11 | 4 | US-10-149-138-1147 | Sequence 1147, Ap |     |    |     |    |   |                    |                   |
| 159 | 11 | 4.7 | 11 | 4 | US-10-149-138-1161 | Sequence 1161, Ap |     |    |     |    |   |                    |                   |
| 160 | 11 | 4.7 | 11 | 4 | US-10-149-138-1280 | Sequence 1280, Ap |     |    |     |    |   |                    |                   |
| 161 | 11 | 4.7 | 11 | 4 | US-10-149-138-1290 | Sequence 1290, Ap |     |    |     |    |   |                    |                   |
| 162 | 11 | 4.7 | 11 | 4 | US-10-149-138-1353 | Sequence 1353, Ap |     |    |     |    |   |                    |                   |
| 163 | 11 | 4.7 | 11 | 4 | US-10-149-138-1369 | Sequence 1369, Ap |     |    |     |    |   |                    |                   |
| 164 | 11 | 4.7 | 11 | 4 | US-10-149-138-1390 | Sequence 1390, Ap |     |    |     |    |   |                    |                   |
| 165 | 11 | 4.7 | 11 | 4 | US-10-149-138-1463 | Sequence 1463, Ap |     |    |     |    |   |                    |                   |
| 166 | 11 | 4.7 | 11 | 4 | US-10-149-138-1467 | Sequence 1467, Ap |     |    |     |    |   |                    |                   |
| 167 | 11 | 4.7 | 11 | 4 | US-10-149-138-1470 | Sequence 1470, Ap |     |    |     |    |   |                    |                   |
| 168 | 11 | 4.7 | 11 | 4 | US-10-149-138-1486 | Sequence 1486, Ap |     |    |     |    |   |                    |                   |
| 169 | 11 | 4.7 | 11 | 4 | US-10-149-138-1495 | Sequence 1495, Ap |     |    |     |    |   |                    |                   |
| 170 | 11 | 4.7 | 11 | 4 | US-10-149-138-1513 | Sequence 1513, Ap |     |    |     |    |   |                    |                   |
| 171 | 11 | 4.7 | 11 | 4 | US-10-149-138-1538 | Sequence 1538, Ap |     |    |     |    |   |                    |                   |
| 172 | 11 | 4.7 | 11 | 4 | US-10-149-138-1553 | Sequence 1553, Ap |     |    |     |    |   |                    |                   |
| 173 | 11 | 4.7 | 11 | 4 | US-10-149-138-1576 | Sequence 1576, Ap |     |    |     |    |   |                    |                   |

## ALIGNMENTS

Sequence 1581, Ap

Sequence 1598, Ap

Sequence 1689, Ap

Sequence 1692, Ap

Sequence 1798, Ap

Sequence 1805, Ap

Sequence 1817, Ap

Sequence 1858, Ap

Sequence 1866, Ap

Sequence 1924, Ap

Sequence 1928, Ap

Sequence 1938, Ap

Sequence 1945, Ap

Sequence 1952, Ap

Sequence 1963, Ap

Sequence 1970, Ap

Sequence 2014, Ap

Sequence 2017, Ap

Sequence 2026, Ap

Sequence 2047, Ap

Sequence 2097, Ap

Sequence 2154, Ap

Sequence 2226, Ap

Sequence 2228, Ap

Sequence 2244, Ap

Sequence 2281, Ap

RESULT 1  
US-10-484-067-13

Sequence 13, Application US/10484067  
Publication No. US20040241686A1

GENERAL INFORMATION:  
APPLICANT: UNIVERSITY OF CALIFORNIA

TITLE OF INVENTION: HBR2/NEU TARGET ANTIGEN AND USE OF SAME TO STIMULATE AN IMMUNE RES

FILE REFERENCE: UC11170-1  
CURRENT APPLICATION NUMBER: US/10/484,067

PRIOR FILING DATE: 2004-01-15  
PRIOR FILING DATE: 2002-07-18

PRIOR APPLICATION NUMBER: PCT/US02/22975  
PRIOR FILING DATE: 2001-07-18

NUMBER OF SEQ ID NOS: 14  
SOFTWARE: Patentin version 3.1

SEQ ID NO 13  
LENGTH: 224

TYPE: PRT  
ORGANISM: Homo sapiens

US-10-484-067-13

Query Match 75.7%; Score 178; DB 5; Length 224;  
Best Local Similarity 100.0%; Pred. No. 7.5e-149;

Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

58 CDDPAPGAGMWHHRSSSTRSGGDTLGLFEBEERAPRPLAPSGAGSDVDDG 117

1 CDDPAPGAGMWHHRSSSTRSGGDTLGLFEBEERAPRPLAPSGAGSDVDDG 60

118 MGAAGLGLSLPHDPSLORVSEDTPLPSETDGVAPLTCSPQPEYVNOQDVAPQPS 177

61 MGAAGLGLSLPHDPSLORVSEDTPLPSETDGVAPLTCSPQPEYVNOQDVAPQPS 120

178 PREGPLPAPRPAATLBRPKTLSPGKNGVXDFVAFGAVENPEYLTTPGGAAPQPH 235

121 PREGPLPAPRPAATLBRPKTLSPGKNGVXDFVAFGAVENPEYLTTPGGAAPQPH 178

RESULT 2

US-09-821-883-25  
; Sequence 25, Application US/09821883  
; Patent No. US2002061310A1  
; GENERAL INFORMATION:  
; APPLICANT: Laus, Reiner  
; APPLICANT: Vidovic, Damir  
; APPLICANT: Gradidis, Thomas  
; TITLE OF INVENTION: Compositions and Methods for Dendritic  
; FILE REFERENCE: 7636-0022.30  
; CURRENT APPLICATION NUMBER: US/09/821,883  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: US 60/193,504  
; PRIOR FILING DATE: 2000-03-30  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 25  
; LENGTH: 217  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-821-883-25

Query Match 56.2%; Score 132; DB 3; Length 217;  
Best Local Similarity 100.0%; Pred. No. 3.2e-108;  
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 GAGCMVHHRRSSSTRSGGDLTLGLPSEBEPSPPLAPSEAGSDVDPDGLGMAAG 123  
DB 1 GAGCMVHHRRSSSTRSGGDLTLGLPSEBEPSPPLAPSEAGSDVDPDGLGMAAG 60

QY 124 LQSLPTHDSPLQRYSEDPVPLPSETDGYVAPLTCSPQPEYVNOQDVAPQPPSPREGPL 183  
DB 61 LQSLPTHDSPLQRYSEDPVPLPSETDGYVAPLTCSPQPEYVNOQDVAPQPPSPREGPL 120

QY 184 PAARPAGATTLER 195  
DB 121 PAARPAGATTLER 132

RESULT 3  
US-11-144-912-25  
; Sequence 25, Application US/11144912  
; Publication No. US20050232932A1  
; GENERAL INFORMATION:  
; APPLICANT: Laus, Reiner  
; APPLICANT: Vidovic, Damir  
; APPLICANT: Gradidis, Thomas  
; TITLE OF INVENTION: Compositions and Methods for Dendritic  
; FILE REFERENCE: 7636-0022.30  
; CURRENT APPLICATION NUMBER: US/11/144,912  
; PRIOR FILING DATE: 2005-06-03  
; PRIOR APPLICATION NUMBER: US/09/821,883  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: US 60/193,504  
; PRIOR FILING DATE: 2000-03-30  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 25  
; LENGTH: 217  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-144-912-25

Query Match 56.2%; Score 132; DB 6; Length 217;  
Best Local Similarity 100.0%; Pred. No. 3.2e-108;  
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 GAGCMVHHRRSSSTRSGGDLTLGLPSEBEPSPPLAPSEAGSDVDPDGLGMAAG 123  
DB 1 GAGCMVHHRRSSSTRSGGDLTLGLPSEBEPSPPLAPSEAGSDVDPDGLGMAAG 60

QY 124 LQSLPTHDSPLQRYSEDPVPLPSETDGYVAPLTCSPQPEYVNOQDVAPQPPSPREGPL 183  
DB 61 LQSLPTHDSPLQRYSEDPVPLPSETDGYVAPLTCSPQPEYVNOQDVAPQPPSPREGPL 120

QY 184 PAARPAGATTLER 195  
DB 121 PAARPAGATTLER 132

DB 61 LQSLPTHDSPLQRYSEDPVPLPSETDGYVAPLTCSPQPEYVNOQDVAPQPPSPREGPL 120  
QY 184 PAARPAGATTLER 195  
DB 121 PAARPAGATTLER 132

RESULT 4  
US-10-029-386-29225  
; Sequence 29225, Application US/10029386  
; Publication No. US20030194704A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharon G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G  
; FILE REFERENCE: AEOMICA-X-2  
; CURRENT APPLICATION NUMBER: US/10/029,386  
; PRIOR FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 34288  
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 29225  
; LENGTH: 88  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO CHR17.1  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1  
; OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 1.5  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.4  
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.91  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.3  
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.9  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.6  
; OTHER INFORMATION: SWISSPROT HIT: P04626, EVALU6 6.00e-45  
US-10-029-386-29225

Query Match 35.7%; Score 84; DB 4; Length 88;  
Best Local Similarity 100.0%; Pred. No. 3.8e-66;  
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 80 SGGGDLTLGLPSEBEPSPPLAPSEAGSDVDPDGLGMAAGLQSLPTHDSPLQRY 139  
DB 3 SGGGDLTLGLPSEBEPSPPLAPSEAGSDVDPDGLGMAAGLQSLPTHDSPLQRY 62

QY 140 EDPVPLPSETDGYVAPLTCSPQ 163  
DB 63 EDPVPLPSETDGYVAPLTCSPQ 86

RESULT 5  
US-09-854-356-5  
; Sequence 5, Application US/09854356  
; Patent No. US20020177567A1  
; GENERAL INFORMATION:  
; APPLICANT: Cheever, Martin A.  
; APPLICANT: Gheyson, Dirk  
; APPLICANT: Corixa Corporation  
; APPLICANT: SmithKline Beecham Biologicals S. A.  
; TITLE OF INVENTION: HER-2/neu Fusion Proteins  
; FILE REFERENCE: 014058-009810PC  
; CURRENT APPLICATION NUMBER: US/09/854,356  
; PRIOR FILING DATE: 2001-05-09  
; PRIOR APPLICATION NUMBER: US 09/493,480  
; PRIOR FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: US 60/117,976  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5

LENGTH: 59  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: fragment of the phosphorylation domain, preferred  
OTHER INFORMATION: portion (delta PD) of human HER-2/neu  
US-09-854-356-5

Query Match 25.1%; Score 59; DB 3; Length 59;  
Best Local Similarity 100.0%; Pred. No. 3.2e-44;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 QNEDGPAASPUDSTFYRSLLBDDMDGLVDAEYLVPOQGFPCPDPAAGAGMHHRR 74  
Db 1 QNEDGPAASPUDSTFYRSLLBDDMDGLVDAEYLVPOQGFPCPDPAAGAGMHHRR 59

RESULT 6  
US-10-425-115-217661

Sequence 217661, Application US/10425115  
Publication No. US20040214272A1

GENERAL INFORMATION:  
APPLICANT: La Rosa, Thomas J.  
APPLICANT: Kovalic, David K.  
APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(53222)B  
CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 217661

LENGTH: 79

TYPE: PRT

ORGANISM: Zea mays

FEATURE:

OTHER INFORMATION: Clone ID: MRT4577\_130104C.1.pep  
US-10-425-115-217661

Query Match 19.1%; Score 45; DB 4; Length 79;  
Best Local Similarity 100.0%; Pred. No. 9.8e-32;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 46 AEEYVPOQGFPCPDPAAGAGMHHRRSSSTRSGGDLTGL 90  
Db 35 AEEYVPOQGFPCPDPAAGAGMHHRRSSSTRSGGDLTGL 79

RESULT 7  
US-09-925-301-1232

Sequence 1232, Application US/09925301  
Patent No. US20020052308A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA106

CURRENT APPLICATION NUMBER: US/09/925,301

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/US00/05882

PRIOR FILING DATE: 2000-03-08

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1694

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1232

LENGTH: 135

TYPE: PRT

ORGANISM: Homo sapiens

US-09-925-301-1232

Query Match 16.6%; Score 39; DB 3; Length 135;  
Best Local Similarity 100.0%; Pred. No. 3.1e-26;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 197 KTLSPGKGVKDVFAFGAVENPEYLTPOGAAPOPHP 235  
Db 51 KTLSPGKGVKDVFAFGAVENPEYLTPOGAAPOPHP 89

RESULT 8  
US-10-484-067-7

Sequence 7, Application US/10484067  
Publication No. US20040241686A1

GENERAL INFORMATION:

APPLICANT: UNIVERSITY OF CALIFORNIA

APPLICANT: NELSON, Edward L.

TITLE OF INVENTION: HER2/NEU TARGET ANTIGEN AND USE OF SAME TO STIMULATE AN IMMUNE RE

FILE REFERENCE: UC1170-1

CURRENT APPLICATION NUMBER: US/10/484,067

CURRENT FILING DATE: 2004-01-15

PRIOR APPLICATION NUMBER: PCT/US02/22975

PRIOR FILING DATE: 2002-07-18

PRIOR APPLICATION NUMBER: US 60/306,250

PRIOR FILING DATE: 2001-07-18

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Patentin Version 3.1

SEQ ID NO 7

LENGTH: 221

TYPE: PRT

ORGANISM: Rat

US-10-484-067-7

Query Match 15.7%; Score 37; DB 5; Length 221;  
Best Local Similarity 100.0%; Pred. No. 2.8e-24;  
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 187 RPAATLPERKTLSPGKGVKDVFAFGAVENPEYL 223  
Db 127 RPAATLPERKTLSPGKGVKDVFAFGAVENPEYL 163

RESULT 9  
US-09-354-533-51

Sequence 51, Application US/09354533  
Publication No. US20020055614A1

GENERAL INFORMATION:

APPLICANT: Cheever, Martin A.

Diels, Mary L.

TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN

FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE

HER-2/neu ONCOGENE IS ASSOCIATED

NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:

ADDRESS: Seed and Berry LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: US

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/354,533

FILING DATE: 15-Jul-1999

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Sharkey, Richard G.

REGISTRATION NUMBER: 32,629

REFERENCE/DOCKET NUMBER: 920010.448C9

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031



INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 51:  
US-09-354-533-51

Query Match 6.4%; Score 15; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 EDDDMGDLVDABEYL 50  
DB 1 EDDDMGDLVDABEYL 15

RESULT 10  
US-09-354-533-52  
Sequence 52, Application US/09354533  
Publication No. US20020055614A1  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
Disls, Mary L.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
HER-2/neu ONCOGENE IS ASSOCIATED  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/354,533  
FILING DATE: 15-Jul-1999  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C9  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 52:  
US-09-354-533-52

Query Match 6.4%; Score 15; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 117 GMAAKGIGSLPTHD 131  
DB 1 GMAAKGIGSLPTHD 15

RESULT 11  
US-09-354-533-53  
Sequence 53, Application US/09354533  
Publication No. US20020055614A1  
GENERAL INFORMATION:

APPLICANT: Cheever, Martin A.  
Disls, Mary L.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
HER-2/neu ONCOGENE IS ASSOCIATED  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/354,533  
FILING DATE: 15-Jul-1999  
CLASSIFICATION: <Unknown>

QY 158 TCSPPEYVNPDPVR 172  
DB 1 TCSPPEYVNPDPVR 15

RESULT 12  
US-09-354-533-54  
Sequence 54, Application US/09354533  
Publication No. US20020055614A1  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
Disls, Mary L.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
HER-2/neu ONCOGENE IS ASSOCIATED  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/354,533  
FILING DATE: 15-Jul-1999  
CLASSIFICATION: <Unknown>

Query Match 6.4%; Score 15; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C9  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 54:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 54:  
US-09-354-533-54

Query Match 6.4%; Score 15; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 192 TLPRKTLSPGKNGV 206  
DB 1 TLPRKTLSPGKNGV 15

RESULT 13  
US-09-354-533-55  
Sequence 55, Application US/09354533  
Publication No. US20020055614A1  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
Diala, Mary L.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
HER-2/neu ONCOGENE IS ASSOCIATED  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/354,533  
FILING DATE: 15-Jul-1999  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C9  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 55:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 55:  
US-09-354-533-55

Query Match 6.4%; Score 15; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 214 GGAIVENPEYLTPOGG 228  
DB 1 GGAIVENPEYLTPOGG 15

RESULT 14  
US-10-245-871-581  
Sequence 581, Application US/10245871  
Publication No. US20030235594A1  
GENERAL INFORMATION:  
APPLICANT: HUMPHREYS, ROBERT  
APPLICANT: XU, MINZHEN  
TITLE OF INVENTION: 11-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES  
FILE REFERENCE: REF-2013  
CURRENT APPLICATION NUMBER: US/10/245,871  
CURRENT FILING DATE: 2003-01-09  
PRIOR APPLICATION NUMBER: 10/197,000  
PRIOR FILING DATE: 2002-07-17  
PRIOR APPLICATION NUMBER: 09/396,813  
PRIOR FILING DATE: 1999-09-14  
NUMBER OF SEQ ID NOS: 905  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 581  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-245-871-581

Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 192 TLPRKTLSPGKNGV 206  
DB 1 TLPRKTLSPGKNGV 15

RESULT 15  
US-10-149-138-3722  
Sequence 3722, Application US/10149138  
Publication No. US20040018971A1  
GENERAL INFORMATION:  
APPLICANT: Fikes, John  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Chesnut, Robert  
APPLICANT: Celis, Esleben  
APPLICANT: Keogh, Elissa  
TITLE OF INVENTION: Inducing Cellular Immune Responses to  
TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions  
FILE REFERENCE: 2060.0140001  
CURRENT APPLICATION NUMBER: US/10/149,138  
CURRENT FILING DATE: 2002-06-10  
PRIOR APPLICATION NUMBER: PCT/US00/33591  
PRIOR FILING DATE: 2000-12-11  
PRIOR APPLICATION NUMBER: US 09/458,299  
PRIOR FILING DATE: 1999-12-11  
NUMBER OF SEQ ID NOS: 4641  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3722  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Artificially Synthesized Peptide  
US-10-149-138-3722

Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 AKGLQSLPTHDPSP 135  
DB 1 AKGLQSLPTHDPSP 15

```
RESULT 16
US-10-149-138-3738
; Sequence 3738, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Betteban
; APPLICANT: Keogh, Elisea
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3738
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-3738

Query Match 6.4%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 DGDLSGMAKGLQSL 127
DB 1 DGDLSGMAKGLQSL 15

RESULT 17
US-10-149-138-3739
; Sequence 3739, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Betteban
; APPLICANT: Keogh, Elisea
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3739
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-3739

Query Match 6.4%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 DLTGLPSESEBAPR 98
DB 1 DLTGLPSESEBAPR 15

RESULT 18
US-10-149-138-3740
; Sequence 3740, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Betteban
; APPLICANT: Keogh, Elisea
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3740
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-3740

Query Match 6.4%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 151 DGVAPLTCSPQPEY 165
DB 1 DGVAPLTCSPQPEY 15

RESULT 19
US-10-149-138-3743
; Sequence 3743, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Betteban
; APPLICANT: Keogh, Elisea
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3743
; LENGTH: 15
```

```
Best Local Similarity 100.0%; Pred. No. 7.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 151 DGVAPLTCSPQPEY 165
DB 1 DGVAPLTCSPQPEY 15

RESULT 18
US-10-149-138-3740
; Sequence 3740, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Betteban
; APPLICANT: Keogh, Elisea
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3740
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-3740

Query Match 6.4%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 DLTGLPSESEBAPR 98
DB 1 DLTGLPSESEBAPR 15

RESULT 19
US-10-149-138-3743
; Sequence 3743, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Betteban
; APPLICANT: Keogh, Elisea
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3743
; LENGTH: 15
```

```

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-3743

```

```
Query Match 6.4%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0
```

```
QY 27 DSTFYRSLLEDDDMG 41
 |||||
Db 1 DSTFYRSLLEDDDMG 15
```

RESULT 20  
US-10-149-138-3748  
; Sequence 3748, Application US/10149138  
; Publication No. US20040018971A1

```

1 APPLICANT: Sette, Alessandro
2 APPLICANT: Sidney, John
3 APPLICANT: Southwood, Scott
4 APPLICANT: Chesnut, Robert
5 APPLICANT: Cells, Esteban
6 APPLICANT: Keogh, Elissa
7 TITLE OF INVENTION: Inducing Cellular Immune Responses to
8 TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
9 FILE REFERENCE: 2060.0140001
10 CURRENT APPLICATION NUMBER: US/10/149,138
11 CURRENT FILING DATE: 2002-06-10
12 PRIOR APPLICATION NUMBER: PCT/US00/33591
13 PRIOR FILING DATE: 2000-12-11
14 PRIOR APPLICATION NUMBER: US 09/458,299
15 PRIOR FILING DATE: 1999-12-11
16 NUMBER OF SEQ ID NOS: 4641
17 SOFTWARE: PatentIn version 3.1
18 SEQ ID NO 3748
19 LENGTH: 15
20 TYPE: PRT
21 ORGANISM: Artificial Sequence
22 FEATURE:
23 OTHER INFORMATION: Artificially Synthesized Peptide
24 US-10-149-138-3748

```

|                       |                 |                    |           |            |
|-----------------------|-----------------|--------------------|-----------|------------|
| Query Match           | 6.4%;           | Score 15;          | DB 4;     | Length 15; |
| Best Local Similarity | 100.0%;         | Pred. No. 7.3e-06; |           |            |
| Matches 15;           | Conservative 0; | Mismatches 0;      | Indels 0; | Gaps 0     |

```

Qy 180 EGPLPARPAGATLE 194
 |||||
Db 1 EGPLPARPAGATLE 15

```

RESULT 21  
US-10-149-138-3755

```

: Sequence 3755, Application US/10149138
: Publication No. US20040018971A1
:
: GENERAL INFORMATION:
: APPLICANT: Fikes, John
: APPLICANT: Sette, Alessandro
: APPLICANT: Sidney, John
: APPLICANT: Southwood, Scott
: APPLICANT: Chesnut, Robert
: APPLICANT: Celis, Esteban
: APPLICANT: Keogh, Elissa
:
: TITLE OF INVENTION: Inducing Cellular Immune Responses to
: TITLE OF INVENTION: HRR2/nu Using Peptide and Nucleic Acid Compositions
: FILE REFERENCE: 2060.0140001
: CURRENT APPLICATION NUMBER: US/10/149,138
: CURRENT FILING DATE: 2002-06-10
: PRIOR APPLICATION NUMBER: PCT/US00/33591
:

```

```

; SEQ ID NO 3755
;
; SOFTWARE: PatentIn version 3.1
;
; NUMBER OF SEQ ID NOS: 4641
;
; PRIOR FILING DATE: 1999-12-11
;
; PRIOR APPLICATION NUMBER: US 09/458,299
;
; PRIOR FILING DATE: 2000-12-11
;
; SEQ ID NO 3755

```

```

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptide
OS-10-149-138-3755

```

Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0

```
QY 12 FVVIQNEDLGPASPL 26
 |||||
Db 1 FVVIQNEDLGPASPL 15
```

```

, RESULT 22
, US-10-149-138-3756
, Sequence 3756, Application US/10149138
, Publication No. US20040018971A1
, GENERAL INFORMATION:
, APPLICANT: Fikes, John
, APPLICANT: Sette, Alessandro
, APPLICANT: Sidney, John
, APPLICANT: Southwood, Scott
, APPLICANT: Chesnut, Robert
, APPLICANT: Celis, Esteban
, APPLICANT: Keogh, Elissa
, TITLE OR INVENTION: Inducing Cellular Immune Responses to
, TITLE OF INVENTION: HER/neu Using Peptide and Nucleic Acid Compositions
, FILE REFERENCE: 2060, 0140001
, CURRENT APPLICATION NUMBER: US/10/149, 138
, CURRENT FILING DATE: 2002-06-10
, PRIOR APPLICATION NUMBER: PCT/US00/33591
, PRIOR FILING DATE: 2000-12-11
, PRIOR APPLICATION NUMBER: US 09/458, 299
, PRIOR FILING DATE: 1999-12-11
, NUMBER OF SEQ ID NOS: 4641
, SOFTWARE: PatentIn version 3.1
, SEQ ID NO 3756
, LENGTH: 15
, TYPE: PRT
, ORGANISM: Artificial Sequence
, FEATURE:
, OTHER INFORMATION: Artificially Synthesized Peptide
, US-10-149-138-3756

```

|                       |                |              |          |           |
|-----------------------|----------------|--------------|----------|-----------|
| Query Match           | 6.4%           | Score 15     | DB 4     | length 15 |
| Best Local Similarity | 100.0%         | Pred. No.    | 7.3e-06  |           |
| Matches 15            | Conservative 0 | Mismatches 0 | Indels 0 | Gaps 0    |

|    |     |                  |     |
|----|-----|------------------|-----|
| Qy | 190 | GATLERPKTILSPGKN | 204 |
|    |     |                  |     |
| Db | 1   | GATLERPKTILSPGKN | 15  |

RESULT 23  
US-10-149-138-3769

Sequence 3769, Application US/10149188  
Publication No. US20040018971A1  
GENERAL INFORMATION:  
APPLICANT: Fikes, John  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Sidewood, Scott  
APPLICANT: Chesnut, Robert  
APPLICANT: Celis, Betteann

```
/ APPLICANT: Keogh, Elisea
/ TITLE OF INVENTION: Inducing Cellular Immune Responses to
/ FILE REFERENCE: 2060.0140001
/ CURRENT APPLICATION NUMBER: US/10/149,138
/ PRIOR FILING DATE: 2002-06-10
/ PRIOR APPLICATION NUMBER: PCT/US00/33591
/ PRIOR FILING DATE: 2000-12-11
/ PRIOR APPLICATION NUMBER: US 09/458,299
/ PRIOR FILING DATE: 1999-12-11
/ NUMBER OF SEQ ID NOS: 4641
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 3769
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-3769

Query Match 6.4%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 GSDVPDGLGMGA 122
DB 1 GSDVPDGLGMGA 15

RESULT 24
US-10-149-138-3793
/ Sequence 3793, Application US/10149138
/ Publication No. US20040018971A1
/ GENERAL INFORMATION:
/ APPLICANT: Fikes, John
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Celis, Bstedan
/ APPLICANT: Keogh, Elisea
/ TITLE OF INVENTION: Inducing Cellular Immune Responses to
/ FILE REFERENCE: 2060.0140001
/ CURRENT APPLICATION NUMBER: US/10/149,138
/ CURRENT FILING DATE: 2002-06-10
/ PRIOR APPLICATION NUMBER: PCT/US00/33591
/ PRIOR FILING DATE: 2000-12-11
/ PRIOR APPLICATION NUMBER: US 09/458,299
/ PRIOR FILING DATE: 1999-12-11
/ NUMBER OF SEQ ID NOS: 4641
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 3793
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-3793

Query Match 6.4%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 208 KDVPFAGAVENPEY 222
DB 1 KDVPFAGAVENPEY 15

RESULT 25
US-10-149-138-3812
/ Sequence 3812, Application US/10149138
/ Publication No. US20040018971A1
```

```
/ GENERAL INFORMATION:
/ APPLICANT: Fikes, John
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Celis, Bstedan
/ APPLICANT: Keogh, Elisea
/ TITLE OF INVENTION: Inducing Cellular Immune Responses to
/ FILE REFERENCE: 2060.0140001
/ CURRENT APPLICATION NUMBER: US/10/149,138
/ CURRENT FILING DATE: 2002-06-10
/ PRIOR APPLICATION NUMBER: PCT/US00/33591
/ PRIOR FILING DATE: 2000-12-11
/ PRIOR APPLICATION NUMBER: US 09/458,299
/ PRIOR FILING DATE: 1999-12-11
/ NUMBER OF SEQ ID NOS: 4641
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 3812
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-3812

Query Match 6.4%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 135 LQRYSDPTVLPSE 149
DB 1 LQRYSDPTVLPSE 15

RESULT 26
US-10-149-138-3813
/ Sequence 3813, Application US/10149138
/ Publication No. US20040018971A1
/ GENERAL INFORMATION:
/ APPLICANT: Fikes, John
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Celis, Bstedan
/ APPLICANT: Keogh, Elisea
/ TITLE OF INVENTION: Inducing Cellular Immune Responses to
/ FILE REFERENCE: 2060.0140001
/ CURRENT APPLICATION NUMBER: US/10/149,138
/ CURRENT FILING DATE: 2002-06-10
/ PRIOR APPLICATION NUMBER: PCT/US00/33591
/ PRIOR FILING DATE: 2000-12-11
/ PRIOR APPLICATION NUMBER: US 09/458,299
/ PRIOR FILING DATE: 1999-12-11
/ NUMBER OF SEQ ID NOS: 4641
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 3813
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-3813

Query Match 6.4%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 LQSLPTDPSLPORY 138
DB 1 LQSLPTDPSLPORY 138
```

Db 1 LOSLPTHDPSPLORY 15

RESULT 27

US-10-149-138-3832

Sequence 3832, Application US/10149138

Publication No. US20040018971A1

GENERAL INFORMATION:

APPLICANT: Fikes, John

APPLICANT: Sidney, John

APPLICANT: Southwood, Scott

APPLICANT: Chesnut, Robert

APPLICANT: Cells, Esteban

APPLICANT: Keogh, Elissa

TITLE OF INVENTION: Inducing Cellular Immune Responses to

FILE REFERENCE: 2060.0140001

CURRENT FILING DATE: 2002-06-10

PRIOR APPLICATION NUMBER: PCT/US00/33591

PRIOR FILING DATE: 2000-12-11

PRIOR APPLICATION NUMBER: US 09/458,299

PRIOR FILING DATE: 1999-12-11

NUMBER OF SEQ ID NOS: 4641

SOFTWARE: PatentIn version 3.1

SEQ ID NO 3832

LENGTH: 15

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Artificially Synthesized Peptide

US-10-149-138-3832

Query Match 6.4%; Score 15; DB 4; Length 15;

Best Local Similarity 100.0%; Pred. No. 7.3e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 NEDLGPASPLDSTFY 15

RESULT 28

US-10-149-138-3834

Sequence 3834, Application US/10149138

Publication No. US20040018971A1

GENERAL INFORMATION:

APPLICANT: Fikes, John

APPLICANT: Sidney, John

APPLICANT: Southwood, Scott

APPLICANT: Chesnut, Robert

APPLICANT: Cells, Esteban

APPLICANT: Keogh, Elissa

TITLE OF INVENTION: Inducing Cellular Immune Responses to

FILE REFERENCE: 2060.0140001

CURRENT APPLICATION NUMBER: US/10/149,138

PRIOR FILING DATE: 2002-06-10

PRIOR APPLICATION NUMBER: PCT/US00/33591

PRIOR FILING DATE: 2000-12-11

PRIOR APPLICATION NUMBER: US 09/458,299

PRIOR FILING DATE: 1999-12-11

NUMBER OF SEQ ID NOS: 4641

SOFTWARE: PatentIn version 3.1

SEQ ID NO 3834

LENGTH: 15

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Artificially Synthesized Peptide

Query Match 6.4%; Score 15; DB 4; Length 15;

Best Local Similarity 100.0%; Pred. No. 7.3e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 NGVYQDVRFPGAVE 15

RESULT 29

US-10-149-138-3845

Sequence 3845, Application US/10149138

Publication No. US20040018971A1

GENERAL INFORMATION:

APPLICANT: Fikes, John

APPLICANT: Sidney, John

APPLICANT: Southwood, Scott

APPLICANT: Chesnut, Robert

APPLICANT: Cells, Esteban

APPLICANT: Keogh, Elissa

TITLE OF INVENTION: Inducing Cellular Immune Responses to

FILE REFERENCE: 2060.0140001

CURRENT FILING DATE: 2002-06-10

PRIOR APPLICATION NUMBER: PCT/US00/33591

PRIOR FILING DATE: 2000-12-11

PRIOR APPLICATION NUMBER: US 09/458,299

PRIOR FILING DATE: 1999-12-11

NUMBER OF SEQ ID NOS: 4641

SOFTWARE: PatentIn version 3.1

SEQ ID NO 3845

LENGTH: 15

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Artificially Synthesized Peptide

US-10-149-138-3845

Query Match 6.4%; Score 15; DB 4; Length 15;

Best Local Similarity 100.0%; Pred. No. 7.3e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 PEYVQPDVRFPPS 15

RESULT 30

US-10-149-138-3854

Sequence 3854, Application US/10149138

Publication No. US20040018971A1

GENERAL INFORMATION:

APPLICANT: Fikes, John

APPLICANT: Sidney, John

APPLICANT: Southwood, Scott

APPLICANT: Chesnut, Robert

APPLICANT: Cells, Esteban

APPLICANT: Keogh, Elissa

TITLE OF INVENTION: Inducing Cellular Immune Responses to

FILE REFERENCE: 2060.0140001

CURRENT APPLICATION NUMBER: US/10/149,138

PRIOR FILING DATE: 2002-06-10

PRIOR APPLICATION NUMBER: PCT/US00/33591

PRIOR FILING DATE: 2000-12-11

PRIOR APPLICATION NUMBER: US 09/458,299

PRIOR FILING DATE: 1999-12-11

NUMBER OF SEQ ID NOS: 4641

SOFTWARE: PatentIn version 3.1

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; SEQ ID NO 3854
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-3854

Query Match 6.4%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 QGFFCPDPAPGAGM 68
Db 1 QGFFCPDPAPGAGM 15

RESULT 31
US-10-149-138-3858
; Sequence 3858, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cellis, Eteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3858
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-3858

Query Match 6.4%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 168 QPDVPPQPPSPRBCP 182
Db 1 QPDVPPQPPSPRBCP 15

RESULT 32
US-10-149-138-3860
; Sequence 3860, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cellis, Eteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
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; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3860
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-3860

Query Match 6.4%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 QGFFCPDPAPGAGG 67
Db 1 QGFFCPDPAPGAGG 15

RESULT 33
US-10-149-138-3870
; Sequence 3870, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cellis, Eteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3870
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-3870

Query Match 6.4%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 RSLLEDDMDGLVDA 46
Db 1 RSLLEDDMDGLVDA 15

RESULT 34
US-10-149-138-3882
; Sequence 3882, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
```

APPLICANT: Cheanut, Robert  
APPLICANT: Cells, Esteban  
APPLICANT: Keogh, Elissa  
TITLE OF INVENTION: Inducing Cellular Immune Responses to  
FILE REFERENCE: 2060.0140001  
CURRENT APPLICATION NUMBER: US/10/149,138  
CURRENT FILING DATE: 2002-06-10  
PRIOR APPLICATION NUMBER: PCT/US00/33591  
PRIOR FILING DATE: 2000-12-11  
PRIOR APPLICATION NUMBER: US 09/458,299  
PRIOR FILING DATE: 1999-12-11  
NUMBER OF SEQ ID NOS: 4641  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3882  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Artificially Synthesized Peptide  
US-10-149-138-3882

Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 150 TDGYVAPLTCSPQPE 164  
Db 1 TDGYVAPLTCSPQPE 15

RESULT 35  
US-10-149-138-3911  
Sequence 3911, Application US/10149138  
Publication No. US20040018971A1  
GENERAL INFORMATION:  
APPLICANT: Fikes, John  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Cheanut, Robert  
APPLICANT: Cells, Esteban  
APPLICANT: Keogh, Elissa  
TITLE OF INVENTION: Inducing Cellular Immune Responses to  
FILE REFERENCE: 2060.0140001  
CURRENT APPLICATION NUMBER: US/10/149,138  
CURRENT FILING DATE: 2002-06-10  
PRIOR APPLICATION NUMBER: PCT/US00/33591  
PRIOR FILING DATE: 2000-12-11  
PRIOR APPLICATION NUMBER: US 09/458,299  
PRIOR FILING DATE: 1999-12-11  
NUMBER OF SEQ ID NOS: 4641  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3911  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Artificially Synthesized Peptide  
US-10-149-138-3911

Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 84 DLTGLGPESEBAPR 98  
Db 1 DLTGLGPESEBAPR 15

RESULT 36  
US-10-149-138-3916

Sequence 3916, Application US/10149138  
Publication No. US20040018971A1  
GENERAL INFORMATION:  
APPLICANT: Fikes, John  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Cheanut, Robert  
APPLICANT: Cells, Esteban  
APPLICANT: Keogh, Elissa  
TITLE OF INVENTION: Inducing Cellular Immune Responses to  
FILE REFERENCE: 2060.0140001  
CURRENT APPLICATION NUMBER: US/10/149,138  
CURRENT FILING DATE: 2002-06-10  
PRIOR APPLICATION NUMBER: PCT/US00/33591  
PRIOR FILING DATE: 2000-12-11  
PRIOR APPLICATION NUMBER: US 09/458,299  
PRIOR FILING DATE: 1999-12-11  
NUMBER OF SEQ ID NOS: 4641  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3916  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Artificially Synthesized Peptide  
US-10-149-138-3916

Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FSRMARDPQRFVVIQ 16  
Db 1 FSRMARDPQRFVVIQ 15

RESULT 37  
US-10-149-138-3917  
Sequence 3917, Application US/10149138  
Publication No. US20040018971A1  
GENERAL INFORMATION:  
APPLICANT: Fikes, John  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Cheanut, Robert  
APPLICANT: Cells, Esteban  
APPLICANT: Keogh, Elissa  
TITLE OF INVENTION: Inducing Cellular Immune Responses to  
FILE REFERENCE: 2060.0140001  
CURRENT APPLICATION NUMBER: US/10/149,138  
CURRENT FILING DATE: 2002-06-10  
PRIOR APPLICATION NUMBER: PCT/US00/33591  
PRIOR FILING DATE: 2000-12-11  
PRIOR APPLICATION NUMBER: US 09/458,299  
PRIOR FILING DATE: 1999-12-11  
NUMBER OF SEQ ID NOS: 4641  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3917  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Artificially Synthesized Peptide  
US-10-149-138-3917

Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Qy 12 FVIONEDLGPA SPL 26  
| | | | | | | | | |  
Db 1 FVIONEDLGPA SPL 15

## RESULT 38

US-10-149-138-3918  
; Sequence 3918, Application US/10149138  
; Publication No. US20040018971A1  
; GENERAL INFORMATION:  
; APPLICANT: Fikes, John  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Sidney, John  
; APPLICANT: Southwood, Scott  
; APPLICANT: Chesnut, Robert  
; APPLICANT: Celis, Esteban  
; APPLICANT: Keogh, Elissa  
; TITLE OF INVENTION: Inducing Cellular Immune Responses to  
; FILE REFERENCE: 2060.0140001  
; CURRENT APPLICATION NUMBER: US/10/149,138  
; CURRENT FILING DATE: 2002-06-10  
; PRIOR APPLICATION NUMBER: PCT/US00/33591  
; PRIOR FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: US 09/458,299  
; PRIOR FILING DATE: 1999-12-11  
; NUMBER OF SEQ ID NOS: 4641  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3918  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificially Synthesized Peptide  
US-10-149-138-3918

Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 41 GDLVDAEYLVPOQG 55  
| | | | | | | | | |  
Db 1 GDLVDAEYLVPOQG 15

## RESULT 39

US-10-149-138-3923  
; Sequence 3923, Application US/10149138  
; Publication No. US20040018971A1  
; GENERAL INFORMATION:  
; APPLICANT: Fikes, John  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Sidney, John  
; APPLICANT: Southwood, Scott  
; APPLICANT: Chesnut, Robert  
; APPLICANT: Celis, Esteban  
; APPLICANT: Keogh, Elissa  
; TITLE OF INVENTION: Inducing Cellular Immune Responses to  
; FILE REFERENCE: 2060.0140001  
; CURRENT APPLICATION NUMBER: US/10/149,138  
; CURRENT FILING DATE: 2002-06-10  
; PRIOR APPLICATION NUMBER: PCT/US00/33591  
; PRIOR FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: US 09/458,299  
; PRIOR FILING DATE: 1999-12-11  
; NUMBER OF SEQ ID NOS: 4641  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3923  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: Artificially Synthesized Peptide  
US-10-149-138-3923

Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 203 KNGVWDVAFPGAV 217  
| | | | | | | | | |  
Db 1 KNGVWDVAFPGAV 15

## RESULT 40

US-10-149-138-3925  
; Sequence 3925, Application US/10149138  
; Publication No. US20040018971A1  
; GENERAL INFORMATION:  
; APPLICANT: Fikes, John  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Sidney, John  
; APPLICANT: Southwood, Scott  
; APPLICANT: Chesnut, Robert  
; APPLICANT: Celis, Esteban  
; APPLICANT: Keogh, Elissa  
; TITLE OF INVENTION: Inducing Cellular Immune Responses to  
; FILE REFERENCE: 2060.0140001  
; CURRENT APPLICATION NUMBER: US/10/149,138  
; CURRENT FILING DATE: 2002-06-10  
; PRIOR APPLICATION NUMBER: PCT/US00/33591  
; PRIOR FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: US 09/458,299  
; PRIOR FILING DATE: 1999-12-11  
; NUMBER OF SEQ ID NOS: 4641  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3925  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificially Synthesized Peptide  
US-10-149-138-3925

Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 135 LQRYSEDPTVLPSE 149  
| | | | | | | | | |  
Db 1 LQRYSEDPTVLPSE 15

## RESULT 41

US-10-149-138-3932  
; Sequence 3932, Application US/10149138  
; Publication No. US20040018971A1  
; GENERAL INFORMATION:  
; APPLICANT: Fikes, John  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Sidney, John  
; APPLICANT: Southwood, Scott  
; APPLICANT: Chesnut, Robert  
; APPLICANT: Celis, Esteban  
; APPLICANT: Keogh, Elissa  
; TITLE OF INVENTION: Inducing Cellular Immune Responses to  
; FILE REFERENCE: 2060.0140001  
; CURRENT APPLICATION NUMBER: US/10/149,138  
; CURRENT FILING DATE: 2002-06-10  
; PRIOR APPLICATION NUMBER: PCT/US00/33591  
; PRIOR FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: US 09/458,299  
; PRIOR FILING DATE: 1999-12-11

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; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3932
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-3932

Query Match 6.4%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 54 QGFPCDPAPGAGM 68
Db 1 QGFPCDPAPGAGM 15

RESULT 42
US-10-149-138-3934
; Sequence 3934, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3934
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-3934

Query Match 6.4%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 RSLLEDDDMGDLVDA 46
Db 1 RSLLEDDDMGDLVDA 15

RESULT 43
US-10-149-138-3935
; Sequence 3935, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3935
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-3935

Query Match 6.4%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 143 TVPLPSRTGYVAPL 157
Db 1 TVPLPSRTGYVAPL 15

RESULT 45
US-10-149-138-3944
; Sequence 3944, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
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; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3935
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-3935

Query Match 6.4%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 109 SDVFDGDLGMGAKG 123
Db 1 SDVFDGDLGMGAKG 15

RESULT 44
US-10-149-138-3939
; Sequence 3939, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3939
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-3939

Query Match 6.4%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 143 TVPLPSRTGYVAPL 157
Db 1 TVPLPSRTGYVAPL 15

RESULT 45
US-10-149-138-3944
; Sequence 3944, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
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APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Chesnut, Robert  
APPLICANT: Celis, Bateban  
APPLICANT: Keogh, Elissa  
TITLE OF INVENTION: Inducing Cellular Immune Responses to  
FILE REFERENCE: 2060.0140001  
CURRENT APPLICATION NUMBER: US/10/149,138  
CURRENT FILING DATE: 2002-06-10  
PRIOR APPLICATION NUMBER: PCT/US00/33591  
PRIOR FILING DATE: 2000-12-11  
PRIOR APPLICATION NUMBER: US 09/458,299  
PRIOR FILING DATE: 1999-12-11  
NUMBER OF SEQ ID NOS: 4641  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3944  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Artificially Synthesized Peptide  
US-10-149-138-3944

Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 YRSLEDDDMGDLVD 45  
DB 1 YRSLEDDDMGDLVD 15

RESULT 46  
US-10-149-138-4486  
Sequence 4486, Application US/10149138  
Publication No. US20040018971A1  
GENERAL INFORMATION:  
APPLICANT: Fikes, John  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Chesnut, Robert  
APPLICANT: Celis, Bateban  
APPLICANT: Keogh, Elissa  
TITLE OF INVENTION: Inducing Cellular Immune Responses to  
FILE REFERENCE: 2060.0140001  
CURRENT APPLICATION NUMBER: US/10/149,138  
CURRENT FILING DATE: 2002-06-10  
PRIOR APPLICATION NUMBER: PCT/US00/33591  
PRIOR FILING DATE: 2000-12-11  
PRIOR APPLICATION NUMBER: US 09/458,299  
PRIOR FILING DATE: 1999-12-11  
NUMBER OF SEQ ID NOS: 4641  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 4486  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Artificial Peptide  
US-10-149-138-4486

Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 QGFPCPPAPGAGM 68  
DB 1 QGFPCPPAPGAGM 15

RESULT 47  
US-10-149-138-4487  
Sequence 4487, Application US/10149138  
Publication No. US20040018971A1  
GENERAL INFORMATION:  
APPLICANT: Fikes, John  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Chesnut, Robert  
APPLICANT: Celis, Bateban  
APPLICANT: Keogh, Elissa  
TITLE OF INVENTION: Inducing Cellular Immune Responses to  
FILE REFERENCE: 2060.0140001  
CURRENT APPLICATION NUMBER: US/10/149,138  
CURRENT FILING DATE: 2002-06-10  
PRIOR APPLICATION NUMBER: PCT/US00/33591  
PRIOR FILING DATE: 2000-12-11  
PRIOR APPLICATION NUMBER: US 09/458,299  
PRIOR FILING DATE: 1999-12-11  
NUMBER OF SEQ ID NOS: 4641  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 4487  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Artificial Peptide  
US-10-149-138-4487

Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 150 TDGYVAPLTCSPPQPE 164  
DB 1 TDGYVAPLTCSPPQPE 15

RESULT 48  
US-10-149-138-4488  
Sequence 4488, Application US/10149138  
Publication No. US20040018971A1  
GENERAL INFORMATION:  
APPLICANT: Fikes, John  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Chesnut, Robert  
APPLICANT: Celis, Bateban  
APPLICANT: Keogh, Elissa  
TITLE OF INVENTION: Inducing Cellular Immune Responses to  
FILE REFERENCE: 2060.0140001  
CURRENT APPLICATION NUMBER: US/10/149,138  
CURRENT FILING DATE: 2002-06-10  
PRIOR APPLICATION NUMBER: PCT/US00/33591  
PRIOR FILING DATE: 2000-12-11  
PRIOR APPLICATION NUMBER: US 09/458,299  
PRIOR FILING DATE: 1999-12-11  
NUMBER OF SEQ ID NOS: 4641  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 4488  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Artificial Peptide  
US-10-149-138-4488

Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.3e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 168 QDVRRPQPPSPREGP 182

Db 1 QDVRRPQPPSPREGP 15

RESULT 49

US-10-149-138-4541

/ Sequence 4541, Application US/10149138

/ Publication No. US20040018971A1

/ GENERAL INFORMATION:

/ APPLICANT: Fikes, John

/ APPLICANT: Sette, Alessandro

/ APPLICANT: Sidney, John

/ APPLICANT: Southwood, Scott

/ APPLICANT: Chesnut, Robert

/ APPLICANT: Celis, Esteban

/ APPLICANT: Keogh, Elissa

/ TITLE OF INVENTION: Inducing Cellular Immune Responses to

/ FILE REFERENCE: 2060.0140001

/ CURRENT FILING DATE: 2002-06-10

/ PRIOR APPLICATION NUMBER: PCT/US00/33591

/ PRIOR FILING DATE: 2000-12-11

/ PRIOR APPLICATION NUMBER: US 09/458,299

/ PRIOR FILING DATE: 1999-12-11

/ NUMBER OF SEQ ID NOS: 4641

/ SOFTWARE: PatentIn version 3.1

/ SEQ ID NO 4541

/ LENGTH: 15

/ TYPE: PRT

/ ORGANISM: Artificial Sequence

/ FEATURE:

/ OTHER INFORMATION: Artificial Peptide

US-10-149-138-4541

Query Match 6.4%; Score 15; DB 4; Length 15;

Best Local Similarity 100.0%; Pred. No. 7.3e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FSRMARDPQRFVVIQ 16

Db 1 FSRMARDPQRFVVIQ 15

RESULT 50

US-10-149-138-4542

/ Sequence 4542, Application US/10149138

/ Publication No. US20040018971A1

/ GENERAL INFORMATION:

/ APPLICANT: Fikes, John

/ APPLICANT: Sette, Alessandro

/ APPLICANT: Sidney, John

/ APPLICANT: Southwood, Scott

/ APPLICANT: Chesnut, Robert

/ APPLICANT: Celis, Esteban

/ APPLICANT: Keogh, Elissa

/ TITLE OF INVENTION: Inducing Cellular Immune Responses to

/ FILE REFERENCE: 2060.0140001

/ CURRENT FILING DATE: 2002-06-10

/ PRIOR APPLICATION NUMBER: PCT/US00/33591

/ PRIOR FILING DATE: 2000-12-11

/ PRIOR APPLICATION NUMBER: US 09/458,299

/ PRIOR FILING DATE: 1999-12-11

/ NUMBER OF SEQ ID NOS: 4641

/ SOFTWARE: PatentIn version 3.1

/ SEQ ID NO 4542

/ LENGTH: 15

/ TYPE: PRT

/ ORGANISM: Artificial Sequence

/ FEATURE:

/ OTHER INFORMATION: Artificial Peptide

US-10-149-138-4542

Query Match 6.4%; Score 15; DB 4; Length 15;

Best Local Similarity 100.0%; Pred. No. 7.3e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 FVVIQEDLGPASPL 26

Db 1 FVVIQEDLGPASPL 15

Search completed: January 18, 2006, 20:59:59

Job time : 121 secs

GenCore version 5.1.6  
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## OM protein - protein search, using SW model

Run on: January 18, 2006, 20:46:59 : Search time 23 Seconds  
(without alignments)  
844.730 Million cell updates/sec

Title: US-09-930-125-2\_COPY\_975\_1209

Perfect score: 235

Sequence: 1 EFSRMARDPQRVVIQNEIDL.....AVENPEYLRPGGAAPQHP 235

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 572060 seqs, 82675679 residues

Word size : 0

Total number of hits satisfying chosen parameters: 454623

Minimum DB seq length: 0

Maximum DB seq length: 235

## Post-Processing: Listing first 200 summaries

Database :

Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/aa/5 COMB.pep:\*  
2: /cgn2\_6/prodata/1/aa/6 COMB.pep:\*  
3: /cgn2\_6/prodata/1/aa/7 COMB.pep:\*  
4: /cgn2\_6/prodata/1/aa/8 COMB.pep:\*  
5: /cgn2\_6/prodata/1/aa/9 COMB.pep:\*  
6: /cgn2\_6/prodata/1/aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description       |
|------------|-------|-------------|--------|-------|-------------------|
| 1          | 41    | 17.4        | 47     | 1     | US-08-625-322-22  |
| 2          | 22    | 9.4         | 47     | 1     | US-08-625-322-23  |
| 3          | 15    | 6.4         | 15     | 1     | US-08-467-083-51  |
| 4          | 15    | 6.4         | 15     | 1     | US-08-467-083-52  |
| 5          | 15    | 6.4         | 15     | 1     | US-08-467-083-53  |
| 6          | 15    | 6.4         | 15     | 1     | US-08-467-083-54  |
| 7          | 15    | 6.4         | 15     | 1     | US-08-467-083-55  |
| 8          | 15    | 6.4         | 15     | 1     | US-08-414-178-51  |
| 9          | 15    | 6.4         | 15     | 1     | US-08-414-178-52  |
| 10         | 15    | 6.4         | 15     | 1     | US-08-414-178-53  |
| 11         | 15    | 6.4         | 15     | 1     | US-08-414-178-54  |
| 12         | 15    | 6.4         | 15     | 1     | US-08-414-178-55  |
| 13         | 15    | 6.4         | 15     | 1     | US-08-486-348A-51 |
| 14         | 15    | 6.4         | 15     | 1     | US-08-486-348A-52 |
| 15         | 15    | 6.4         | 15     | 1     | US-08-486-348A-53 |
| 16         | 15    | 6.4         | 15     | 1     | US-08-486-348A-54 |
| 17         | 15    | 6.4         | 15     | 1     | US-08-486-348A-55 |
| 18         | 15    | 6.4         | 15     | 1     | US-08-468-545B-51 |
| 19         | 15    | 6.4         | 15     | 1     | US-08-468-545B-52 |
| 20         | 15    | 6.4         | 15     | 1     | US-08-468-545B-53 |
| 21         | 15    | 6.4         | 15     | 1     | US-08-468-545B-54 |
| 22         | 15    | 6.4         | 15     | 1     | US-08-468-545B-55 |
| 23         | 15    | 6.4         | 15     | 1     | US-08-466-680B-51 |
| 24         | 15    | 6.4         | 15     | 1     | US-08-466-680B-52 |
| 25         | 15    | 6.4         | 15     | 1     | US-08-466-680B-53 |
| 26         | 15    | 6.4         | 15     | 1     | US-08-466-680B-54 |
| 27         | 15    | 6.4         | 15     | 1     | US-08-466-680B-55 |

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|-----|----|-----|-----|---|----------------------|-------------------|
| 28  | 15 | 6.4 | 15  | 2 | US-09-354-533-51     | Sequence 51, Appl |
| 29  | 15 | 6.4 | 15  | 2 | US-09-354-533-52     | Sequence 52, Appl |
| 30  | 15 | 6.4 | 15  | 2 | US-09-354-533-53     | Sequence 53, Appl |
| 31  | 15 | 6.4 | 15  | 2 | US-09-354-533-54     | Sequence 54, Appl |
| 32  | 15 | 6.4 | 15  | 2 | US-09-354-533-55     | Sequence 55, Appl |
| 33  | 13 | 5.5 | 13  | 2 | US-08-403-459-45     | Sequence 45, Appl |
| 34  | 11 | 4.7 | 48  | 1 | US-08-625-322-25     | Sequence 25, Appl |
| 35  | 10 | 4.3 | 10  | 2 | US-08-159-339A-268   | Sequence 268, App |
| 36  | 10 | 4.3 | 10  | 2 | US-08-403-459-16     | Sequence 16, Appl |
| 37  | 10 | 4.3 | 10  | 2 | US-08-403-459-44     | Sequence 44, Appl |
| 38  | 10 | 4.3 | 13  | 2 | US-08-403-459-40     | Sequence 40, Appl |
| 39  | 10 | 4.3 | 14  | 1 | US-08-467-083-64     | Sequence 64, Appl |
| 40  | 10 | 4.3 | 14  | 1 | US-08-414-178-64     | Sequence 64, Appl |
| 41  | 10 | 4.3 | 14  | 1 | US-08-486-348A-64    | Sequence 64, Appl |
| 42  | 10 | 4.3 | 14  | 1 | US-08-468-545B-64    | Sequence 64, Appl |
| 43  | 10 | 4.3 | 14  | 2 | US-08-466-680B-64    | Sequence 64, Appl |
| 44  | 10 | 4.3 | 14  | 2 | US-09-354-533-64     | Sequence 64, Appl |
| 45  | 10 | 4.3 | 17  | 2 | US-08-197-484-11     | Sequence 11, Appl |
| 46  | 10 | 4.3 | 17  | 4 | PCT-US95-02121-11    | Sequence 11, Appl |
| 47  | 10 | 4.3 | 21  | 1 | US-08-423-646A-46    | Sequence 46, Appl |
| 48  | 9  | 3.8 | 9   | 1 | US-08-467-083-23     | Sequence 23, Appl |
| 49  | 9  | 3.8 | 9   | 1 | US-08-467-083-24     | Sequence 24, Appl |
| 50  | 9  | 3.8 | 9   | 1 | US-08-467-083-25     | Sequence 25, Appl |
| 51  | 9  | 3.8 | 9   | 1 | US-08-414-178-10     | Sequence 10, Appl |
| 52  | 9  | 3.8 | 9   | 1 | US-08-414-178-23     | Sequence 23, Appl |
| 53  | 9  | 3.8 | 9   | 1 | US-08-414-178-24     | Sequence 24, Appl |
| 54  | 9  | 3.8 | 9   | 1 | US-08-414-178-25     | Sequence 25, Appl |
| 55  | 9  | 3.8 | 9   | 1 | US-08-486-348A-10    | Sequence 10, Appl |
| 56  | 9  | 3.8 | 9   | 1 | US-08-486-348A-23    | Sequence 23, Appl |
| 57  | 9  | 3.8 | 9   | 1 | US-08-486-348A-24    | Sequence 24, Appl |
| 58  | 9  | 3.8 | 9   | 1 | US-08-486-348A-25    | Sequence 25, Appl |
| 59  | 9  | 3.8 | 9   | 1 | US-08-468-545B-10    | Sequence 10, Appl |
| 60  | 9  | 3.8 | 9   | 1 | US-08-468-545B-23    | Sequence 23, Appl |
| 61  | 9  | 3.8 | 9   | 1 | US-08-468-545B-24    | Sequence 24, Appl |
| 62  | 9  | 3.8 | 9   | 1 | US-08-468-545B-25    | Sequence 25, Appl |
| 63  | 9  | 3.8 | 9   | 1 | US-08-159-339A-257   | Sequence 257, App |
| 64  | 9  | 3.8 | 9   | 2 | US-08-466-680B-10    | Sequence 10, Appl |
| 65  | 9  | 3.8 | 9   | 2 | US-08-466-680B-23    | Sequence 23, Appl |
| 66  | 9  | 3.8 | 9   | 2 | US-08-466-680B-24    | Sequence 24, Appl |
| 67  | 9  | 3.8 | 9   | 2 | US-08-466-680B-25    | Sequence 25, Appl |
| 68  | 9  | 3.8 | 9   | 2 | US-08-403-459-29     | Sequence 29, Appl |
| 69  | 9  | 3.8 | 9   | 2 | US-09-354-533-10     | Sequence 10, Appl |
| 70  | 9  | 3.8 | 9   | 2 | US-09-354-533-23     | Sequence 23, Appl |
| 71  | 9  | 3.8 | 9   | 2 | US-09-354-533-24     | Sequence 24, Appl |
| 72  | 9  | 3.8 | 9   | 2 | US-09-354-533-25     | Sequence 25, Appl |
| 73  | 9  | 3.8 | 15  | 2 | US-08-467-083-50     | Sequence 50, Appl |
| 74  | 8  | 3.4 | 15  | 1 | US-08-414-178-50     | Sequence 50, Appl |
| 75  | 8  | 3.4 | 15  | 1 | US-08-486-348A-50    | Sequence 50, Appl |
| 76  | 8  | 3.4 | 15  | 1 | US-08-468-545B-50    | Sequence 50, Appl |
| 77  | 8  | 3.4 | 15  | 2 | US-08-466-680B-50    | Sequence 50, Appl |
| 78  | 8  | 3.4 | 15  | 2 | US-09-354-533-50     | Sequence 50, Appl |
| 79  | 8  | 3.4 | 15  | 2 | US-09-354-533-50     | Sequence 50, Appl |
| 80  | 8  | 3.4 | 15  | 2 | US-09-354-533-50     | Sequence 50, Appl |
| 81  | 8  | 3.4 | 16  | 2 | US-09-587-066-4      | Sequence 4, Appl1 |
| 82  | 8  | 3.0 | 10  | 2 | US-08-159-339A-296   | Sequence 296, App |
| 83  | 7  | 3.0 | 11  | 2 | US-08-403-459-37     | Sequence 37, Appl |
| 84  | 7  | 3.0 | 14  | 2 | US-08-403-459-38     | Sequence 38, Appl |
| 85  | 7  | 3.0 | 14  | 2 | US-08-403-459-39     | Sequence 39, Appl |
| 86  | 7  | 3.0 | 14  | 2 | US-08-403-459-65     | Sequence 65, Appl |
| 87  | 7  | 3.0 | 14  | 2 | US-08-403-459-66     | Sequence 66, Appl |
| 88  | 7  | 3.0 | 14  | 2 | US-08-403-459-66     | Sequence 66, Appl |
| 89  | 7  | 3.0 | 48  | 1 | US-08-625-322-21     | Sequence 21, Appl |
| 90  | 7  | 3.0 | 48  | 1 | US-08-625-322-21     | Sequence 21, Appl |
| 91  | 7  | 3.0 | 66  | 2 | US-09-270-767-45835  | Sequence 45835, A |
| 92  | 7  | 3.0 | 93  | 2 | US-09-270-767-40746  | Sequence 40746, A |
| 93  | 7  | 3.0 | 93  | 2 | US-09-270-767-55962  | Sequence 55962, A |
| 94  | 7  | 3.0 | 137 | 2 | US-09-270-767-37229  | Sequence 37229, A |
| 95  | 7  | 3.0 | 137 | 2 | US-09-270-767-52446  | Sequence 52446, A |
| 96  | 7  | 3.0 | 139 | 2 | US-09-302-540-12596  | Sequence 12596, A |
| 97  | 7  | 3.0 | 159 | 2 | US-09-252-991A-28117 | Sequence 28117, A |
| 98  | 7  | 3.0 | 170 | 2 | US-09-252-991A-16793 | Sequence 16793, A |
| 99  | 7  | 3.0 | 174 | 2 | US-09-252-991A-19493 | Sequence 19493, A |
| 100 | 7  | 3.0 | 215 | 2 | US-09-270-767-45569  | Sequence 45569, A |



Best Local Similarity 100.0%; Pred. No. 3.4e-31;  
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EFSRMDPQRFVIVQNEIDGSPASPLDSTFYRSLLEDDMG 41  
Db 7 EFSRMDPQRFVIVQNEIDGSPASPLDSTFYRSLLEDDMG 47

## RESULT 2

US-08-625-322-23  
Sequence 23, Application US/08625322

Patent No. 5804412

GENERAL INFORMATION:

APPLICANT: Gill, Gordon N.

APPLICANT: Kuten, Richard C.

APPLICANT: Cadena, Deborah L.

TITLE OF INVENTION: Sorting Nexins and Methods of Using Same

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell and Flores

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/625.322

FILING DATE: 01-APR-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-UD 1955

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 47 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-625-322-23

Query Match 9.4%; Score 22; DB 1; Length 47;

Best Local Similarity 100.0%; Pred. No. 2.6e-13;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EFSRMDPQRFVIVQNEIDGSP 22

Db 7 EFSRMDPQRFVIVQNEIDGSP 26

## RESULT 3

US-08-467-083-51

Sequence 51, Application US/08467083

Patent No. 5726023

GENERAL INFORMATION:

APPLICANT: Cheever, Martin A.

APPLICANT: Disis, Mary L.

TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN

TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE

TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED

NUMBER OF SEQUENCES: 68

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed and Berry

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: US  
ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/467,083

FILING DATE: 06-JUN-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/414,417

FILING DATE: 06-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Sharkey, Richard G.

REGISTRATION NUMBER: 32,629

REFERENCE/DOCKET NUMBER: 920010.448C2

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

TELEX: 3723836 SEBDAABERY

INFORMATION FOR SEQ ID NO: 51:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-467-083-51

Query Match 6.4%; Score 15; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 3.4e-07;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 36 EDDMGDLVDAERYL 50

Db 1 EDDMGDLVDAERYL 15

## RESULT 4

US-08-467-083-52

Sequence 52, Application US/08467083

Patent No. 5726023

GENERAL INFORMATION:

APPLICANT: Cheever, Martin A.

APPLICANT: Disis, Mary L.

TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN

TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE

TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED

NUMBER OF SEQUENCES: 68

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed and Berry

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: US

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/467,083

FILING DATE: 06-JUN-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/414,417

FILING DATE: 06-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Sharkey, Richard G.

REGISTRATION NUMBER: 32,629

REFERENCE/DOCKET NUMBER: 920010.448C2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
TELEX: 3723836 SEEDANBERRY  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-467-083-52

Query Match 6.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 117 GNGAKGLOSLPTHD 131  
DB 1 GNGAKGLOSLPTHD 15

## RESULT 5

US-08-467-083-53  
Sequence 53, Application US/08467083  
Patent No. 5726023  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
APPLICANT: Disib, Mary L.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN  
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,083  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/414,417  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
TELEX: 3723836 SEEDANBERRY  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-467-083-53

Query Match 6.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 158 TCSPOPEYVNOPDVR 172  
DB 1 TCSPOPEYVNOPDVR 15

RESULT 6  
US-08-467-083-54  
Sequence 54, Application US/08467083  
Patent No. 5726023  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
APPLICANT: Disib, Mary L.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN  
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,083  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/414,417  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
TELEX: 3723836 SEEDANBERRY  
INFORMATION FOR SEQ ID NO: 54:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-467-083-54

Query Match 6.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 192 TLERPXTLSPGKNGV 206  
DB 1 TLERPXTLSPGKNGV 15

RESULT 7  
US-08-467-083-55  
Sequence 55, Application US/08467083  
Patent No. 5726023  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
APPLICANT: Disib, Mary L.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN  
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,083  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/414,417  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
TELEX: 3723836 SEEDANBERRY  
INFORMATION FOR SEQ ID NO: 55:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-467-083-55



MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,083  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/414,417  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
TELEX: 3723836 SEDANBERRY  
INFORMATION FOR SEQ ID NO: 55:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-467-083-55

Query Match 6.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 214 GGAIVENPEYLTPOGG 228  
DB 1 GGAIVENPEYLTPOGG 15

RESULT 8  
US-08-414-417B-51  
Sequence 51, Application US/08414417B  
Patent No. 5801005  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
TELEX: 3723836 SEDANBERRY  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid

TOPOLOGY: linear  
US-08-414-417B-51

Query Match 6.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 EDDMGDLVDAREYL 50  
DB 1 EDDMGDLVDAREYL 15

RESULT 9  
US-08-414-417B-52  
Sequence 52, Application US/08414417B  
Patent No. 5801005  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
TELEX: 3723836 SEDANBERRY  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-414-417B-52

Query Match 6.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 117 GGAAGKGLSLPPTH 131  
DB 1 GGAAGKGLSLPPTH 15

RESULT 10  
US-08-414-417B-53  
Sequence 53, Application US/08414417B  
Patent No. 5801005  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
TELEX: 3723836 SEDANBERRY  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid

;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Seed and Berry LLP  
;; STREET: 6300 Columbia Center, 701 Fifth Avenue  
;; CITY: Seattle  
;; STATE: Washington  
;; COUNTRY: US  
;; ZIP: 98104-7092  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentin Release #1.0, Version #1.25  
;;  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/414,417B  
;; FILING DATE: 31-MAR-1995  
;; CLASSIFICATION: 424  
;;  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Sharkey, Richard G.  
;; REGISTRATION NUMBER: 32,629  
;; REFERENCE/DOCKET NUMBER: 920010.448C2  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (206) 622-4900  
;; TELEFAX: (206) 682-6031  
;; INFORMATION FOR SEQ ID NO: 53:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 15 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;;  
US-08-414-417B-53

Query Match 6.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 158 TCSPQPEYVNOQDVR 172  
DB 1 TCSPQPEYVNOQDVR 15

RESULT 11  
US-08-414-417B-54  
; Sequence 54, Application US/08414417B  
; Patent No. 5801005  
; GENERAL INFORMATION:  
; APPLICANT: Cheever, Martin A.  
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/414,417B  
; FILING DATE: 31-MAR-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sharkey, Richard G.  
; REGISTRATION NUMBER: 32,629  
; REFERENCE/DOCKET NUMBER: 920010.448C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031

;; INFORMATION FOR SEQ ID NO: 54:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 15 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;;  
US-08-414-417B-54

Query Match 6.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 192 TLERPKTISPGKNGV 206  
DB 1 TLERPKTISPGKNGV 15

RESULT 12  
US-08-414-417B-55  
; Sequence 55, Application US/08414417B  
; Patent No. 5801005  
; GENERAL INFORMATION:  
; APPLICANT: Cheever, Martin A.  
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/414,417B  
; FILING DATE: 31-MAR-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sharkey, Richard G.  
; REGISTRATION NUMBER: 32,629  
; REFERENCE/DOCKET NUMBER: 920010.448C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 55:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
;;  
US-08-414-417B-55

Query Match 6.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 214 GGAIVENPEYLTPOGG 228  
DB 1 GGAIVENPEYLTPOGG 15

RESULT 13  
US-08-486-348A-51  
; Sequence 51, Application US/08486348A  
; Patent No. 5846538  
; GENERAL INFORMATION:  
; APPLICANT: Cheever, Martin A.  
; APPLICANT: Disis, Mary L.

TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,348A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C6  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 682-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-486-348A-51

Query Match 6.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 EDDMDGLVDAEYL 50  
DB 1 EDDMDGLVDAEYL 15

RESULT 14  
US-08-486-348A-52  
Sequence 52, Application US/08486348A  
Patent No. 5846538  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,348A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C6  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 682-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-486-348A-53

REFERENCE/DOCKET NUMBER: 920010.448C6  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 682-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-486-348A-52

Query Match 6.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 117 GMGAAGLQSLPTHD 131  
DB 1 GMGAAGLQSLPTHD 15

RESULT 15  
US-08-486-348A-53  
Sequence 53, Application US/08486348A  
Patent No. 5846538  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,348A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C6  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 682-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-486-348A-53

Query Match 6.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 158 TCSPOPEYVQPDVR 172  
DB 1 TCSPOPEYVQPDVR 15

RESULT 16  
US-08-486-348A-54  
Sequence 54, Application US/08486348A

```
/ Patent No. 5846538
/ GENERAL INFORMATION:
/ APPLICANT: Cheever, Martin A.
/ APPLICANT: Disig, Mary L.
/ TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
/ TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
/ TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
/ NUMBER OF SEQUENCES: 69
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Seed and Berry LLP
/ STREET: 6300 Columbia Center, 701 Fifth Avenue
/ CITY: Seattle
/ STATE: Washington
/ COUNTRY: US
/ ZIP: 98104-7092
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/486,348A
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sharkey, Richard G.
/ REGISTRATION NUMBER: 32,629
/ REFERENCE/DOCKET NUMBER: 920010.448C6
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 622-4900
/ TELEFAX: (206) 682-6031
/ INFORMATION FOR SEQ ID NO: 54:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ US-08-486-348A-54

Query Match 6.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 192 TLERPRTLSPGKNGV 206
Db 1 TLERPRTLSPGKNGV 15

RESULT 17
US-08-486-348A-55
/ Sequence 55, Application US/08486348A
/ Patent No. 5846538
/ GENERAL INFORMATION:
/ APPLICANT: Cheever, Martin A.
/ APPLICANT: Disig, Mary L.
/ TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
/ TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
/ TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
/ NUMBER OF SEQUENCES: 69
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Seed and Berry LLP
/ STREET: 6300 Columbia Center, 701 Fifth Avenue
/ CITY: Seattle
/ STATE: Washington
/ COUNTRY: US
/ ZIP: 98104-7092
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/486,348A
/ FILING DATE: 07-JUN-1995
```

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/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sharkey, Richard G.
/ REGISTRATION NUMBER: 32,629
/ REFERENCE/DOCKET NUMBER: 920010.448C6
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 622-4900
/ TELEFAX: (206) 682-6031
/ INFORMATION FOR SEQ ID NO: 55:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ US-08-486-348A-55

Query Match 6.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 214 GGAVENPEYLTPOGG 228
Db 1 GGAVENPEYLTPOGG 15

RESULT 18
US-08-468-545B-51
/ Sequence 51, Application US/08468545B
/ Patent No. 5876712
/ GENERAL INFORMATION:
/ APPLICANT: Cheever, Martin A.
/ APPLICANT: Disig, Mary L.
/ TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
/ TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
/ TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
/ NUMBER OF SEQUENCES: 69
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Seed and Berry LLP
/ STREET: 6300 Columbia Center, 701 Fifth Avenue
/ CITY: Seattle
/ STATE: Washington
/ COUNTRY: US
/ ZIP: 98104-7092
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/468,545B
/ FILING DATE: 06-JUN-1995
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sharkey, Richard G.
/ REGISTRATION NUMBER: 32,629
/ REFERENCE/DOCKET NUMBER: 920010.448C5
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 622-4900
/ TELEFAX: (206) 682-6031
/ INFORMATION FOR SEQ ID NO: 51:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ US-08-468-545B-51

Query Match 6.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 36 EDDMDGLVDVDAEYL 50
Db 1 EDDMDGLVDVDAEYL 15
```

RESULT 19  
US-08-468-545B-52  
Sequence 52, Application US/08468545B  
Patent No. 5876712  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/468,545B  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION/DOCKET NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 682-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-468-545B-52

Query Match 6.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 117 GCGAKGLQSLPTHD 131  
DB 1 GCGAKGLQSLPTHD 15

RESULT 20  
US-08-468-545B-53  
Sequence 53, Application US/08468545B  
Patent No. 5876712  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/468,545B  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION/DOCKET NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 682-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 54:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-468-545B-54

SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/468,545B  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION/DOCKET NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 682-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-468-545B-53

Query Match 6.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 158 TCSPQPEYVNPQDVR 172  
DB 1 TCSPQPEYVNPQDVR 15

RESULT 21  
US-08-468-545B-54  
Sequence 54, Application US/08468545B  
Patent No. 5876712  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/468,545B  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION/DOCKET NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 682-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 54:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-468-545B-54

Query Match 6.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 192 TLERPKTSLPGKNGV 206  
|||||  
Db 1 TLERPKTSLPGKNGV 15

## RESULT 22

US-08-468-545B-55  
; Sequence 55, Application US/08468545B  
; Patent No. 5876712  
; GENERAL INFORMATION:  
; APPLICANT: Cheever, Martin A.  
; APPLICANT: Diels, Mary L.  
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/468,545B  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sharkey, Richard G.  
; REGISTRATION NUMBER: 32,629  
; REFERENCE/DOCKET NUMBER: 920010.448C5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 682-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 55:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; US-08-468-545B-55  
; Query Match 6.4%; Score 15; DB 1; Length 15;  
; Best Local Similarity 100.0%; Pred. No. 3.4e-07;  
; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 214 GGAVNPEYLTPOGG 228  
|||||  
Db 1 GGAVNPEYLTPOGG 15

## RESULT 23

US-08-466-680B-51  
; Sequence 51, Application US/08466680B  
; Patent No. 6075122  
; GENERAL INFORMATION:  
; APPLICANT: Cheever, Martin A.  
; APPLICANT: Diels, Mary L.  
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98104-7092

## COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/466,680B  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sharkey, Richard G.  
; REGISTRATION NUMBER: 32,629  
; REFERENCE/DOCKET NUMBER: 920010.448C4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 682-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 51:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; US-08-466-680B-51

Query Match 6.4%; Score 15; DB 2; Length 15;  
; Best Local Similarity 100.0%; Pred. No. 3.4e-07;  
; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 36 EDDDMGDLVDAEYTL 50  
|||||  
Db 1 EDDDMGDLVDAEYTL 15

## RESULT 24

US-08-466-680B-52  
; Sequence 52, Application US/08466680B  
; Patent No. 6075122  
; GENERAL INFORMATION:  
; APPLICANT: Cheever, Martin A.  
; APPLICANT: Diels, Mary L.  
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/466,680B  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sharkey, Richard G.  
; REGISTRATION NUMBER: 32,629  
; REFERENCE/DOCKET NUMBER: 920010.448C4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 682-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 52:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; US-08-466-680B-52

Query Match 6.4%; Score 15; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 117 GNGAKGLOSLPTHD 131  
DB 1 GNGAKGLOSLPTHD 15

## RESULT 25

US-08-466-680B-53  
Sequence 53, Application US/08466680B  
Patent No. 6075122

## GENERAL INFORMATION:

APPLICANT: Cheever, Martin A.  
APPLICANT: Disls, Mary L.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/466,680B  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

## US-08-466-680B-53

Query Match 6.4%; Score 15; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 158 TCSPOPEYVQPDVR 172  
DB 1 TCSPOPEYVQPDVR 15

## RESULT 26

US-08-466-680B-54  
Sequence 54, Application US/08466680B  
Patent No. 6075122

## GENERAL INFORMATION:

APPLICANT: Cheever, Martin A.  
APPLICANT: Disls, Mary L.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/466,680B  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 54:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

## US-08-466-680B-54

Query Match 6.4%; Score 15; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 192 TLERPKTSLPGKNGV 206  
DB 1 TLERPKTSLPGKNGV 15

## RESULT 27

US-08-466-680B-55  
Sequence 55, Application US/08466680B  
Patent No. 6075122

## GENERAL INFORMATION:

APPLICANT: Cheever, Martin A.  
APPLICANT: Disls, Mary L.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/466,680B  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 55:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids

TYPE: amino acid  
TOPOLOGY: linear  
US-08-466-680B-55

Query Match 6.4%; Score 15; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 214 GGAVENPEYLTPOGG 228  
Db 1 GGAVENPEYLTPOGG 15

RESULT 28  
US-09-354-533-51  
Sequence 51, Application US/09354533  
Patent No. 6664370  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
Dialb, Mary L.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
HER-2/neu ONCOGENE IS ASSOCIATED  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/354,533  
FILING DATE: 15-Jul-1999  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C9  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 51:  
US-09-354-533-51

Query Match 6.4%; Score 15; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 36 EDDMGDLVDABEYL 50  
Db 1 EDDMGDLVDABEYL 15

RESULT 29  
US-09-354-533-52  
Sequence 52, Application US/09354533  
Patent No. 6664370  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
Dialb, Mary L.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE

HER-2/neu ONCOGENE IS ASSOCIATED  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/354,533  
FILING DATE: 15-Jul-1999  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C9

US-09-354-533-52

Query Match 6.4%; Score 15; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 117 GMAAKGLQSLPTHD 131  
Db 1 GMAAKGLQSLPTHD 15

RESULT 30  
US-09-354-533-53  
Sequence 53, Application US/09354533  
Patent No. 6664370  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
Dialb, Mary L.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
HER-2/neu ONCOGENE IS ASSOCIATED  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/354,533  
FILING DATE: 15-Jul-1999  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C9



```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 53:
US-09-354-533-53
;
Query Match 6.4%; Score 15; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 158 TCSPQPEYVNPQDVR 172
DB 1 TCSPQPEYVNPQDVR 15

RESULT 31
US-09-354-533-54
; Sequence 54, Application US/09354533
; Patent No. 6664370
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/354,533
; FILING DATE: 15-Jul-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 54:
US-09-354-533-54
;
Query Match 6.4%; Score 15; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 192 TLSPKTLSPKNGV 206
DB 1 TLSPKTLSPKNGV 15

RESULT 32
US-09-354-533-55
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```

; Sequence 55, Application US/09354533
; Patent No. 6664370
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/354,533
; FILING DATE: 15-Jul-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 55:
US-09-354-533-55
;
Query Match 6.4%; Score 15; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 214 GGAVENPEYLTPOGG 228
DB 1 GGAVENPEYLTPOGG 15

RESULT 33
US-08-403-459-45
; Sequence 45, Application US/08403459
; Patent No. 651942
; GENERAL INFORMATION:
; APPLICANT: Ioannides, Constantine G.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STIMULATING
; TITL OF INVENTION: T-LYMPHOCYTES
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
```

APPLICATION NUMBER: US/08/403,459  
FILING DATE: Concurrently Herewith  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Kitchell, Barbara S.  
REGISTRATION NUMBER: 33,928  
REFERENCE/DOCKET NUMBER: UTSC:390/KIT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (713) 789-2679  
TELEX: 79-0924  
INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-403-459-45

Query Match 5.5%; Score 13; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.3e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 112 PDGDLGMGAAGL 124  
Db 1 PDGDLGMGAAGL 13

RESULT 34  
US-08-625-322-25  
Sequence 25, Application US/08625322  
Patent No. 5804412

GENERAL INFORMATION:  
APPLICANT: G11, Gordon N.  
APPLICANT: Kurren, Richard C.  
APPLICANT: Cadena, Deborah L.  
TITLE OF INVENTION: Sorting Nexins and Methods of Using Same  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell and Flores  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/625,322  
FILING DATE: 01-APR-1996  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,615  
REFERENCE/DOCKET NUMBER: P-UD 1955  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 48 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-625-322-25

Query Match 4.7%; Score 11; DB 1; Length 48;  
Best Local Similarity 100.0%; Pred. No. 0.0059;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EFSRWARDPOR 11  
Db 7 EFSRWARDPOR 17

RESULT 35  
US-08-159-339A-268  
Sequence 268, Application US/08159339A  
Patent No. 6037135

GENERAL INFORMATION:  
APPLICANT: Kubo, Ralph T.  
APPLICANT: Grey, Howard W.  
APPLICANT: Sette, Alessandro  
APPLICANT: Celis, Esteban  
TITLE OF INVENTION: HLA Binding peptides and Their  
TITLE OF INVENTION: Uses  
NUMBER OF SEQUENCES: 1254  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111-3834

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/159,339A  
FILING DATE: 29-NOV-1993  
CLASSIFICATION: 424

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/926,666  
FILING DATE: 07-AUG-1992  
APPLICATION NUMBER: US 08/027,746  
FILING DATE: 05-MAR-1993  
APPLICATION NUMBER: US 08/103,396  
FILING DATE: 06-AUG-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Eilen Lauver  
REGISTRATION NUMBER: 32,762  
REFERENCE/DOCKET NUMBER: 018623-005030US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
TELEX:

INFORMATION FOR SEQ ID NO: 268:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-159-339A-268

Query Match 4.3%; Score 10; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.012;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 MGDVDAEEY 49  
Db 1 MGDVDAEEY 10

RESULT 36  
US-08-403-459-16  
Sequence 16, Application US/08403459  
Patent No. 6514942

GENERAL INFORMATION:  
APPLICANT: Ioannides, Constantine G.  
APPLICANT: Fisk, Bryan A.

APPLICANT: Ioannides, Maria G.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STIMULATING  
TITLE OF INVENTION: T-LYMPHOCYTES  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: United States of America  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/403,459  
FILING DATE: Concurrently Herewith  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Kitchell, Barbara S.  
REGISTRATION NUMBER: 33,928  
REFERENCE/DOCKET NUMBER: UTSC:390/KIT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (713) 789-2679  
TELEX: 79-0924  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-403-459-16

Query Match 4.3%; Score 10; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.012;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 115 DLGMAAKGL 124  
DB 1 DLGMAAKGL 10

RESULT 37  
US-08-403-459-44  
Sequence 44: Application US/08403459  
Patent No. 6514942  
GENERAL INFORMATION:  
APPLICANT: Ioannides, Constantn G.  
APPLICANT: Fisk, Bryan A.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STIMULATING  
TITLE OF INVENTION: T-LYMPHOCYTES  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: United States of America  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/403,459  
FILING DATE: Concurrently Herewith  
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:  
NAME: Kitchell, Barbara S.  
REGISTRATION NUMBER: 33,928  
REFERENCE/DOCKET NUMBER: UTSC:390/KIT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (713) 789-2679  
TELEX: 79-0924  
INFORMATION FOR SEQ ID NO: 44:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-403-459-44

Query Match 4.3%; Score 10; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.012;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 115 DLGMAAKGL 124  
DB 1 DLGMAAKGL 10

RESULT 38  
US-08-403-459-40  
Sequence 40: Application US/08403459  
Patent No. 6514942  
GENERAL INFORMATION:  
APPLICANT: Ioannides, Constantn G.  
APPLICANT: Fisk, Bryan A.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STIMULATING  
TITLE OF INVENTION: T-LYMPHOCYTES  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: United States of America  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/403,459  
FILING DATE: Concurrently Herewith  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Kitchell, Barbara S.  
REGISTRATION NUMBER: 33,928  
REFERENCE/DOCKET NUMBER: UTSC:390/KIT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (713) 789-2679  
TELEX: 79-0924  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-403-459-40

Query Match 4.3%; Score 10; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.015;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 EFSRMARDPQ 10  
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Db 4 EFSRMARDPQ 13

## RESULT 39

US-08-467-083-64  
; Sequence 64, Application US/08467083  
; Patent No. 5726023

## GENERAL INFORMATION:

APPLICANT: Cheever, Martin A.

APPLICANT: Disib, Mary L.

TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN

TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE

TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED

NUMBER OF SEQUENCES: 68

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed and Berry

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: US

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/467,083

FILING DATE: 06-JUN-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/414,417

FILING DATE: 06-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Sharkey, Richard G.

REGISTRATION NUMBER: 32,629

REFERENCE/DOCKET NUMBER: 920010.448C2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

TELEFAX: 3723836 SEEDANBERRY

INFORMATION FOR SEQ ID NO: 64:

SEQUENCE CHARACTERISTICS:

LENGTH: 14 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

US-08-467-083-64

Query Match 4.3%; Score 10; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 0.016;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 EFSRMARDPQ 10

|||||

Db 5 EFSRMARDPQ 14

## RESULT 40

US-08-414-417B-64

; Sequence 64, Application US/08414417B

; Patent No. 5801005

GENERAL INFORMATION:

APPLICANT: Cheever, Martin A.

APPLICANT: Disib, Mary L.

TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN

TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE

TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED

NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/414,417B

FILING DATE: 31-MAR-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Sharkey, Richard G.

REGISTRATION NUMBER: 32,629

REFERENCE/DOCKET NUMBER: 920010.448C2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 64:

SEQUENCE CHARACTERISTICS:

LENGTH: 14 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

US-08-414-417B-64

Query Match 4.3%; Score 10; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 0.016;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 EFSRMARDPQ 10

|||||

Db 5 EFSRMARDPQ 14

## RESULT 41

US-08-486-348A-64

; Sequence 64, Application US/08486348A

; Patent No. 5846338

GENERAL INFORMATION:

APPLICANT: Cheever, Martin A.

APPLICANT: Disib, Mary L.

TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN

TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE

TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED

NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed and Berry LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: US

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/486,348A

FILING DATE: 07-JUN-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Sharkey, Richard G.

REGISTRATION NUMBER: 32,629

REFERENCE/DOCKET NUMBER: 920010.448C6

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 64:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-468-348A-64

Query Match 4.3%; Score 10; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.016;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EFSRMAPDQ 10  
DB 5 EFSRMAPDQ 14

RESULT 42  
US-08-468-545B-64  
Sequence 64, Application US/08468545B  
Patent No. 5876712  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
APPLICANT: Disis, Mary L.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESSES:  
ADDRESSER: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/468,545B  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448CS  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 64:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-468-545B-64

Query Match 4.3%; Score 10; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.016;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EFSRMAPDQ 10  
DB 5 EFSRMAPDQ 14

RESULT 43  
US-08-466-680B-64  
Sequence 64, Application US/08466680B  
Patent No. 6075122  
GENERAL INFORMATION:

APPLICANT: Cheever, Martin A.  
APPLICANT: Disis, Mary L.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESSES:  
ADDRESSER: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/466,680B  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 64:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-466-680B-64

Query Match 4.3%; Score 10; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.016;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EFSRMAPDQ 10  
DB 5 EFSRMAPDQ 14

RESULT 44  
US-09-354-533-64  
Sequence 64, Application US/09354533  
Patent No. 6664370  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
APPLICANT: Disis, Mary L.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESSES:  
ADDRESSER: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/354,533  
FILING DATE: 15-JUL-1999  
CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C9  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 64:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 64:  
US-09-354-533-64

Query Match 4.3%; Score 10; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.016;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EFSRWARDPQ 10  
Db 5 EFSRWARDPQ 14

RESULT 45  
US-08-197-484-11  
Sequence 11, Application US/08197484  
Patent No. 6419931  
GENERAL INFORMATION:  
APPLICANT: VITIELLO, Maria A.  
APPLICANT: CHESTNUT, Robert W.  
APPLICANT: SETTE, Alessandro D.  
APPLICANT: CELIS, Bateban  
APPLICANT: GRAY, Howard  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING  
TITLE OF INVENTION: CTL IMMUNITY  
NUMBER OF SEQUENCES: 153  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: Stewart Street Tower, One Market Plaza  
CITY: San Francisco  
STATE: California  
COUNTRY: US  
ZIP: 94105-1493  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/197,484  
FILING DATE: 16-FEB-1994  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/935,811  
FILING DATE: 26-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/874,491  
FILING DATE: 27-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/827,682  
FILING DATE: 29-JAN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/749,568  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Parmelee, Steven W.  
REGISTRATION NUMBER: 31,990  
REFERENCE/DOCKET NUMBER: 14137-26-4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 467-9600  
TELEFAX: (206) 623-6793

INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-197-484-11

Query Match 4.3%; Score 10; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0.019;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EFSRWARDPQ 10  
Db 8 EFSRWARDPQ 17

RESULT 46  
PCT-US95-02121-11  
Sequence 11, Application PC/TUS9502121  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING  
TITLE OF INVENTION: CTL IMMUNITY  
NUMBER OF SEQUENCES: 153  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/02121  
FILING DATE: 16-FEB-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/197,484  
FILING DATE: 16-FEB-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/935,811  
FILING DATE: 26-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/874,491  
FILING DATE: 27-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/827,682  
FILING DATE: 29-JAN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/749,568  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Parmelee, Steven W.  
REGISTRATION NUMBER: 31,990  
REFERENCE/DOCKET NUMBER: 14137-26-4PC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 467-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
PCT-US95-02121-11

Query Match 4.3%; Score 10; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0.019;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EFSRWARDPQ 10  
Db 8 EFSRWARDPQ 17

RESULT 47  
US-08-423-646A-46  
Sequence 46, Application US/08423646A  
Patent No. 6280964  
GENERAL INFORMATION:  
APPLICANT: Kavanaugh, William M.  
APPLICANT: Williams, Lewis T.  
TITLE OF INVENTION: Binding Sites for Phosphotyrosine  
TITLE OF INVENTION: Binding Domains  
NUMBER OF SEQUENCES: 74  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/423,646A  
FILING DATE: 14-APR-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Dow, Karen B.  
REGISTRATION NUMBER: 29,684  
REFERENCE/DOCKET NUMBER: 2307K-059100  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Region  
LOCATION: one-of(11)  
OTHER INFORMATION: /note="Xaa is phosphotyrosine."  
US-08-423-646A-46

Query Match 4.3%; Score 10; DB 2; Length 21;  
Best Local Similarity 100.0%; Pred. No. 0.024;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 212 AFGGAVENPE 221  
DB 1 AFGGAVENPE 10

RESULT 48  
US-08-467-083-10  
Sequence 10, Application US/08467083  
Patent No. 5726023  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
APPLICANT: Disla, Mary L.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN  
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Seed and Berry  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington

COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,083  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/414,417  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
TELEX: 3723836 SEBANDERRY  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-467-083-10

Query Match 3.8%; Score 9; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 198 TISPGKGV 206  
DB 1 TISPGKGV 9

RESULT 49  
US-08-467-083-23  
Sequence 23, Application US/08467083  
Patent No. 5726023  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
APPLICANT: Disla, Mary L.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN  
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Seed and Berry  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,083  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/414,417  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C2  
TELECOMMUNICATION INFORMATION:

Search completed: January 18, 2006, 20:50:09  
Job time : 31 secs

TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
TELEX: 3723836 SEDDANBERY  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-467-083-23

Query Match 3.8%; Score 9; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 DLVDAEYL 50  
|||||||  
Db 1 DLVDAEYL 9

# RESULT 50

US-08-467-083-24  
Sequence 24, Application US/08467083  
Patent No. 5726023  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
APPLICANT: Disig, Mary L.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN  
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,083  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/414,417  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
TELEX: 3723836 SEDDANBERY  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-467-083-24

Query Match 3.8%; Score 9; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 88 GLPSEEEA 96  
|||||||  
Db 1 GLPSEEEA 9



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OM protein - protein search, using SW model

Run on: January 18, 2006, 20:49:47 ; Search time 30 Seconds  
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79.382 Million cell updates/sec

Title: US-09-930-125-2\_COPY\_975\_1209

Profile score: 235  
Sequence: 1 EERSRRARDQGRVIVIGNEDL.....AVENPEYLTPGGAAAPQHP 235

Scoring table: OLIGO  
Gapop 60.0, Gapext 60.0

Searched: 70606 seqs, 10133881 residues

Word size: 0

Total number of hits satisfying chosen parameters: 54762

Minimum DB seq length: 0  
Maximum DB seq length: 235

Post-processing: Listing first 200 summaries

Database:

Published Applications AA New:\*  
1: /cgn2\_6/prodata/1/pubppa/US06\_NEW\_PUB.pep:\*  
2: /cgn2\_6/prodata/1/pubppa/US07\_NEW\_PUB.pep:\*  
3: /cgn2\_6/prodata/1/pubppa/US09\_NEW\_PUB.pep:\*  
4: /cgn2\_6/prodata/1/pubppa/US10\_NEW\_PUB.pep:\*  
5: /cgn2\_6/prodata/1/pubppa/US11\_NEW\_PUB.pep:\*  
6: /cgn2\_6/prodata/1/pubppa/US12\_NEW\_PUB.pep:\*  
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8: /cgn2\_6/prodata/1/pubppa/US14\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARYS

| Result No. | Score | Query Match | Length | ID                 | Description        |
|------------|-------|-------------|--------|--------------------|--------------------|
| 1          | 15    | 6.4         | 15     | US-11-033-039-581  | Sequence 581, App  |
| 2          | 12    | 5.1         | 12     | US-11-033-039-574  | Sequence 574, App  |
| 3          | 10    | 4.3         | 14     | US-11-033-039-584  | Sequence 584, App  |
| 4          | 9     | 3.8         | 9      | US-11-033-039-554  | Sequence 554, App  |
| 5          | 9     | 3.8         | 9      | US-11-033-039-560  | Sequence 560, App  |
| 6          | 9     | 3.8         | 9      | US-11-033-039-567  | Sequence 567, App  |
| 7          | 9     | 3.8         | 14     | US-11-033-039-589  | Sequence 589, App  |
| 8          | 9     | 3.8         | 14     | US-11-033-039-593  | Sequence 593, App  |
| 9          | 7     | 3.0         | 12     | US-11-033-039-575  | Sequence 575, App  |
| 10         | 7     | 3.0         | 161    | US-10-467-657-1338 | Sequence 1338, App |
| 11         | 7     | 3.0         | 216    | US-11-186-284-217  | Sequence 217, App  |
| 12         | 6     | 2.6         | 9      | US-11-033-039-586  | Sequence 586, App  |
| 13         | 6     | 2.6         | 10     | US-11-057-708-25   | Sequence 25, App   |
| 14         | 6     | 2.6         | 14     | US-11-033-039-594  | Sequence 594, App  |
| 15         | 6     | 2.6         | 112    | US-10-510-386-140  | Sequence 140, App  |
| 16         | 6     | 2.6         | 122    | US-09-978-360A-604 | Sequence 604, App  |
| 17         | 6     | 2.6         | 147    | US-10-793-626-2502 | Sequence 2502, App |
| 18         | 6     | 2.6         | 156    | US-10-467-657-112  | Sequence 112, App  |
| 19         | 6     | 2.6         | 156    | US-10-467-657-8550 | Sequence 8550, App |
| 20         | 6     | 2.6         | 195    | US-10-995-561-526  | Sequence 561, App  |
| 21         | 6     | 2.6         | 233    | US-11-022-562-26   | Sequence 226, App  |
| 22         | 5     | 2.1         | 8      | US-11-045-024-1111 | Sequence 1111, App |
| 23         | 5     | 2.1         | 8      | US-11-045-024-6406 | Sequence 6406, App |
| 24         | 5     | 2.1         | 8      | US-11-062-186-2    | Sequence 2, App    |
| 25         | 5     | 2.1         | 9      | US-10-467-657-4572 | Sequence 4572, App |

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|----|---|-----|----|---------------------|---------------------|
| 26 | 5 | 2.1 | 9  | US-11-045-024-1231  | Sequence 1231, App  |
| 27 | 5 | 2.1 | 9  | US-11-045-024-5189  | Sequence 5189, App  |
| 28 | 5 | 2.1 | 9  | US-11-045-024-7291  | Sequence 7291, App  |
| 29 | 5 | 2.1 | 9  | US-11-045-024-13707 | Sequence 13707, App |
| 30 | 5 | 2.1 | 10 | US-10-431-638-29    | Sequence 29, App    |
| 31 | 5 | 2.1 | 10 | US-11-045-024-1348  | Sequence 1348, App  |
| 32 | 5 | 2.1 | 10 | US-11-045-024-5218  | Sequence 5218, App  |
| 33 | 5 | 2.1 | 10 | US-11-045-024-7293  | Sequence 7293, App  |
| 34 | 5 | 2.1 | 10 | US-11-045-024-9197  | Sequence 9197, App  |
| 35 | 5 | 2.1 | 10 | US-11-062-186-128   | Sequence 128, App   |
| 36 | 5 | 2.1 | 10 | US-11-146-854-46    | Sequence 46, App    |
| 37 | 5 | 2.1 | 11 | US-11-033-365-22    | Sequence 22, App    |
| 38 | 5 | 2.1 | 11 | US-11-058-735-69    | Sequence 69, App    |
| 39 | 5 | 2.1 | 11 | US-11-119-098-67    | Sequence 67, App    |
| 40 | 5 | 2.1 | 11 | US-11-045-024-1456  | Sequence 1456, App  |
| 41 | 5 | 2.1 | 11 | US-11-045-024-4215  | Sequence 4215, App  |
| 42 | 5 | 2.1 | 11 | US-11-045-024-7286  | Sequence 7286, App  |
| 43 | 5 | 2.1 | 11 | US-11-045-024-9071  | Sequence 9071, App  |
| 44 | 5 | 2.1 | 12 | US-10-986-501-220   | Sequence 220, App   |
| 45 | 5 | 2.1 | 12 | US-11-054-515-2364  | Sequence 2364, App  |
| 46 | 5 | 2.1 | 14 | US-11-054-515-2390  | Sequence 2390, App  |
| 47 | 5 | 2.1 | 14 | US-11-054-515-2417  | Sequence 2417, App  |
| 48 | 5 | 2.1 | 14 | US-11-054-515-2420  | Sequence 2420, App  |
| 49 | 5 | 2.1 | 14 | US-11-054-515-2445  | Sequence 2445, App  |
| 50 | 5 | 2.1 | 14 | US-11-054-515-2464  | Sequence 2464, App  |
| 51 | 5 | 2.1 | 14 | US-11-054-515-2551  | Sequence 2551, App  |
| 52 | 5 | 2.1 | 14 | US-11-054-515-2557  | Sequence 2557, App  |
| 53 | 5 | 2.1 | 14 | US-11-054-515-2562  | Sequence 2562, App  |
| 54 | 5 | 2.1 | 14 | US-11-054-515-2672  | Sequence 2672, App  |
| 55 | 5 | 2.1 | 15 | US-11-024-251-4     | Sequence 4, App     |
| 56 | 5 | 2.1 | 15 | US-11-045-024-13008 | Sequence 13008, App |
| 57 | 5 | 2.1 | 15 | US-11-045-024-13051 | Sequence 13051, App |
| 58 | 5 | 2.1 | 17 | US-10-655-658-23    | Sequence 23, App    |
| 59 | 5 | 2.1 | 17 | US-10-655-658-2371  | Sequence 2871, App  |
| 60 | 5 | 2.1 | 18 | US-10-431-638-41    | Sequence 41, App    |
| 61 | 5 | 2.1 | 18 | US-10-431-638-43    | Sequence 43, App    |
| 62 | 5 | 2.1 | 19 | US-10-495-664-2     | Sequence 2, App     |
| 63 | 5 | 2.1 | 19 | US-11-051-481-1     | Sequence 1, App     |
| 64 | 5 | 2.1 | 32 | US-10-467-657-3840  | Sequence 3840, App  |
| 65 | 5 | 2.1 | 34 | US-10-467-657-9207  | Sequence 9207, App  |
| 66 | 5 | 2.1 | 42 | US-11-043-590-15    | Sequence 15, App    |
| 67 | 5 | 2.1 | 43 | US-10-864-079-16    | Sequence 16, App    |
| 68 | 5 | 2.1 | 45 | US-10-986-501-211   | Sequence 211, App   |
| 69 | 5 | 2.1 | 50 | US-10-467-657-6044  | Sequence 6044, App  |
| 70 | 5 | 2.1 | 52 | US-10-467-657-3780  | Sequence 3780, App  |
| 71 | 5 | 2.1 | 53 | US-11-188-281-15    | Sequence 15, App    |
| 72 | 5 | 2.1 | 57 | US-11-123-896-98    | Sequence 98, App    |
| 73 | 5 | 2.1 | 57 | US-11-123-896-143   | Sequence 143, App   |
| 74 | 5 | 2.1 | 62 | US-11-123-896-273   | Sequence 273, App   |
| 75 | 5 | 2.1 | 63 | US-11-174-166-2     | Sequence 2, App     |
| 76 | 5 | 2.1 | 63 | US-11-174-166-6     | Sequence 6, App     |
| 77 | 5 | 2.1 | 63 | US-11-174-166-8     | Sequence 8, App     |
| 78 | 5 | 2.1 | 63 | US-11-174-166-10    | Sequence 10, App    |
| 79 | 5 | 2.1 | 63 | US-11-174-166-12    | Sequence 12, App    |
| 80 | 5 | 2.1 | 63 | US-11-174-166-14    | Sequence 14, App    |
| 81 | 5 | 2.1 | 63 | US-11-174-166-16    | Sequence 16, App    |
| 82 | 5 | 2.1 | 63 | US-11-000-463-353   | Sequence 353, App   |
| 83 | 5 | 2.1 | 63 | US-11-000-463-825   | Sequence 825, App   |
| 84 | 5 | 2.1 | 63 | US-11-123-896-272   | Sequence 272, App   |
| 85 | 5 | 2.1 | 76 | US-11-000-463-842   | Sequence 842, App   |
| 86 | 5 | 2.1 | 79 | US-10-821-234-1153  | Sequence 1153, App  |
| 87 | 5 | 2.1 | 81 | US-10-821-234-370   | Sequence 370, App   |
| 88 | 5 | 2.1 | 82 | US-09-978-360A-418  | Sequence 418, App   |
| 89 | 5 | 2.1 | 83 | US-10-821-234-1346  | Sequence 1346, App  |
| 90 | 5 | 2.1 | 85 | US-09-978-360A-601  | Sequence 601, App   |
| 91 | 5 | 2.1 | 85 | US-09-978-360A-602  | Sequence 602, App   |
| 92 | 5 | 2.1 | 85 | US-09-978-360A-779  | Sequence 779, App   |
| 93 | 5 | 2.1 | 85 | US-11-102-476-22    | Sequence 22, App    |
| 94 | 5 | 2.1 | 87 | US-11-082-389-360   | Sequence 360, App   |
| 95 | 5 | 2.1 | 90 | US-11-102-476-7     | Sequence 7, App     |
| 96 | 5 | 2.1 | 90 | US-10-467-657-328   | Sequence 328, App   |
| 97 | 5 | 2.1 | 92 | US-11-000-463-380   | Sequence 380, App   |
| 98 | 5 | 2.1 | 92 | US-11-000-463-380   | Sequence 380, App   |

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| 99  | 5 | 2.1 | 92  | 7 | US-11-000-463-852  | Sequence 852, App  |
| 100 | 5 | 2.1 | 94  | 7 | US-11-097-812-9    | Sequence 9, Appl   |
| 101 | 5 | 2.1 | 94  | 7 | US-11-097-812-12   | Sequence 12, Appl  |
| 102 | 5 | 2.1 | 96  | 7 | US-11-097-812-7    | Sequence 7, Appl   |
| 103 | 5 | 2.1 | 96  | 7 | US-11-097-812-10   | Sequence 10, Appl  |
| 104 | 5 | 2.1 | 96  | 7 | US-11-097-812-11   | Sequence 11, Appl  |
| 105 | 5 | 2.1 | 98  | 7 | US-11-025-712-1    | Sequence 1, Appl   |
| 106 | 5 | 2.1 | 100 | 6 | US-10-793-626-848  | Sequence 848, App  |
| 107 | 5 | 2.1 | 100 | 6 | US-10-821-234-876  | Sequence 876, App  |
| 108 | 5 | 2.1 | 100 | 7 | US-11-025-712-7    | Sequence 7, Appl   |
| 109 | 5 | 2.1 | 103 | 6 | US-10-986-501-169  | Sequence 169, App  |
| 110 | 5 | 2.1 | 103 | 6 | US-10-467-657-8695 | Sequence 8695, App |
| 111 | 5 | 2.1 | 103 | 6 | US-10-995-561-590  | Sequence 590, App  |
| 112 | 5 | 2.1 | 103 | 7 | US-11-075-351-48   | Sequence 48, Appl  |
| 113 | 5 | 2.1 | 103 | 7 | US-11-124-368A-322 | Sequence 322, App  |
| 114 | 5 | 2.1 | 104 | 6 | US-10-793-626-422  | Sequence 422, App  |
| 115 | 5 | 2.1 | 104 | 6 | US-10-834-397-168  | Sequence 168, App  |
| 116 | 5 | 2.1 | 108 | 6 | US-09-978-360A-547 | Sequence 547, App  |
| 117 | 5 | 2.1 | 108 | 5 | US-09-978-360A-703 | Sequence 703, App  |
| 118 | 5 | 2.1 | 108 | 5 | US-10-510-880-5    | Sequence 5, Appl   |
| 119 | 5 | 2.1 | 108 | 6 | US-10-875-800-1    | Sequence 1, Appl   |
| 120 | 5 | 2.1 | 108 | 6 | US-10-467-657-2560 | Sequence 2560, App |
| 121 | 5 | 2.1 | 108 | 6 | US-10-299-977-1    | Sequence 1, Appl   |
| 122 | 5 | 2.1 | 109 | 7 | US-11-082-389-330  | Sequence 330, App  |
| 123 | 5 | 2.1 | 111 | 6 | US-10-821-234-1547 | Sequence 1547, App |
| 124 | 5 | 2.1 | 111 | 6 | US-10-771-257-34   | Sequence 34, Appl  |
| 125 | 5 | 2.1 | 111 | 7 | US-11-127-677-34   | Sequence 34, Appl  |
| 126 | 5 | 2.1 | 112 | 6 | US-10-821-234-1035 | Sequence 1035, App |
| 127 | 5 | 2.1 | 112 | 7 | US-11-020-772-19   | Sequence 19, Appl  |
| 128 | 5 | 2.1 | 114 | 6 | US-10-821-234-1370 | Sequence 1370, App |
| 129 | 5 | 2.1 | 115 | 6 | US-10-821-234-1404 | Sequence 1404, App |
| 130 | 5 | 2.1 | 115 | 6 | US-10-821-234-1433 | Sequence 1433, App |
| 131 | 5 | 2.1 | 116 | 6 | US-10-793-626-908  | Sequence 908, App  |
| 132 | 5 | 2.1 | 116 | 6 | US-10-793-626-2386 | Sequence 2386, App |
| 133 | 5 | 2.1 | 117 | 7 | US-11-020-772-12   | Sequence 12, Appl  |
| 134 | 5 | 2.1 | 117 | 7 | US-11-054-669-119  | Sequence 119, App  |
| 135 | 5 | 2.1 | 117 | 7 | US-11-096-070-34   | Sequence 34, Appl  |
| 136 | 5 | 2.1 | 118 | 7 | US-11-020-772-13   | Sequence 13, Appl  |
| 137 | 5 | 2.1 | 120 | 7 | US-11-096-070-35   | Sequence 35, Appl  |
| 138 | 5 | 2.1 | 120 | 7 | US-11-004-590-391  | Sequence 391, App  |
| 139 | 5 | 2.1 | 121 | 6 | US-10-467-657-3556 | Sequence 3556, App |
| 140 | 5 | 2.1 | 121 | 6 | US-10-665-658-24   | Sequence 24, Appl  |
| 141 | 5 | 2.1 | 125 | 6 | US-10-467-657-2128 | Sequence 2128, App |
| 142 | 5 | 2.1 | 125 | 6 | US-10-599-866-1    | Sequence 1, Appl   |
| 143 | 5 | 2.1 | 125 | 7 | US-11-061-821-1    | Sequence 1, Appl   |
| 144 | 5 | 2.1 | 128 | 7 | US-11-116-144-144  | Sequence 144, App  |
| 145 | 5 | 2.1 | 128 | 7 | US-11-052-554A-244 | Sequence 244, App  |
| 146 | 5 | 2.1 | 130 | 5 | US-09-978-360A-690 | Sequence 690, App  |
| 147 | 5 | 2.1 | 133 | 7 | US-11-047-757-9    | Sequence 9, Appl   |
| 148 | 5 | 2.1 | 133 | 7 | US-11-088-008-1    | Sequence 1, Appl   |
| 149 | 5 | 2.1 | 134 | 6 | US-10-510-880-1    | Sequence 1, Appl   |
| 150 | 5 | 2.1 | 134 | 6 | US-10-886-501-114  | Sequence 114, App  |
| 151 | 5 | 2.1 | 134 | 6 | US-10-986-501-199  | Sequence 199, App  |
| 152 | 5 | 2.1 | 134 | 6 | US-10-875-800-2    | Sequence 2, Appl   |
| 153 | 5 | 2.1 | 134 | 7 | US-11-043-590-12   | Sequence 12, Appl  |
| 154 | 5 | 2.1 | 135 | 6 | US-10-821-234-1018 | Sequence 1018, App |
| 155 | 5 | 2.1 | 137 | 6 | US-09-978-360A-765 | Sequence 765, App  |
| 156 | 5 | 2.1 | 138 | 6 | US-10-789-273-4    | Sequence 4, Appl   |
| 157 | 5 | 2.1 | 138 | 6 | US-10-789-273-8    | Sequence 8, Appl   |
| 158 | 5 | 2.1 | 138 | 6 | US-10-789-273-12   | Sequence 12, Appl  |
| 159 | 5 | 2.1 | 138 | 6 | US-10-527-500-15   | Sequence 15, Appl  |
| 160 | 5 | 2.1 | 140 | 6 | US-10-055-877-331  | Sequence 331, App  |
| 161 | 5 | 2.1 | 140 | 6 | US-10-055-877-333  | Sequence 333, App  |
| 162 | 5 | 2.1 | 140 | 6 | US-10-055-877-334  | Sequence 334, App  |
| 163 | 5 | 2.1 | 140 | 7 | US-11-193-512-27   | Sequence 27, Appl  |
| 164 | 5 | 2.1 | 141 | 7 | US-11-119-098-1    | Sequence 1, Appl   |
| 165 | 5 | 2.1 | 142 | 6 | US-10-793-626-3038 | Sequence 3038, App |
| 166 | 5 | 2.1 | 142 | 7 | US-11-055-822-64   | Sequence 64, Appl  |
| 167 | 5 | 2.1 | 142 | 7 | US-11-186-284-105  | Sequence 105, App  |
| 168 | 5 | 2.1 | 143 | 6 | US-10-467-657-274  | Sequence 274, App  |
| 169 | 5 | 2.1 | 143 | 6 | US-10-467-657-3770 | Sequence 3720, App |
| 170 | 5 | 2.1 | 143 | 7 | US-11-116-144-166  | Sequence 166, App  |
| 171 | 5 | 2.1 | 144 | 6 | US-10-821-234-1254 | Sequence 1254, App |

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|-----|---|-----|-----|---|--------------------|--------------------|
| 172 | 5 | 2.1 | 145 | 6 | US-10-467-657-6506 | Sequence 6506, App |
| 173 | 5 | 2.1 | 145 | 7 | US-11-215-721-3    | Sequence 3, Appl   |
| 174 | 5 | 2.1 | 146 | 6 | US-10-793-626-2694 | Sequence 2694, App |
| 175 | 5 | 2.1 | 146 | 7 | US-11-083-800-8    | Sequence 8, Appl   |
| 176 | 5 | 2.1 | 146 | 7 | US-10-793-626-824  | Sequence 824, App  |
| 177 | 5 | 2.1 | 148 | 6 | US-11-055-822-1076 | Sequence 1076, App |
| 178 | 5 | 2.1 | 148 | 7 | US-10-467-657-270  | Sequence 270, App  |
| 179 | 5 | 2.1 | 149 | 6 | US-10-467-657-3668 | Sequence 3668, App |
| 180 | 5 | 2.1 | 150 | 7 | US-11-152-497-4    | Sequence 4, Appl   |
| 181 | 5 | 2.1 | 152 | 6 | US-10-994-820A-13  | Sequence 13, Appl  |
| 182 | 5 | 2.1 | 152 | 6 | US-10-467-657-4310 | Sequence 4310, App |
| 183 | 5 | 2.1 | 152 | 7 | US-11-152-497-6    | Sequence 6, Appl   |
| 184 | 5 | 2.1 | 153 | 5 | US-09-978-360A-490 | Sequence 490, App  |
| 185 | 5 | 2.1 | 153 | 5 | US-09-978-360A-760 | Sequence 760, App  |
| 186 | 5 | 2.1 | 154 | 6 | US-10-821-234-1469 | Sequence 1469, App |
| 187 | 5 | 2.1 | 155 | 6 | US-10-793-626-2990 | Sequence 2990, App |
| 188 | 5 | 2.1 | 155 | 6 | US-10-467-657-4490 | Sequence 4490, App |
| 189 | 5 | 2.1 | 155 | 7 | US-11-116-144-169  | Sequence 169, App  |
| 190 | 5 | 2.1 | 156 | 6 | US-10-821-234-1424 | Sequence 1424, App |
| 191 | 5 | 2.1 | 156 | 7 | US-11-116-144-31   | Sequence 31, Appl  |
| 192 | 5 | 2.1 | 156 | 7 | US-11-116-144-168  | Sequence 168, App  |
| 193 | 5 | 2.1 | 157 | 6 | US-10-994-820A-14  | Sequence 14, Appl  |
| 194 | 5 | 2.1 | 158 | 6 | US-10-995-561-585  | Sequence 585, App  |
| 195 | 5 | 2.1 | 158 | 6 | US-10-995-561-586  | Sequence 586, App  |
| 196 | 5 | 2.1 | 158 | 7 | US-11-157-049-40   | Sequence 40, Appl  |
| 197 | 5 | 2.1 | 160 | 6 | US-10-793-626-940  | Sequence 940, App  |
| 198 | 5 | 2.1 | 160 | 7 | US-11-157-049-23   | Sequence 23, Appl  |
| 199 | 5 | 2.1 | 160 | 7 | US-11-157-049-39   | Sequence 39, Appl  |
| 200 | 5 | 2.1 | 160 | 7 | US-11-215-721-1    | Sequence 1, Appl   |

## ALIGNMENTS

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RESULT 1
US-11-033-039-581
; Sequence 581, Application US/11033039
; Publication No. US2006002947A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2017US01
; CURRENT APPLICATION NUMBER: US/11/033,039
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 581
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-033-039-581

Query Match 6.4%; Score 15; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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192 TLRRPTLSPGKNGV 206  
Db 1 TLRRPTLSPGKNGV 15

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RESULT 2
US-11-033-039-574
; Sequence 574, Application US/11033039
; Publication No. US2006002947A1
; GENERAL INFORMATION:
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APPLICANT: HUMPHREYS, ROBERT
APPLICANT: XU, MINZHEN
TITLE OF INVENTION: LI-KEY/ANTIGENIC EPIOTOPE HYBRID PEPTIDE VACCINES
FILE REFERENCE: REH-2017US01
CURRENT APPLICATION NUMBER: US/11/033,039
CURRENT FILING DATE: 2005-01-11
PRIOR APPLICATION NUMBER: 10/245,871
PRIOR FILING DATE: 2002-09-17
PRIOR APPLICATION NUMBER: 10/197,000
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: 09/396,813
PRIOR FILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 1452
SOFTWARE: PatentIn version 3.3
SEQ ID NO 574
LENGTH: 12
TYPE: PRT
ORGANISM: Homo sapiens
US-11-033-039-574
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Query Match 5.1%; Score 12; DB 7; Length 12;
Best Local Similarity 100.0%; Pred.No. 1.1e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 EFRRMARDPQRF 12
Db 1 EFRRMARDPQRF 12
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RESULT 3
US-11-033-039-584
Sequence 584, Application US/11033039
Publication No. US20060002947A1
GENERAL INFORMATION:
APPLICANT: HUMPHREYS, ROBERT
APPLICANT: XU, MINZHEN
TITLE OF INVENTION: LI-KEY/ANTIGENIC EPIOTOPE HYBRID PEPTIDE VACCINES
FILE REFERENCE: REH-2017US01
CURRENT APPLICATION NUMBER: US/11/033,039
CURRENT FILING DATE: 2005-01-11
PRIOR APPLICATION NUMBER: 10/245,871
PRIOR FILING DATE: 2002-09-17
PRIOR APPLICATION NUMBER: 10/197,000
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: 09/396,813
PRIOR FILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 1452
SOFTWARE: PatentIn version 3.3
SEQ ID NO 584
LENGTH: 14
TYPE: PRT
ORGANISM: Homo sapiens
US-11-033-039-584
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Query Match 4.3%; Score 10; DB 7; Length 14;
Best Local Similarity 100.0%; Pred.No. 0.0011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 5 EFRRMARDPQ 14
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RESULT 4
US-11-033-039-554
Sequence 554, Application US/11033039
Publication No. US20060002947A1
GENERAL INFORMATION:
APPLICANT: HUMPHREYS, ROBERT
APPLICANT: XU, MINZHEN
TITLE OF INVENTION: LI-KEY/ANTIGENIC EPIOTOPE HYBRID PEPTIDE VACCINES
FILE REFERENCE: REH-2017US01
CURRENT APPLICATION NUMBER: US/11/033,039
```

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CURRENT FILING DATE: 2005-01-11
PRIOR APPLICATION NUMBER: 10/245,871
PRIOR FILING DATE: 2002-09-17
PRIOR APPLICATION NUMBER: 10/197,000
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: 09/396,813
PRIOR FILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 1452
SOFTWARE: PatentIn version 3.3
SEQ ID NO 554
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-11-033-039-554
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Best Local Similarity 100.0%; Pred.No. 5.5e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 12 FVVIQNEDL 20
Db 1 FVVIQNEDL 9
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RESULT 5
US-11-033-039-560
Sequence 560, Application US/11033039
Publication No. US20060002947A1
GENERAL INFORMATION:
APPLICANT: HUMPHREYS, ROBERT
APPLICANT: XU, MINZHEN
TITLE OF INVENTION: LI-KEY/ANTIGENIC EPIOTOPE HYBRID PEPTIDE VACCINES
FILE REFERENCE: REH-2017US01
CURRENT APPLICATION NUMBER: US/11/033,039
CURRENT FILING DATE: 2005-01-11
PRIOR APPLICATION NUMBER: 10/245,871
PRIOR FILING DATE: 2002-09-17
PRIOR APPLICATION NUMBER: 10/197,000
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: 09/396,813
PRIOR FILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 1452
SOFTWARE: PatentIn version 3.3
SEQ ID NO 560
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-11-033-039-560
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Query Match 3.8%; Score 9; DB 7; Length 9;
Best Local Similarity 100.0%; Pred.No. 5.5e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 68 MVYHRRSS 76
Db 1 MVYHRRSS 9
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RESULT 6
US-11-033-039-607
Sequence 607, Application US/11033039
Publication No. US20060002947A1
GENERAL INFORMATION:
APPLICANT: HUMPHREYS, ROBERT
APPLICANT: XU, MINZHEN
TITLE OF INVENTION: LI-KEY/ANTIGENIC EPIOTOPE HYBRID PEPTIDE VACCINES
FILE REFERENCE: REH-2017US01
CURRENT APPLICATION NUMBER: US/11/033,039
CURRENT FILING DATE: 2005-01-11
PRIOR APPLICATION NUMBER: 10/245,871
PRIOR FILING DATE: 2002-09-17
PRIOR APPLICATION NUMBER: 10/197,000
PRIOR FILING DATE: 2002-07-17
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PRIOR APPLICATION NUMBER: 09/396,813  
PRIOR FILING DATE: 1999-09-14  
NUMBER OF SEQ ID NOS: 1452  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 607  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-033-039-607

Query Match 3.8%; Score 9; DB 7; Length 9;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 48 EYLVPQGGF 56  
Db 1 EYLVPQGGF 9

RESULT 7  
US-11-033-039-589

Sequence 589, Application US/11033039  
Publication No. US20060002947A1  
GENERAL INFORMATION:  
APPLICANT: HUMPHREYS, ROBERT  
APPLICANT: XU, MINZHEN  
TITLE OF INVENTION: LI-KEY/ANTIGENIC EPI TOPE HYBRID PEPTIDE VACCINES  
FILE REFERENCE: REH-2017US01  
CURRENT APPLICATION NUMBER: US/11/033,039  
CURRENT FILING DATE: 2005-01-11  
PRIOR APPLICATION NUMBER: 10/245,871  
PRIOR FILING DATE: 2002-09-17  
PRIOR APPLICATION NUMBER: 10/197,000  
PRIOR FILING DATE: 2002-07-17  
PRIOR APPLICATION NUMBER: 09/396,813  
PRIOR FILING DATE: 1999-09-14  
NUMBER OF SEQ ID NOS: 1452  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 589  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: hybrid peptide  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (5)..(5)  
OTHER INFORMATION: Ava  
US-11-033-039-589

Query Match 3.8%; Score 9; DB 7; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 FVVIQNEPL 20  
Db 6 FVVIQNEPL 14

RESULT 8  
US-11-033-039-593

Sequence 593, Application US/11033039  
Publication No. US20060002947A1  
GENERAL INFORMATION:  
APPLICANT: HUMPHREYS, ROBERT  
APPLICANT: XU, MINZHEN  
TITLE OF INVENTION: LI-KEY/ANTIGENIC EPI TOPE HYBRID PEPTIDE VACCINES  
FILE REFERENCE: REH-2017US01  
CURRENT APPLICATION NUMBER: US/11/033,039  
CURRENT FILING DATE: 2005-01-11  
PRIOR APPLICATION NUMBER: 10/245,871  
PRIOR FILING DATE: 2002-09-17

PRIOR APPLICATION NUMBER: 10/197,000  
PRIOR FILING DATE: 2002-07-17  
PRIOR APPLICATION NUMBER: 09/396,813  
PRIOR FILING DATE: 1999-09-14  
NUMBER OF SEQ ID NOS: 1452  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 593  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: hybrid peptide  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (5)..(5)  
OTHER INFORMATION: Ava  
US-11-033-039-593

Query Match 3.8%; Score 9; DB 7; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 68 MVHRHRSS 76  
Db 6 MVHRHRSS 14

RESULT 9  
US-11-033-039-575

Sequence 575, Application US/11033039  
Publication No. US20060002947A1  
GENERAL INFORMATION:  
APPLICANT: HUMPHREYS, ROBERT  
APPLICANT: XU, MINZHEN  
TITLE OF INVENTION: LI-KEY/ANTIGENIC EPI TOPE HYBRID PEPTIDE VACCINES  
FILE REFERENCE: REH-2017US01  
CURRENT APPLICATION NUMBER: US/11/033,039  
CURRENT FILING DATE: 2005-01-11  
PRIOR APPLICATION NUMBER: 10/245,871  
PRIOR FILING DATE: 2002-09-17  
PRIOR APPLICATION NUMBER: 10/197,000  
PRIOR FILING DATE: 2002-07-17  
PRIOR APPLICATION NUMBER: 09/396,813  
PRIOR FILING DATE: 1999-09-14  
NUMBER OF SEQ ID NOS: 1452  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 575  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-033-039-575

Query Match 3.0%; Score 7; DB 7; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.87;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 112 FDGDLGM 118  
Db 1 FDGDLGM 7

RESULT 10  
US-10-467-1338

Sequence 1338, Application US/10467657  
Publication No. US20050260581A1  
GENERAL INFORMATION:  
APPLICANT: CHIRON SPA  
APPLICANT: FONTANA Maria Rita  
APPLICANT: PIZZA Mariagrazia  
APPLICANT: MASIGNANI Vega  
APPLICANT: MONACI Elisabetta  
TITLE OF INVENTION: GOMOCOCCAL PROTEINS AND NUCLEIC ACIDS

FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/10/467,657  
CURRENT FILING DATE: 2003-08-11  
PRIOR APPLICATION NUMBER: GB-0103424.8  
PRIOR FILING DATE: 2001-02-12  
NUMBER OF SEQ ID NOS: 9218  
SOFTWARE: SeqMin99, version 1.04  
SEQ ID NO: 1338  
LENGTH: 161  
TYPE: PRT  
ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-1338

Query Match 3.0%; Score 7; DB 6; Length 161;  
Best Local Similarity 100.0%; Pred. No. 8.9;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 141 DPTVPLP 147  
DB 129 DPTVPLP 135

RESULT 11  
US-11-186-284-217  
Sequence 217, Application US/11186284  
Publication No. US2005026493A1  
GENERAL INFORMATION:  
APPLICANT: Millennium Pharmaceuticals, Inc.  
APPLICANT: Berger, Allison  
APPLICANT: Guillemette, Tracy L.  
APPLICANT: Kamatkar, Shubhang  
APPLICANT: Schlegel, Robert  
APPLICANT: Monahan, John E.  
APPLICANT: Thibodeau, Stephen N.  
APPLICANT: Burgart, Lawrence J.  
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND  
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
TITLE OF INVENTION: THERAPY OF COLON CANCER  
FILE REFERENCE: MPM01-029P2RNM  
CURRENT APPLICATION NUMBER: US/11/186,284  
CURRENT FILING DATE: 2005-07-21  
PRIOR APPLICATION NUMBER: US/10/301,822  
PRIOR FILING DATE: 2002-11-21  
PRIOR APPLICATION NUMBER: US 60/339,971  
PRIOR FILING DATE: 2001-12-10  
PRIOR APPLICATION NUMBER: US 60/361,978  
PRIOR FILING DATE: 2002-03-05  
PRIOR APPLICATION NUMBER: US 60/381,988  
PRIOR FILING DATE: 2002-05-20  
NUMBER OF SEQ ID NOS: 228  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 217  
LENGTH: 216  
TYPE: PRT  
ORGANISM: Homo Sapiens  
US-11-186-284-217

Query Match 3.0%; Score 7; DB 7; Length 216;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 98 RSPLAPS 104  
DB 206 RSPLAPS 212

RESULT 12  
US-11-033-039-586  
Sequence 586, Application US/11033039  
Publication No. US20060002947A1  
GENERAL INFORMATION:  
APPLICANT: HUMPHREYS, ROBERT  
APPLICANT: XU, MINZHEN

TITLE OF INVENTION: LI-KEY/ANTIGENIC EPIOTOPE HYBRID PEPTIDE VACCINES  
FILE REFERENCE: REH-2017US01  
CURRENT APPLICATION NUMBER: US/11/033,039  
CURRENT FILING DATE: 2005-01-11  
PRIOR APPLICATION NUMBER: 10/245,871  
PRIOR FILING DATE: 2002-09-17  
PRIOR APPLICATION NUMBER: 10/197,000  
PRIOR FILING DATE: 2002-07-17  
PRIOR APPLICATION NUMBER: 09/396,813  
PRIOR FILING DATE: 1999-09-14  
NUMBER OF SEQ ID NOS: 1452  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO: 586  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-033-039-586

Query Match 2.6%; Score 6; DB 7; Length 9;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EFSRMA 6  
DB 4 EFSRMA 9

RESULT 13  
US-11-057-708-25  
Sequence 25, Application US/11057708  
Publication No. US20050250702A1  
GENERAL INFORMATION:  
APPLICANT: Universiteit Utrecht  
APPLICANT: Strous, Gerardus  
APPLICANT: Van Kerkhof, Petrus  
APPLICANT: Govers, Roland  
TITLE OF INVENTION: CONTROLLING AVAILABILITY OR ACTIVITY OF PROTEINS BY USE OF PROTEAS  
TITLE OF INVENTION: INHIBITORS OR RECEPTOR FRAGMENTS  
FILE REFERENCE: 2183-4525US  
CURRENT APPLICATION NUMBER: US/11/057,708  
CURRENT FILING DATE: 2005-02-14  
PRIOR APPLICATION NUMBER: US/09/660,302  
PRIOR FILING DATE: 2000-09-12  
PRIOR APPLICATION NUMBER: PCT/NL99/00136  
PRIOR FILING DATE: 1999-03-12  
PRIOR APPLICATION NUMBER: EP98200799.9  
PRIOR FILING DATE: 1998-03-12  
NUMBER OF SEQ ID NOS: 51  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO: 25  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: Uneure, ERB2 TKR (neu-oncogene)  
US-11-057-708-25

Query Match 2.6%; Score 6; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.1;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 218 ENPEYL 223  
DB 1 ENPEYL 6

RESULT 14  
US-11-033-039-594  
Sequence 594, Application US/11033039  
Publication No. US20060002947A1  
GENERAL INFORMATION:  
APPLICANT: HUMPHREYS, ROBERT  
APPLICANT: XU, MINZHEN

```
/ TITLE OF INVENTION: LI-KEY/ANTIGENIC EPIOTOPE HYBRID PEPTIDE VACCINES
/ FILE REFERENCE: REF-2017US01
/ CURRENT APPLICATION NUMBER: US/11/033,039
/ CURRENT FILING DATE: 2005-01-11
/ PRIOR APPLICATION NUMBER: 10/245,871
/ PRIOR FILING DATE: 2002-09-17
/ PRIOR APPLICATION NUMBER: 10/197,000
/ PRIOR FILING DATE: 2002-07-17
/ PRIOR APPLICATION NUMBER: 09/396,813
/ PRIOR FILING DATE: 1999-09-14
/ NUMBER OF SEQ ID NOS: 1452
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 594
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
/ FEATURE:
/ OTHER INFORMATION: hybrid peptide
/ NAME/KEY: MOD_RES
/ LOCATION: (5)..(5)
/ OTHER INFORMATION: Ava
/ US-11-033-039-594

Query Match 2.6%; Score 6; DB 7; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EFSRMA 6
 |||||
 9 EFSRMA 14

RESULT 15
US-10-510-386-140
/ Sequence 140, Application US/10510386
/ Publication No. US20050244922A1
/ GENERAL INFORMATION:
/ APPLICANT: Andersen, Jens Tonne
/ APPLICANT: Clausen, ID Groth
/ APPLICANT: Jorgensen, Steen Tyroels
/ APPLICANT: Olsen, Peter Bjarkle
/ APPLICANT: Rasmussen, Michael Dolberg
/ TITLE OF INVENTION: Improved Bacillus Host Cell
/ FILE REFERENCE: 10294.204-US
/ CURRENT APPLICATION NUMBER: US/10/510,386
/ CURRENT FILING DATE: 2004-10-04
/ NUMBER OF SEQ ID NOS: 248
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 140
/ LENGTH: 112
/ TYPE: PRT
/ ORGANISM: Bacillus licheniformis
/ US-10-510-386-140

Query Match 2.6%; Score 6; DB 6; Length 112;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 TRSGG 83
 |||||
 105 TRSGG 110

RESULT 16
US-09-978-360A-604
/ Sequence 604, Application US/09978360A
/ Publication No. US20060009633A9
/ GENERAL INFORMATION:
/ APPLICANT: Edwards, Jean-Baptiste Dumas Milne
/ APPLICANT: Duclet, Aymeric
/ APPLICANT: Bougueleret, Lydie

/ APPLICANT: Jobert, Severin
/ APPLICANT: Clusel, Catherine
/ TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
/ FILE REFERENCE: 56 US4, CIP
/ CURRENT APPLICATION NUMBER: US/09/978,360A
/ CURRENT FILING DATE: 2001-10-15
/ PRIOR APPLICATION NUMBER: US 60/066,677
/ PRIOR FILING DATE: 1997-11-13
/ PRIOR APPLICATION NUMBER: US 60/069,957
/ PRIOR FILING DATE: 1997-12-17
/ PRIOR APPLICATION NUMBER: US 60/074,121
/ PRIOR FILING DATE: 1998-02-09
/ PRIOR APPLICATION NUMBER: US 60/081,563
/ PRIOR FILING DATE: 1998-04-13
/ PRIOR APPLICATION NUMBER: US 60/096,116
/ PRIOR FILING DATE: 1998-08-10
/ PRIOR APPLICATION NUMBER: US 60/099,273
/ PRIOR FILING DATE: -03-04
/ PRIOR APPLICATION NUMBER: US 09/191,997
/ PRIOR FILING DATE: 1998-11-13
/ PRIOR APPLICATION NUMBER: US 09/215,435
/ PRIOR FILING DATE: 1998-12-17
/ PRIOR APPLICATION NUMBER: PCT/IB98/02122
/ PRIOR FILING DATE: 1998-12-17
/ PRIOR APPLICATION NUMBER: US 09/247,155
/ PRIOR FILING DATE: 1999-02-09
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 810
/ SOFTWARE: Patent.pm
/ SEQ ID NO 604
/ LENGTH: 122
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: SIGNAL
/ LOCATION: -56...-1
/ FEATURES:
/ NAME/KEY: misc_feature
/ LOCATION: (-13, 4)
/ OTHER INFORMATION: unknown
/ US-09-978-360A-604

Query Match 2.6%; Score 6; DB 5; Length 122;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 LPTHP 132
 |||||
 22 LPTHP 27

RESULT 17
US-10-793-626-2502
/ Sequence 2502, Application US/10793626
/ Publication No. US20050255478A1
/ GENERAL INFORMATION:
/ APPLICANT: KIMMERLY, WILLIAM JOHN
/ TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
/ FILE REFERENCE: PUS480US
/ CURRENT APPLICATION NUMBER: US/10/793,626
/ CURRENT FILING DATE: 2004-03-04
/ PRIOR APPLICATION NUMBER: 60/164,258
/ PRIOR FILING DATE: 1999-11-09
/ NUMBER OF SEQ ID NOS: 4472
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2502
/ LENGTH: 147
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: synthetic
/ OTHER INFORMATION: amino acid sequence
/ US-10-793-626-2502
```

Query Match 2.6%; Score 6; DB 6; Length 147;  
Best Local Similarity 100.0%; Pred. No. 79;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 90 PSEER 95  
|||||  
Db 112 PSEER 117

RESULT 18  
US-10-467-657-112  
; Sequence 112, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SpA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 112  
; LENGTH: 156  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-112

Query Match 2.6%; Score 6; DB 6; Length 156;  
Best Local Similarity 100.0%; Pred. No. 83;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 EGAGSD 110  
|||||  
Db 73 EGAGSD 78

RESULT 19  
US-10-467-657-8550  
; Sequence 8550, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SpA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 8550  
; LENGTH: 156  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-8550

Query Match 2.6%; Score 6; DB 6; Length 156;  
Best Local Similarity 100.0%; Pred. No. 83;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 EGAGSD 110  
|||||

Db 73 EGAGSD 78

RESULT 20  
US-10-995-561-563  
; Sequence 563, Application US/10995561  
; Publication No. US20050272054A1  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF  
; TITLE OF INVENTION: DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001559  
; CURRENT APPLICATION NUMBER: US/10/995,561  
; CURRENT FILING DATE: 2004-11-24  
; NUMBER OF SEQ ID NOS: 85702  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 563  
; LENGTH: 195  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-995-561-563

Query Match 2.6%; Score 6; DB 6; Length 195;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 91 PSEER 96  
|||||  
Db 167 PSEER 172

RESULT 21  
US-11-022-562-226  
; Sequence 226, Application US/11022562  
; Publication No. US20050249742A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruprecht, Ruth M.  
; APPLICANT: Shieong, Jiang  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING  
; TITLE OF INVENTION: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE  
; FILE REFERENCE: DFN-043CN  
; CURRENT APPLICATION NUMBER: US/11/022,562  
; CURRENT FILING DATE: 2004-12-22  
; PRIOR APPLICATION NUMBER: PCT/US03/20322  
; PRIOR FILING DATE: 2003-06-27  
; PRIOR APPLICATION NUMBER: 60/392718  
; PRIOR FILING DATE: 2002-06-27  
; NUMBER OF SEQ ID NOS: 340  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 226  
; LENGTH: 233  
; TYPE: PRT  
; ORGANISM: Staphylococcus aureus  
US-11-022-562-226

Query Match 2.6%; Score 6; DB 7; Length 233;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 109 SDVFDG 114  
|||||  
Db 172 SDVFDG 177

RESULT 22  
US-11-045-024-1111  
; Sequence 1111, Application US/11045024  
; Publication No. US20050271676A1  
; GENERAL INFORMATION:  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Sidney, John  
; APPLICANT: Southwood, Scott

APPLICANT: Livingston, Brian  
APPLICANT: Chesnut, Robert  
APPLICANT: Baker, Denise Marie  
APPLICANT: Celis, Esreban  
APPLICANT: Kubo, Ralph  
APPLICANT: Grey, Howard M.  
APPLICANT: Epimmune Inc.  
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency  
TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions  
FILE REFERENCE: 2060.0040007  
CURRENT APPLICATION NUMBER: US/11/045,024  
CURRENT FILING DATE: 2005-01-28  
PRIOR APPLICATION NUMBER: US 09/412,863  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: US 08/027,146  
PRIOR FILING DATE: 1993-03-05  
PRIOR APPLICATION NUMBER: US 08/073,205  
PRIOR FILING DATE: 1993-06-04  
PRIOR APPLICATION NUMBER: US 08/103,396  
PRIOR FILING DATE: 1993-08-06  
PRIOR APPLICATION NUMBER: US 08/159,184  
PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/159,339  
PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/205,713  
PRIOR FILING DATE: 1994-03-04  
PRIOR APPLICATION NUMBER: US 08/347,610  
PRIOR FILING DATE: 1994-12-01  
NUMBER OF SEQ ID NOS: 14528  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1111  
LENGTH: 8  
TYPE: PRT  
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-11-045-024-1111

Query Match 2.1% Score 5; DB 7; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 190 GATLE 194  
|||||  
Db 1 GATLE 5

RESULT 23  
US-11-045-024-6406  
Sequence 6406, Application US/11045024  
Publication No. US20050271676A1  
GENERAL INFORMATION:  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Livingston, Brian  
APPLICANT: Chesnut, Robert  
APPLICANT: Baker, Denise Marie  
APPLICANT: Celis, Esreban  
APPLICANT: Kubo, Ralph  
APPLICANT: Grey, Howard M.  
APPLICANT: Epimmune Inc.  
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency  
TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions  
FILE REFERENCE: 2060.0040007  
CURRENT APPLICATION NUMBER: US/11/045,024  
CURRENT FILING DATE: 2005-01-28  
PRIOR APPLICATION NUMBER: US 09/412,863  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: US 08/027,146  
PRIOR FILING DATE: 1993-03-05  
PRIOR APPLICATION NUMBER: US 08/073,205  
PRIOR FILING DATE: 1993-06-04  
PRIOR APPLICATION NUMBER: US 08/103,396  
PRIOR FILING DATE: 1993-08-06

PRIOR APPLICATION NUMBER: US 08/159,184  
PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/159,339  
PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/205,713  
PRIOR FILING DATE: 1994-03-04  
PRIOR APPLICATION NUMBER: US 08/347,610  
PRIOR FILING DATE: 1994-12-01  
NUMBER OF SEQ ID NOS: 14528  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6406  
LENGTH: 8  
TYPE: PRT  
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-11-045-024-6406

Query Match 2.1% Score 5; DB 7; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 190 GATLE 194  
|||||  
Db 1 GATLE 5

RESULT 24  
US-11-062-186-2  
Sequence 2, Application US/11062186  
Publication No. US20050272097A1  
GENERAL INFORMATION:  
APPLICANT: CALENOFF, EMANUEL  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING AND TREATING  
TITLE OF INVENTION: AUTOIMMUNE DISEASES  
FILE REFERENCE: 21417-98470  
CURRENT APPLICATION NUMBER: US/11/062,186  
CURRENT FILING DATE: 2005-02-18  
PRIOR APPLICATION NUMBER: 60/545,062  
PRIOR FILING DATE: 2004-02-18  
PRIOR APPLICATION NUMBER: 60/545,980  
PRIOR FILING DATE: 2004-02-18  
NUMBER OF SEQ ID NOS: 172  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 2  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-062-186-2

Query Match 2.1% Score 5; DB 7; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 200 SPGKN 204  
|||||  
Db 2 SPGKN 6

RESULT 25  
US-10-467-657-4572  
Sequence 4572, Application US/10467657  
Publication No. US20050260581A1  
GENERAL INFORMATION:  
APPLICANT: CHIRON SPA  
APPLICANT: FONTANA Maria Rita  
APPLICANT: PIZZA Mariagrazia  
APPLICANT: MASTRONI Vega  
APPLICANT: MONACI Elisabetta  
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/10/467,657  
CURRENT FILING DATE: 2003-08-11  
PRIOR APPLICATION NUMBER: GB-0103424.8  
PRIOR FILING DATE: 2001-02-12



NUMBER OF SEQ ID NOS: 9218  
SOFTWARE: SeqMin99, version 1.04  
SEQ ID NO: 4572  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-4572

Query Match 2.1%; Score 5; DB 6; Length 9;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 64 GAGGM 68  
Db 4 GAGGM 8

RESULT 26  
US-11-045-024-1231  
Sequence 1231, Application US/11045024  
Publication No. US20050271676A1  
GENERAL INFORMATION:  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Livingston, Brian  
APPLICANT: Chesnut, Robert  
APPLICANT: Baker, Denise Marie  
APPLICANT: Celis, Esleben  
APPLICANT: Kubo, Ralph  
APPLICANT: Grey, Howard M.  
APPLICANT: EpiImmune Inc.  
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency  
FILE REFERENCE: 2060.0040007  
CURRENT APPLICATION NUMBER: US/11/045,024  
CURRENT FILING DATE: 2005-01-28  
PRIOR APPLICATION NUMBER: US 09/412,863  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: US 08/027,146  
PRIOR FILING DATE: 1993-03-05  
PRIOR APPLICATION NUMBER: US 08/073,205  
PRIOR FILING DATE: 1993-06-04  
PRIOR APPLICATION NUMBER: US 08/103,396  
PRIOR FILING DATE: 1993-08-06  
PRIOR APPLICATION NUMBER: US 08/159,184  
PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/159,339  
PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/205,713  
PRIOR FILING DATE: 1994-03-04  
PRIOR APPLICATION NUMBER: US 08/347,610  
PRIOR FILING DATE: 1994-12-01  
NUMBER OF SEQ ID NOS: 14528  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 1231  
LENGTH: 9  
TYPE: PRT  
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-11-045-024-1231

Query Match 2.1%; Score 5; DB 7; Length 9;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 190 GATLE 194  
Db 1 GATLE 5

RESULT 27  
US-11-045-024-5189  
Sequence 5189, Application US/11045024

Publication No. US20050271676A1  
GENERAL INFORMATION:  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Livingston, Brian  
APPLICANT: Chesnut, Robert  
APPLICANT: Baker, Denise Marie  
APPLICANT: Celis, Esleben  
APPLICANT: Kubo, Ralph  
APPLICANT: Grey, Howard M.  
APPLICANT: EpiImmune Inc.  
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency  
FILE REFERENCE: 2060.0040007  
CURRENT APPLICATION NUMBER: US/11/045,024  
CURRENT FILING DATE: 2005-01-28  
PRIOR APPLICATION NUMBER: US 09/412,863  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: US 08/027,146  
PRIOR FILING DATE: 1993-03-05  
PRIOR APPLICATION NUMBER: US 08/073,205  
PRIOR FILING DATE: 1993-06-04  
PRIOR APPLICATION NUMBER: US 08/103,396  
PRIOR FILING DATE: 1993-08-06  
PRIOR APPLICATION NUMBER: US 08/159,184  
PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/159,339  
PRIOR FILING DATE: 1994-03-04  
PRIOR APPLICATION NUMBER: US 08/205,713  
PRIOR FILING DATE: 1994-12-01  
NUMBER OF SEQ ID NOS: 14528  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 5189  
LENGTH: 9  
TYPE: PRT  
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-11-045-024-5189

Query Match 2.1%; Score 5; DB 7; Length 9;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 190 GATLE 194  
Db 3 GATLE 7

RESULT 28  
US-11-045-024-7291  
Sequence 7291, Application US/11045024  
Publication No. US20050271676A1  
GENERAL INFORMATION:  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Livingston, Brian  
APPLICANT: Chesnut, Robert  
APPLICANT: Baker, Denise Marie  
APPLICANT: Celis, Esleben  
APPLICANT: Kubo, Ralph  
APPLICANT: Grey, Howard M.  
APPLICANT: EpiImmune Inc.  
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency  
FILE REFERENCE: 2060.0040007  
CURRENT APPLICATION NUMBER: US/11/045,024  
CURRENT FILING DATE: 2005-01-28  
PRIOR APPLICATION NUMBER: US 09/412,863  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: US 08/027,146

```

; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7291
; LENGTH: 9
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-7291
```

```
Query Match 2.1%; Score 5; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 190 GATLE 194

DB 3 GATLE 7

RESULT 29

```
US-11-045-024-13707
; Sequence 13707, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13707
; LENGTH: 9
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-13707
```

```
Query Match 2.1%; Score 5; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 190 GATLE 194

DB 4 GATLE 8

RESULT 30

```
US-10-431-638-29
; Sequence 29, Application US/10431638
; Publication No. US2006003939A1
; GENERAL INFORMATION:
; APPLICANT: The Rockefeller Institute
; APPLICANT: Stetler, Hermann
; TITLE OF INVENTION: PEPTIDES AND METHODS FOR CELL DEATH REGULATION
; FILE REFERENCE: P-5004-US
; CURRENT APPLICATION NUMBER: US/10/431,638
; CURRENT FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 29
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-431-638-29
```

```
Query Match 2.1%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 74 RSSST 78

DB 3 RSSST 7

RESULT 31

```
US-11-045-024-1348
; Sequence 1348, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
```

;; PRIOR FILING DATE: 1994-12-01  
;; NUMBER OF SEQ ID NOS: 14528  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 1348  
;; LENGTH: 10  
;; TYPE: PRT  
;; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-11-045-024-1348

Query Match 2.1%; Score 5; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 68;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 190 GATLE 194  
Db 1 GATLE 5

## RESULT 32

US-11-045-024-5218  
;; Sequence 5218, Application US/11045024  
;; Publication No. US20050271676A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Sette, Alessandro  
;; APPLICANT: Sidney, John  
;; APPLICANT: Southwood, Scott  
;; APPLICANT: Livingston, Brian  
;; APPLICANT: Chesnut, Robert  
;; APPLICANT: Baker, Denise Marie  
;; APPLICANT: Celis, Basteen  
;; APPLICANT: Kubo, Ralph  
;; APPLICANT: Grey, Howard M.  
;; APPLICANT: Eptimmune Inc.  
;; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency  
;; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions  
;; FILE REFERENCE: 2060.0040007  
;; CURRENT APPLICATION NUMBER: US/11/045,024  
;; CURRENT FILING DATE: 2005-01-28  
;; PRIOR APPLICATION NUMBER: US 09/412,863  
;; PRIOR FILING DATE: 1999-10-05  
;; PRIOR APPLICATION NUMBER: US 08/027,146  
;; PRIOR FILING DATE: 1993-03-05  
;; PRIOR APPLICATION NUMBER: US 08/073,205  
;; PRIOR FILING DATE: 1993-06-04  
;; PRIOR APPLICATION NUMBER: US 08/103,396  
;; PRIOR FILING DATE: 1993-08-06  
;; PRIOR APPLICATION NUMBER: US 08/159,184  
;; PRIOR FILING DATE: 1993-11-29  
;; PRIOR APPLICATION NUMBER: US 08/159,339  
;; PRIOR FILING DATE: 1993-11-29  
;; PRIOR APPLICATION NUMBER: US 08/205,713  
;; PRIOR FILING DATE: 1994-03-04  
;; PRIOR APPLICATION NUMBER: US 08/347,610  
;; PRIOR FILING DATE: 1994-12-01  
;; NUMBER OF SEQ ID NOS: 14528  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 5218  
;; LENGTH: 10  
;; TYPE: PRT  
;; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-11-045-024-5218

Query Match 2.1%; Score 5; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 68;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 190 GATLE 194  
Db 3 GATLE 7

## RESULT 33

US-11-045-024-7293

;; Sequence 7293, Application US/11045024  
;; Publication No. US20050271676A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Sette, Alessandro  
;; APPLICANT: Sidney, John  
;; APPLICANT: Southwood, Scott  
;; APPLICANT: Livingston, Brian  
;; APPLICANT: Chesnut, Robert  
;; APPLICANT: Baker, Denise Marie  
;; APPLICANT: Celis, Basteen  
;; APPLICANT: Kubo, Ralph  
;; APPLICANT: Grey, Howard M.  
;; APPLICANT: Eptimmune Inc.  
;; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency  
;; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions  
;; FILE REFERENCE: 2060.0040007  
;; CURRENT APPLICATION NUMBER: US/11/045,024  
;; CURRENT FILING DATE: 2005-01-28  
;; PRIOR APPLICATION NUMBER: US 09/412,863  
;; PRIOR FILING DATE: 1999-10-05  
;; PRIOR APPLICATION NUMBER: US 08/027,146  
;; PRIOR FILING DATE: 1993-03-05  
;; PRIOR APPLICATION NUMBER: US 08/073,205  
;; PRIOR FILING DATE: 1993-06-04  
;; PRIOR APPLICATION NUMBER: US 08/103,396  
;; PRIOR FILING DATE: 1993-08-06  
;; PRIOR APPLICATION NUMBER: US 08/159,184  
;; PRIOR FILING DATE: 1993-11-29  
;; PRIOR APPLICATION NUMBER: US 08/159,339  
;; PRIOR FILING DATE: 1993-11-29  
;; PRIOR APPLICATION NUMBER: US 08/205,713  
;; PRIOR FILING DATE: 1994-03-04  
;; PRIOR APPLICATION NUMBER: US 08/347,610  
;; PRIOR FILING DATE: 1994-12-01  
;; NUMBER OF SEQ ID NOS: 14528  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 7293  
;; LENGTH: 10  
;; TYPE: PRT  
;; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-11-045-024-7293

Query Match 2.1%; Score 5; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 68;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 190 GATLE 194  
Db 3 GATLE 7

RESULT 34  
US-11-045-024-9197  
;; Sequence 9197, Application US/11045024  
;; Publication No. US20050271676A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Sette, Alessandro  
;; APPLICANT: Sidney, John  
;; APPLICANT: Southwood, Scott  
;; APPLICANT: Livingston, Brian  
;; APPLICANT: Chesnut, Robert  
;; APPLICANT: Baker, Denise Marie  
;; APPLICANT: Celis, Basteen  
;; APPLICANT: Kubo, Ralph  
;; APPLICANT: Grey, Howard M.  
;; APPLICANT: Eptimmune Inc.  
;; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency  
;; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions  
;; FILE REFERENCE: 2060.0040007  
;; CURRENT APPLICATION NUMBER: US/11/045,024  
;; CURRENT FILING DATE: 2005-01-28  
;; PRIOR APPLICATION NUMBER: US 09/412,863  
;; PRIOR FILING DATE: 1999-10-05

Query Match 2.1%; Score 5; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 68;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 9197
; LENGTH: 10
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-9197
```

```
Query Match 2.1%; Score 5; DB 7; Length 10;
Best Local Similarity 100.0%; Pred.No. 68;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 190 GATLE 194
DB 1 GATLE 5
```

```

RESULT 35
US-11-062-186-128
; Sequence 128, Application US/11062186
; Publication No. US20050272097A1
; GENERAL INFORMATION:
; APPLICANT: CALENOFF, EMANUEL
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING AND TREATING
; FILE REFERENCE: 21417-98470
; CURRENT APPLICATION NUMBER: US/11/062,186
; CURRENT FILING DATE: 2005-02-18
; PRIOR APPLICATION NUMBER: 60/546,062
; PRIOR FILING DATE: 2004-02-18
; PRIOR APPLICATION NUMBER: 60/545,980
; PRIOR FILING DATE: 2004-02-18
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 128
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-062-186-128
```

```
Query Match 2.1%; Score 5; DB 7; Length 10;
Best Local Similarity 100.0%; Pred.No. 68;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 22 PASPL 26
DB 1 PASPL 5
```

```

RESULT 36
US-11-146-854-46
; Sequence 46, Application US/11146854
; Publication No. US2005027161A1
; GENERAL INFORMATION:
; APPLICANT: University of Virginia Patent Foundation
; APPLICANT: Engelhard, Victor H
; APPLICANT: Zarling, Angela
; APPLICANT: Hunt, Donald F
; APPLICANT: Evans, Anne M
```

```

; APPLICANT: Shabanowitz, Jeffrey
; TITLE OF INVENTION: PHOSPHOPEPTIDE ANTIGENS ASSOCIATED WITH MHC MOLECULES
; FILE REFERENCE: 01015-02
; CURRENT APPLICATION NUMBER: US/11/146,854
; CURRENT FILING DATE: 2005-06-07
; PRIOR APPLICATION NUMBER: US 60/578,205
; PRIOR FILING DATE: 2004-06-09
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 46
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (4)-(4)
; OTHER INFORMATION: PHOSPHORYLATION
US-11-146-854-46
```

```
Query Match 2.1%; Score 5; DB 7; Length 10;
Best Local Similarity 100.0%; Pred.No. 68;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 96 APRSP 100
DB 1 APRSP 5
```

```

RESULT 37
US-11-033-365-22
; Sequence 22, Application US/11033365
; Publication No. US20050250678A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies Inc.
; APPLICANT: Deerees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Wang, Zhigang
; APPLICANT: Clausen, Henrik
; TITLE OF INVENTION: O-Linked Glycosylation of peptides
; FILE REFERENCE: 040853-01-5138
; CURRENT APPLICATION NUMBER: US/11/033,365
; CURRENT FILING DATE: 2005-01-10
; PRIOR APPLICATION NUMBER: 60/535,284
; PRIOR FILING DATE: 2004-01-08
; PRIOR APPLICATION NUMBER: 60/544,411
; PRIOR FILING DATE: 2004-02-12
; PRIOR APPLICATION NUMBER: 60/546,631
; PRIOR FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/555,813
; PRIOR FILING DATE: 2004-03-23
; PRIOR APPLICATION NUMBER: 60/570,891
; PRIOR FILING DATE: 2004-05-12
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 22
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-033-365-22
```

```
Query Match 2.1%; Score 5; DB 7; Length 11;
Best Local Similarity 100.0%; Pred.No. 74;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 20 LGPAS 24
DB 7 LGPAS 11
```

```

RESULT 38
US-11-058-735-69
; Sequence 69, Application US/11058735
; Publication No. US20050261475A1
```

```

; GENERAL INFORMATION:
; APPLICANT: TSENG, HUANG-CHUN
; TITLE OF INVENTION: SOLID-PHASE CAPTURE-RELEASE-TAG METHODS FOR
; FILE REFERENCE: PHOSPHOPROTEOMIC ANALYSES
; CURRENT APPLICATION NUMBER: US/11/058,735
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,748
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: Patencin Ver. 3.3
; SEQ ID NO 69
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Mus musculus
; US-11-058-735-69

Query Match 2.1% Score 5; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 80 SGGGD 84
 |||||
Db 5 SGGGD 9

RESULT 39
US-11-119-098-67
; Sequence 67, Application US/11119098
; Publication No. US20050267030A1
; GENERAL INFORMATION:
; APPLICANT: Tsao, Philip S.
; TITLE OF INVENTION: Use of deltaPKC peptides for modulation of Reactive Oxygen Species
; FILE REFERENCE: 58600-8213, US00
; CURRENT APPLICATION NUMBER: US/11/119,098
; CURRENT FILING DATE: 2005-04-29
; PRIOR APPLICATION NUMBER: US 60/567,315
; PRIOR FILING DATE: 2004-04-30
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified delta V1-2 peptide
; US-11-119-098-67

Query Match 2.1% Score 5; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 195 RPKTL 199
 |||||
Db 6 RPKTL 10

RESULT 40
US-11-045-024-1456
; Sequence 1456, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Bastejan
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; US-11-045-024-1456
```

```

; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060, 0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1994-03-04
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1456
; LENGTH: 11
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
; US-11-045-024-1456

Query Match 2.1% Score 5; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 190 GATLE 194
 |||||
Db 5 GATLE 9

RESULT 41
US-11-045-024-4215
; Sequence 4215, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Bastejan
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060, 0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
```

```

; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 4215
; LENGTH: 11
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-4215

Query Match 2.1%; Score 5; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 190 GATLE 194
DB 5 GATLE 9

RESULT 42
US-11-045-024-7286
; Sequence 7286; Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Estebean
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 7286
; LENGTH: 11
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-7286

Query Match 2.1%; Score 5; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 190 GATLE 194
DB 5 GATLE 9

RESULT 43
US-11-045-024-9071
; Sequence 9071; Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Estebean
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 9071
; LENGTH: 11
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-9071

Query Match 2.1%; Score 5; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 190 GATLE 194
DB 2 GATLE 6

RESULT 44
US-10-986-501-220
; Sequence 220; Application US/10986501
; Publication No. US2005024845A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: P2013P2C1
; CURRENT APPLICATION NUMBER: US/10/986,501
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US/10/621,363
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/969,730
; PRIOR FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: 09/774,639
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/238,291
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: PCT/US98/16235
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; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/056,371
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,732
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,366
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,364
; PRIOR FILING DATE: 1997-08-19
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 373
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 220
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-986-501-220
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Query Match
Best Local Similarity 2.1%; Score 5; DB 6; Length 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 24 SPLDS 28
Db 2 SPLDS 6
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RESULT 45
US-11-054-515-2364
; Sequence 2364, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2364
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2364
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Query Match
Best Local Similarity 2.1%; Score 5; DB 7; Length 14;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 22 PASPL 26
Db 8 PASPL 12
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```

RESULT 46
US-11-054-515-2390
; Sequence 2390, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2390
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2390
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```

Query Match
Best Local Similarity 2.1%; Score 5; DB 7; Length 14;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 22 PASPL 26
Db 8 PASPL 12
```

```

RESULT 47
US-11-054-515-2417
; Sequence 2417, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
```

```

; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2417
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2417

Query Match 2.1% Score 5; DB 7; Length 14;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 PASPL 26
DB 8 PASPL 12

RESULT 48
US-11-054-515-2420
; Sequence 2420, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2420
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2420

Query Match 2.1% Score 5; DB 7; Length 14;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 PASPL 26
DB 8 PASPL 12

RESULT 49
US-11-054-515-2445
; Sequence 2445, Application US/11054515
; Publication No. US20050255532A1
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; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17

US-11-054-515-2464
; Sequence 2464, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17

US-11-054-515-2445

Query Match 2.1% Score 5; DB 7; Length 14;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 99 SPLAP 103
DB 10 SPLAP 14

RESULT 50
US-11-054-515-2464
; Sequence 2464, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
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Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 3247  
 ; SEQ ID NO 2464  
 ; LENGTH: 14  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-11-054-515-2464

Query Match 2.1%; Score 5; DB 7; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 92;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 99 SPLAP 103  
 Db 10 SPLAP 14

Search completed: January 18, 2006, 21:00:34  
 Job time : 32 secs

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GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: January 18, 2006, 21:06:40 ; Search time 30 Seconds  
(without alignments)  
3.378 Million cell updates/sec

Title: US-09-930-125-3  
Perfect score: 10  
Sequence: 1 EXLVFQGSF 10

Scoring table: Oligo  
Gapop 60.0 , Gapext 60.0

Searched: 70606 seqs, 10133861 residues

Word size : 6

Total number of hits satisfying chosen parameters: 21200

Minimum DB seq length: 0  
Maximum DB seq length: 10

Post-processing: Listing first 200 summaries

Database :

Published Applications AA New:  
1: /cgn2\_6/ptcodata/1/pubpaa/US08\_NEW\_PUB.pep:\*  
2: /cgn2\_6/ptcodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptcodata/1/pubpaa/US07\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptcodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*  
5: /cgn2\_6/ptcodata/1/pubpaa/US09\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptcodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
7: /cgn2\_6/ptcodata/1/pubpaa/US11\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptcodata/1/pubpaa/US00\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID              | Description        |
|------------|-------|-------------|--------|--------------------|--------------------|
| 1          | 90.0  | 9           | 7      | US-11-033-039-607  | Sequence 607, App  |
| 2          | 40.0  | 9           | 7      | US-11-110-274-308  | Sequence 308, App  |
| 3          | 40.0  | 10          | 7      | US-11-057-708-24   | Sequence 24, App1  |
| 4          | 40.0  | 10          | 7      | US-11-057-708-32   | Sequence 32, App1  |
| 5          | 30.0  | 5           | 6      | US-10-997-066-17   | Sequence 17, App1  |
| 6          | 30.0  | 5           | 7      | US-11-035-682-13   | Sequence 13, App1  |
| 7          | 30.0  | 6           | 6      | US-10-969-314-36   | Sequence 36, App1  |
| 8          | 30.0  | 6           | 6      | US-10-485-788A-458 | Sequence 458, App  |
| 9          | 30.0  | 6           | 7      | US-11-014-629-4    | Sequence 4, App1   |
| 10         | 30.0  | 6           | 7      | US-11-148-074-8    | Sequence 8, App1   |
| 11         | 30.0  | 6           | 7      | US-11-107-539-2    | Sequence 2, App1   |
| 12         | 30.0  | 7           | 6      | US-10-467-657-9179 | Sequence 9179, App |
| 13         | 30.0  | 7           | 6      | US-10-485-788A-459 | Sequence 459, App  |
| 14         | 30.0  | 7           | 6      | US-10-880-238-133  | Sequence 133, App  |
| 15         | 30.0  | 7           | 7      | US-11-201-341-14   | Sequence 14, App1  |
| 16         | 30.0  | 7           | 7      | US-11-150-533-53   | Sequence 53, App1  |
| 17         | 30.0  | 8           | 6      | US-10-485-788A-370 | Sequence 370, App  |
| 18         | 30.0  | 8           | 6      | US-10-485-788A-460 | Sequence 460, App  |
| 19         | 30.0  | 8           | 7      | US-11-044-051-91   | Sequence 91, App1  |
| 20         | 30.0  | 8           | 7      | US-11-044-051-92   | Sequence 92, App1  |
| 21         | 30.0  | 8           | 7      | US-11-045-024-189  | Sequence 189, App  |
| 22         | 30.0  | 8           | 7      | US-11-045-024-1573 | Sequence 1573, App |
| 23         | 30.0  | 8           | 7      | US-11-045-024-1090 | Sequence 3090, App |
| 24         | 30.0  | 8           | 7      | US-11-045-024-4235 | Sequence 4235, App |
| 25         | 30.0  | 8           | 7      | US-11-045-024-4237 | Sequence 4237, App |

|    |      |   |   |                     |                    |
|----|------|---|---|---------------------|--------------------|
| 26 | 30.0 | 8 | 7 | US-11-045-024-5505  | Sequence 5505, App |
| 27 | 30.0 | 8 | 7 | US-11-045-024-7435  | Sequence 7435, App |
| 28 | 30.0 | 8 | 7 | US-11-045-024-7461  | Sequence 7461, App |
| 29 | 30.0 | 8 | 7 | US-11-045-024-9375  | Sequence 9375, App |
| 30 | 30.0 | 8 | 7 | US-11-045-024-9399  | Sequence 9399, App |
| 31 | 30.0 | 8 | 7 | US-11-045-024-9713  | Sequence 9713, App |
| 32 | 30.0 | 8 | 7 | US-11-045-024-9714  | Sequence 9714, App |
| 33 | 30.0 | 8 | 7 | US-11-045-024-11467 | Sequence 11467, A  |
| 34 | 30.0 | 8 | 7 | US-11-045-024-11705 | Sequence 11705, A  |
| 35 | 30.0 | 8 | 7 | US-11-045-024-12655 | Sequence 12655, A  |
| 36 | 30.0 | 8 | 7 | US-11-041-270A-9    | Sequence 9, App1   |
| 37 | 30.0 | 8 | 7 | US-11-064-416-4     | Sequence 4, App1   |
| 38 | 30.0 | 8 | 7 | US-11-064-416-5     | Sequence 5, App1   |
| 39 | 30.0 | 9 | 6 | US-10-969-314-30    | Sequence 30, App1  |
| 40 | 30.0 | 9 | 6 | US-10-969-314-31    | Sequence 31, App1  |
| 41 | 30.0 | 9 | 6 | US-10-969-314-32    | Sequence 32, App1  |
| 42 | 30.0 | 9 | 6 | US-10-969-314-33    | Sequence 33, App1  |
| 43 | 30.0 | 9 | 6 | US-10-925-366A-33   | Sequence 33, App1  |
| 44 | 30.0 | 9 | 6 | US-10-925-366A-33   | Sequence 33, App1  |
| 45 | 30.0 | 9 | 6 | US-10-925-366A-33   | Sequence 33, App1  |
| 46 | 30.0 | 9 | 6 | US-10-966-483-8     | Sequence 8, App1   |
| 47 | 30.0 | 9 | 6 | US-10-859-643-19    | Sequence 19, App1  |
| 48 | 30.0 | 9 | 6 | US-10-859-643-32    | Sequence 32, App1  |
| 49 | 30.0 | 9 | 6 | US-10-859-643-271   | Sequence 271, App  |
| 50 | 30.0 | 9 | 6 | US-10-859-643-352   | Sequence 352, App  |
| 51 | 30.0 | 9 | 6 | US-10-859-643-352   | Sequence 352, App  |
| 52 | 30.0 | 9 | 6 | US-10-859-643-352   | Sequence 352, App  |
| 53 | 30.0 | 9 | 6 | US-10-859-643-352   | Sequence 352, App  |
| 54 | 30.0 | 9 | 7 | US-11-010-748A-309  | Sequence 309, App  |
| 55 | 30.0 | 9 | 7 | US-11-010-748A-313  | Sequence 313, App  |
| 56 | 30.0 | 9 | 7 | US-11-010-748A-315  | Sequence 315, App  |
| 57 | 30.0 | 9 | 7 | US-11-010-748A-318  | Sequence 318, App  |
| 58 | 30.0 | 9 | 7 | US-11-010-748A-321  | Sequence 321, App  |
| 59 | 30.0 | 9 | 7 | US-11-010-748A-325  | Sequence 325, App  |
| 60 | 30.0 | 9 | 7 | US-11-010-748A-327  | Sequence 327, App  |
| 61 | 30.0 | 9 | 7 | US-11-044-051-89    | Sequence 89, App1  |
| 62 | 30.0 | 9 | 7 | US-11-054-515-2981  | Sequence 2981, App |
| 63 | 30.0 | 9 | 7 | US-11-073-347-92    | Sequence 92, App1  |
| 64 | 30.0 | 9 | 7 | US-11-009-939-40    | Sequence 40, App1  |
| 65 | 30.0 | 9 | 7 | US-11-097-864-19    | Sequence 19, App1  |
| 66 | 30.0 | 9 | 7 | US-11-097-864-32    | Sequence 32, App1  |
| 67 | 30.0 | 9 | 7 | US-11-097-864-271   | Sequence 271, App  |
| 68 | 30.0 | 9 | 7 | US-11-097-864-352   | Sequence 352, App  |
| 69 | 30.0 | 9 | 7 | US-11-097-864-487   | Sequence 487, App  |
| 70 | 30.0 | 9 | 7 | US-11-097-864-580   | Sequence 580, App  |
| 71 | 30.0 | 9 | 7 | US-11-097-864-676   | Sequence 676, App  |
| 72 | 30.0 | 9 | 7 | US-11-097-912-19    | Sequence 19, App1  |
| 73 | 30.0 | 9 | 7 | US-11-097-912-32    | Sequence 32, App1  |
| 74 | 30.0 | 9 | 7 | US-11-097-912-271   | Sequence 271, App  |
| 75 | 30.0 | 9 | 7 | US-11-097-912-352   | Sequence 352, App  |
| 76 | 30.0 | 9 | 7 | US-11-097-912-487   | Sequence 487, App  |
| 77 | 30.0 | 9 | 7 | US-11-097-912-580   | Sequence 580, App  |
| 78 | 30.0 | 9 | 7 | US-11-097-912-676   | Sequence 676, App  |
| 79 | 30.0 | 9 | 7 | US-11-045-024-197   | Sequence 197, App  |
| 80 | 30.0 | 9 | 7 | US-11-045-024-199   | Sequence 199, App  |
| 81 | 30.0 | 9 | 7 | US-11-045-024-1522  | Sequence 1522, App |
| 82 | 30.0 | 9 | 7 | US-11-045-024-1786  | Sequence 1786, App |
| 83 | 30.0 | 9 | 7 | US-11-045-024-3203  | Sequence 3203, App |
| 84 | 30.0 | 9 | 7 | US-11-045-024-4258  | Sequence 4258, App |
| 85 | 30.0 | 9 | 7 | US-11-045-024-4260  | Sequence 4260, App |
| 86 | 30.0 | 9 | 7 | US-11-045-024-4262  | Sequence 4262, App |
| 87 | 30.0 | 9 | 7 | US-11-045-024-5132  | Sequence 5132, App |
| 88 | 30.0 | 9 | 7 | US-11-045-024-6478  | Sequence 6478, App |
| 89 | 30.0 | 9 | 7 | US-11-045-024-6929  | Sequence 6929, App |
| 90 | 30.0 | 9 | 7 | US-11-045-024-7438  | Sequence 7438, App |
| 91 | 30.0 | 9 | 7 | US-11-045-024-9403  | Sequence 9403, App |
| 92 | 30.0 | 9 | 7 | US-11-045-024-9709  | Sequence 9709, App |
| 93 | 30.0 | 9 | 7 | US-11-045-024-9724  | Sequence 9724, App |
| 94 | 30.0 | 9 | 7 | US-11-045-024-11712 | Sequence 11712, A  |
| 95 | 30.0 | 9 | 7 | US-11-045-024-12656 | Sequence 12656, A  |
| 96 | 30.0 | 9 | 7 | US-11-045-024-13758 | Sequence 13758, A  |
| 97 | 30.0 | 9 | 7 | US-11-045-024-13767 | Sequence 13767, A  |
| 98 | 30.0 | 9 | 7 | US-11-045-024-13769 | Sequence 13769, A  |

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| 99  | 3 | 30.0 | 9  | 7 | US-11-045-024-13771 | Sequence 13771, A  |
| 100 | 3 | 30.0 | 9  | 7 | US-11-045-024-13773 | Sequence 13773, A  |
| 101 | 3 | 30.0 | 9  | 7 | US-11-193-512-45    | Sequence 45, Appl  |
| 102 | 3 | 30.0 | 9  | 7 | US-11-033-039-13    | Sequence 13, Appl  |
| 103 | 3 | 30.0 | 9  | 7 | US-11-033-039-72    | Sequence 72, Appl  |
| 104 | 3 | 30.0 | 9  | 7 | US-11-033-039-107   | Sequence 107, Appl |
| 105 | 3 | 30.0 | 9  | 7 | US-11-033-039-281   | Sequence 281, Appl |
| 106 | 3 | 30.0 | 9  | 7 | US-11-033-039-286   | Sequence 286, Appl |
| 107 | 3 | 30.0 | 9  | 7 | US-11-033-039-328   | Sequence 328, Appl |
| 108 | 3 | 30.0 | 9  | 7 | US-11-033-039-867   | Sequence 867, Appl |
| 109 | 3 | 30.0 | 9  | 7 | US-11-107-539-5     | Sequence 5, Appl   |
| 110 | 3 | 30.0 | 9  | 7 | US-11-107-539-27    | Sequence 27, Appl  |
| 111 | 3 | 30.0 | 9  | 7 | US-11-107-539-28    | Sequence 28, Appl  |
| 112 | 3 | 30.0 | 10 | 6 | US-10-835-615-830   | Sequence 830, Appl |
| 113 | 3 | 30.0 | 10 | 6 | US-10-969-314-13    | Sequence 13, Appl  |
| 114 | 3 | 30.0 | 10 | 6 | US-10-969-314-16    | Sequence 16, Appl  |
| 115 | 3 | 30.0 | 10 | 6 | US-10-989-226-51    | Sequence 51, Appl  |
| 116 | 3 | 30.0 | 10 | 6 | US-10-517-784-36    | Sequence 36, Appl  |
| 117 | 3 | 30.0 | 10 | 6 | US-10-859-643-88    | Sequence 88, Appl  |
| 118 | 3 | 30.0 | 10 | 6 | US-10-859-643-89    | Sequence 89, Appl  |
| 119 | 3 | 30.0 | 10 | 6 | US-10-859-643-92    | Sequence 92, Appl  |
| 120 | 3 | 30.0 | 10 | 6 | US-10-859-643-95    | Sequence 95, Appl  |
| 121 | 3 | 30.0 | 10 | 6 | US-10-859-643-176   | Sequence 176, Appl |
| 122 | 3 | 30.0 | 10 | 6 | US-10-859-643-181   | Sequence 181, Appl |
| 123 | 3 | 30.0 | 10 | 6 | US-10-859-643-206   | Sequence 206, Appl |
| 124 | 3 | 30.0 | 10 | 6 | US-10-859-643-215   | Sequence 215, Appl |
| 125 | 3 | 30.0 | 10 | 6 | US-10-859-643-237   | Sequence 237, Appl |
| 126 | 3 | 30.0 | 10 | 6 | US-10-859-643-244   | Sequence 244, Appl |
| 127 | 3 | 30.0 | 10 | 6 | US-10-859-643-301   | Sequence 301, Appl |
| 128 | 3 | 30.0 | 10 | 6 | US-10-859-643-341   | Sequence 341, Appl |
| 129 | 3 | 30.0 | 10 | 6 | US-10-859-643-408   | Sequence 408, Appl |
| 130 | 3 | 30.0 | 10 | 6 | US-10-859-643-449   | Sequence 449, Appl |
| 131 | 3 | 30.0 | 10 | 6 | US-10-859-643-504   | Sequence 504, Appl |
| 132 | 3 | 30.0 | 10 | 6 | US-10-859-643-608   | Sequence 608, Appl |
| 133 | 3 | 30.0 | 10 | 7 | US-11-057-708-6     | Sequence 6, Appl   |
| 134 | 3 | 30.0 | 10 | 7 | US-11-057-708-10    | Sequence 10, Appl  |
| 135 | 3 | 30.0 | 10 | 7 | US-11-057-708-13    | Sequence 13, Appl  |
| 136 | 3 | 30.0 | 10 | 7 | US-11-057-708-20    | Sequence 20, Appl  |
| 137 | 3 | 30.0 | 10 | 7 | US-11-057-708-21    | Sequence 21, Appl  |
| 138 | 3 | 30.0 | 10 | 7 | US-11-057-708-22    | Sequence 22, Appl  |
| 139 | 3 | 30.0 | 10 | 7 | US-11-057-708-23    | Sequence 23, Appl  |
| 140 | 3 | 30.0 | 10 | 7 | US-11-057-708-25    | Sequence 25, Appl  |
| 141 | 3 | 30.0 | 10 | 7 | US-11-057-708-26    | Sequence 26, Appl  |
| 142 | 3 | 30.0 | 10 | 7 | US-11-057-708-41    | Sequence 41, Appl  |
| 143 | 3 | 30.0 | 10 | 7 | US-11-057-708-42    | Sequence 42, Appl  |
| 144 | 3 | 30.0 | 10 | 7 | US-11-057-708-43    | Sequence 43, Appl  |
| 145 | 3 | 30.0 | 10 | 7 | US-11-152-747-40    | Sequence 40, Appl  |
| 146 | 3 | 30.0 | 10 | 7 | US-11-044-051-90    | Sequence 90, Appl  |
| 147 | 3 | 30.0 | 10 | 7 | US-11-056-470-7     | Sequence 7, Appl   |
| 148 | 3 | 30.0 | 10 | 7 | US-11-073-347-93    | Sequence 93, Appl  |
| 149 | 3 | 30.0 | 10 | 7 | US-11-073-347-94    | Sequence 94, Appl  |
| 150 | 3 | 30.0 | 10 | 7 | US-11-097-864-88    | Sequence 88, Appl  |
| 151 | 3 | 30.0 | 10 | 7 | US-11-097-864-89    | Sequence 89, Appl  |
| 152 | 3 | 30.0 | 10 | 7 | US-11-097-864-92    | Sequence 92, Appl  |
| 153 | 3 | 30.0 | 10 | 7 | US-11-097-864-95    | Sequence 95, Appl  |
| 154 | 3 | 30.0 | 10 | 7 | US-11-097-864-176   | Sequence 176, Appl |
| 155 | 3 | 30.0 | 10 | 7 | US-11-097-864-181   | Sequence 181, Appl |
| 156 | 3 | 30.0 | 10 | 7 | US-11-097-864-206   | Sequence 206, Appl |
| 157 | 3 | 30.0 | 10 | 7 | US-11-097-864-215   | Sequence 215, Appl |
| 158 | 3 | 30.0 | 10 | 7 | US-11-097-864-237   | Sequence 237, Appl |
| 159 | 3 | 30.0 | 10 | 7 | US-11-097-864-244   | Sequence 244, Appl |
| 160 | 3 | 30.0 | 10 | 7 | US-11-097-864-301   | Sequence 301, Appl |
| 161 | 3 | 30.0 | 10 | 7 | US-11-097-864-341   | Sequence 341, Appl |
| 162 | 3 | 30.0 | 10 | 7 | US-11-097-864-408   | Sequence 408, Appl |
| 163 | 3 | 30.0 | 10 | 7 | US-11-097-864-449   | Sequence 449, Appl |
| 164 | 3 | 30.0 | 10 | 7 | US-11-097-864-504   | Sequence 504, Appl |
| 165 | 3 | 30.0 | 10 | 7 | US-11-097-864-608   | Sequence 608, Appl |
| 166 | 3 | 30.0 | 10 | 7 | US-11-097-912-88    | Sequence 88, Appl  |
| 167 | 3 | 30.0 | 10 | 7 | US-11-097-912-89    | Sequence 89, Appl  |
| 168 | 3 | 30.0 | 10 | 7 | US-11-097-912-92    | Sequence 92, Appl  |
| 169 | 3 | 30.0 | 10 | 7 | US-11-097-912-95    | Sequence 95, Appl  |
| 170 | 3 | 30.0 | 10 | 7 | US-11-097-912-176   | Sequence 176, Appl |
| 171 | 3 | 30.0 | 10 | 7 | US-11-097-912-181   | Sequence 181, Appl |

|     |   |      |    |   |                    |                     |
|-----|---|------|----|---|--------------------|---------------------|
| 172 | 3 | 30.0 | 10 | 7 | US-11-097-912-206  | Sequence 206, Appl  |
| 173 | 3 | 30.0 | 10 | 7 | US-11-097-912-215  | Sequence 215, Appl  |
| 174 | 3 | 30.0 | 10 | 7 | US-11-097-912-237  | Sequence 237, Appl  |
| 175 | 3 | 30.0 | 10 | 7 | US-11-097-912-244  | Sequence 244, Appl  |
| 176 | 3 | 30.0 | 10 | 7 | US-11-097-912-301  | Sequence 301, Appl  |
| 177 | 3 | 30.0 | 10 | 7 | US-11-097-912-341  | Sequence 341, Appl  |
| 178 | 3 | 30.0 | 10 | 7 | US-11-097-912-408  | Sequence 408, Appl  |
| 179 | 3 | 30.0 | 10 | 7 | US-11-097-912-449  | Sequence 449, Appl  |
| 180 | 3 | 30.0 | 10 | 7 | US-11-097-912-504  | Sequence 504, Appl  |
| 181 | 3 | 30.0 | 10 | 7 | US-11-097-912-608  | Sequence 608, Appl  |
| 182 | 3 | 30.0 | 10 | 7 | US-11-156-843-2    | Sequence 2, Appl    |
| 183 | 3 | 30.0 | 10 | 7 | US-11-156-843-4    | Sequence 4, Appl    |
| 184 | 3 | 30.0 | 10 | 7 | US-11-156-843-5    | Sequence 5, Appl    |
| 185 | 3 | 30.0 | 10 | 7 | US-11-156-843-8    | Sequence 8, Appl    |
| 186 | 3 | 30.0 | 10 | 7 | US-11-156-843-11   | Sequence 11, Appl   |
| 187 | 3 | 30.0 | 10 | 7 | US-11-156-843-12   | Sequence 12, Appl   |
| 188 | 3 | 30.0 | 10 | 7 | US-11-156-843-15   | Sequence 15, Appl   |
| 189 | 3 | 30.0 | 10 | 7 | US-11-156-843-21   | Sequence 21, Appl   |
| 190 | 3 | 30.0 | 10 | 7 | US-11-156-843-22   | Sequence 22, Appl   |
| 191 | 3 | 30.0 | 10 | 7 | US-11-156-843-125  | Sequence 125, Appl  |
| 192 | 3 | 30.0 | 10 | 7 | US-11-045-024-204  | Sequence 204, Appl  |
| 193 | 3 | 30.0 | 10 | 7 | US-11-045-024-1545 | Sequence 1545, Appl |
| 194 | 3 | 30.0 | 10 | 7 | US-11-045-024-3273 | Sequence 3273, Appl |
| 195 | 3 | 30.0 | 10 | 7 | US-11-045-024-4276 | Sequence 4276, Appl |
| 196 | 3 | 30.0 | 10 | 7 | US-11-045-024-4278 | Sequence 4278, Appl |
| 197 | 3 | 30.0 | 10 | 7 | US-11-045-024-5743 | Sequence 5743, Appl |
| 198 | 3 | 30.0 | 10 | 7 | US-11-045-024-7428 | Sequence 7428, Appl |
| 199 | 3 | 30.0 | 10 | 7 | US-11-045-024-7439 | Sequence 7439, Appl |
| 200 | 3 | 30.0 | 10 | 7 | US-11-045-024-9364 | Sequence 9364, Appl |

## ALIGNMENTS

```
RESULT 1
US-11-033-039-607
; Sequence 607, Application US/11033039
; Publication No. US2006002947A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REF-20170501
; CURRENT APPLICATION NUMBER: US/11/033,039
; PRIOR FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 607
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-033-039-607

Query Match 90.0%; Score 9; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EYLVPOQGF 10
Db 1 EYLVPOQGF 9

RESULT 2
US-11-110-274-308
; Sequence 308, Application US/11110274
; Publication No. US20050266502A1
; GENERAL INFORMATION:
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APPLICANT: Merchiers, Pascal G.  
APPLICANT: Hoffmann, Marcel  
TITLE OF INVENTION: Methods, Compositions and Compound Assays for Inhibiting  
FILE REFERENCE: P27,697-A USA  
CURRENT APPLICATION NUMBER: US/11/110,274  
PRIOR FILING DATE: 2005-04-20  
PRIOR APPLICATION NUMBER: US 60/563,661  
NUMBER OF SEQ ID NOS: 620  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 308  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-110-274-308

Query Match 40.0%; Score 4; DB 7; Length 9;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLVP 6  
DB 1 YLVP 4

RESULT 3  
US-11-057-708-24  
Sequence 24, Application US/11057708  
Publication No. US20050250702A1  
GENERAL INFORMATION:  
APPLICANT: Universiteit Utrecht  
APPLICANT: Strous, Gerardus  
APPLICANT: Van Kerkhof, Petrus  
APPLICANT: Govers, Roland  
TITLE OF INVENTION: CONTROLLING AVAILABILITY OR ACTIVITY OF PROTEINS BY USE OF PROTEIN  
TITLE OF INVENTION: INHIBITORS OR RECEPTOR FRAGMENTS  
FILE REFERENCE: 2183-4525US  
CURRENT APPLICATION NUMBER: US/11/057,708  
PRIOR FILING DATE: 2005-02-14  
PRIOR APPLICATION NUMBER: US/09/660,302  
PRIOR FILING DATE: 2000-09-12  
PRIOR APPLICATION NUMBER: PCT/NL99/00136  
PRIOR FILING DATE: 1999-03-12  
PRIOR APPLICATION NUMBER: EP98200799.9  
PRIOR FILING DATE: 1998-03-12  
NUMBER OF SEQ ID NOS: 51  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 24  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Rattus unknown species (Rat)  
FEATURE:  
OTHER INFORMATION: MHC-II(BETA)  
US-11-057-708-24

Query Match 40.0%; Score 4; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYL 4  
DB 3 EBYL 6

RESULT 4  
US-11-057-708-32  
Sequence 32, Application US/11057708  
Publication No. US20050250702A1  
GENERAL INFORMATION:  
APPLICANT: Universiteit Utrecht  
APPLICANT: Strous, Gerardus

APPLICANT: Van Kerkhof, Petrus  
APPLICANT: Govers, Roland  
TITLE OF INVENTION: CONTROLLING AVAILABILITY OR ACTIVITY OF PROTEINS BY USE OF PROTEIN  
TITLE OF INVENTION: INHIBITORS OR RECEPTOR FRAGMENTS  
FILE REFERENCE: 2183-4525US  
CURRENT APPLICATION NUMBER: US/11/057,708  
CURRENT FILING DATE: 2005-02-14  
PRIOR APPLICATION NUMBER: US/09/660,302  
PRIOR FILING DATE: 2000-09-12  
PRIOR APPLICATION NUMBER: PCT/NL99/00136  
PRIOR FILING DATE: 1999-03-12  
PRIOR APPLICATION NUMBER: EP98200799.9  
NUMBER OF SEQ ID NOS: 51  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 32  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: Unsuure, RHESUS BLOOD GROUP-ASSOCIATED GLYCOPROTEIN  
US-11-057-708-32

Query Match 40.0%; Score 4; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EBYL 5  
DB 4 EBYL 7

RESULT 5  
US-10-997-066-17  
Sequence 17, Application US/10997066  
Publication No. US20050244891A1  
GENERAL INFORMATION:  
APPLICANT: GRAHAM, RONALD J.  
APPLICANT: LEE, LINDA G.  
APPLICANT: SUN, HONGYE  
TITLE OF INVENTION: LIGAND-CONTAINING MICELLES AND USES THEREOF  
FILE REFERENCE: 375461-0110US  
CURRENT APPLICATION NUMBER: US/10/997,066  
CURRENT FILING DATE: 2004-11-24  
PRIOR APPLICATION NUMBER: 60/525,492  
PRIOR FILING DATE: 2003-11-26  
PRIOR APPLICATION NUMBER: 60/628,509  
PRIOR FILING DATE: 2004-11-15  
NUMBER OF SEQ ID NOS: 47  
SOFTWARE: PatentIn Ver. 3.3  
SEQ ID NO 17  
LENGTH: 5  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-997-066-17

Query Match 30.0%; Score 3; DB 6; Length 5;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBY 3  
DB 2 EBY 4

RESULT 6  
US-11-035-682-13  
Sequence 13, Application US/11035682  
Publication No. US20050245726A1  
GENERAL INFORMATION:

APPLICANT: LEE, LINDA G.  
APPLICANT: SUN, HONGYE  
TITLE OF INVENTION: FLUORESCENT KINASE ASSAYS AND SUBSTRATES  
FILE REFERENCE: 375461-023US  
CURRENT APPLICATION NUMBER: US/11/035,682  
CURRENT FILING DATE: 2005-01-14  
PRIOR APPLICATION NUMBER: 60/537,416  
PRIOR FILING DATE: 2004-01-16  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: PatentIn Ver. 3.3  
SEQ ID NO 13  
LENGTH: 5  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-11-035-682-13

Query Match 30.0%; Score 3; DB 7; Length 5;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 BEY 3  
DB 2 BEY 4

RESULT 7  
US-10-969-314-36  
Sequence 36, Application US/10969314  
Publication No. US20050249719A1  
GENERAL INFORMATION:  
APPLICANT: SHAN, LU  
APPLICANT: BETHUNE, MICHAEL  
APPLICANT: KHOSLA, CHAITAN  
APPLICANT: GASS, JONATHAN  
APPLICANT: PYLE, GAIL G.  
APPLICANT: GRAY, GARY  
APPLICANT: ISAACS, INDU  
APPLICANT: STROHMAYER, GREGG  
TITLE OF INVENTION: ENZYME TREATMENT OF FOODSTUFFS FOR  
FILE REFERENCE: STAN-361  
CURRENT APPLICATION NUMBER: US/10/969,314  
CURRENT FILING DATE: 2004-10-19  
PRIOR APPLICATION NUMBER: 60/565,668  
PRIOR FILING DATE: 2004-04-26  
PRIOR APPLICATION NUMBER: 10/367,405  
PRIOR FILING DATE: 2003-02-14  
PRIOR APPLICATION NUMBER: 60/357,238  
PRIOR FILING DATE: 2002-02-14  
PRIOR APPLICATION NUMBER: 60/380,761  
PRIOR FILING DATE: 2002-05-14  
PRIOR APPLICATION NUMBER: 60/392,782  
PRIOR FILING DATE: 2002-06-28  
PRIOR APPLICATION NUMBER: 60/422,933  
PRIOR FILING DATE: 2002-10-31  
NUMBER OF SEQ ID NOS: 46  
SOFTWARE: PatentIn Version 4.0  
SEQ ID NO 36  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Triticum aestivum  
US-10-969-314-36

Query Match 30.0%; Score 3; DB 6; Length 6;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PQO 8  
DB 2 PQO 4

RESULT 8  
US-10-485-788A-458  
Sequence 458, Application US/10485788A  
Publication No. US20050282743A1  
GENERAL INFORMATION:  
APPLICANT: LU, Peter S.  
APPLICANT: Rabinowitz, Joshua D.  
APPLICANT: Schweitzer, Johannes  
APPLICANT: Carrick, Deanna Marie  
APPLICANT: Arbor Vita Corporation  
TITLE OF INVENTION: Molecular Interactions in Cells  
FILE REFERENCE: 20054-00320US  
CURRENT APPLICATION NUMBER: US/10/485,788A  
CURRENT FILING DATE: 2004-02-03  
PRIOR APPLICATION NUMBER: US 60/309,841  
PRIOR FILING DATE: 2001-08-03  
PRIOR APPLICATION NUMBER: US 60/360,061  
PRIOR FILING DATE: 2002-02-25  
PRIOR APPLICATION NUMBER: WO PCT/US02/24655  
PRIOR FILING DATE: 2002-08-02  
NUMBER OF SEQ ID NOS: 841  
SOFTWARE: PatentIn Version 3.1  
SEQ ID NO 458  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-485-788A-458

Query Match 30.0%; Score 3; DB 6; Length 6;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLV 5  
DB 1 YLV 3

RESULT 9  
US-11-014-629-4  
Sequence 4, Application US/11014629  
Publication No. US20050244376A1  
GENERAL INFORMATION:  
APPLICANT: Hall, Frederick L.  
APPLICANT: Gordon, Erlinda M.  
TITLE OF INVENTION: TARGETED GENE DELIVERY TO EXTRACELLULAR MATRIX  
FILE REFERENCE: 30863-704.302  
CURRENT APPLICATION NUMBER: US/11/014,629  
CURRENT FILING DATE: 2004-12-15  
PRIOR APPLICATION NUMBER: US 08/837,223  
PRIOR FILING DATE: 1997-04-10  
PRIOR APPLICATION NUMBER: US 09/904,923  
PRIOR FILING DATE: 2001-07-13  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: PatentIn Version 3.1  
SEQ ID NO 4  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Peptide cleavage site  
US-11-014-629-4

Query Match 30.0%; Score 3; DB 7; Length 6;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LVP 6  
DB 1 LVP 3

RESULT 10  
US-11-148-074-8  
; Sequence 8, Application US/11148074  
; Publication No. US20050272919A1  
; GENERAL INFORMATION:  
; APPLICANT: Duellman, Sarah  
; APPLICANT: Thompson, Nancy  
; APPLICANT: Burgess, Richard  
; TITLE OF INVENTION: Immunoaffinity Chromatography Using Epitope Tags to  
; FILE REFERENCE: 09820.315  
; CURRENT APPLICATION NUMBER: US/11/148,074  
; PRIOR FILING DATE: 2005-06-08  
; PRIOR APPLICATION NUMBER: US 60/577,944  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 8  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Thrombin protease recognition sequence  
US-11-148-074-8

Query Match 30.0%; Score 3; DB 7; Length 6;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LVP 6  
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DB 1 LVP 3

RESULT 11  
US-11-107-539-2  
; Sequence 2, Application US/11107539  
; Publication No. US20060002917A1  
; GENERAL INFORMATION:  
; APPLICANT: PIPER, JUSTIN L.  
; APPLICANT: GRAY, GARY M.  
; APPLICANT: KHOSLA, CHAITAN  
; TITLE OF INVENTION: EFFECT OF PROLYL ENDOPEPTIDASE ON  
; FILE REFERENCE: STAN-362  
; CURRENT APPLICATION NUMBER: US/11/107,539  
; PRIOR FILING DATE: 2005-04-15  
; PRIOR APPLICATION NUMBER: 60/565,684  
; PRIOR FILING DATE: 2004-04-26  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Trilicium aestivum  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (6)...(6)  
; OTHER INFORMATION: Tyrosine modified with NO2  
US-11-107-539-2

Query Match 30.0%; Score 3; DB 7; Length 6;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PQQ 8  
|||  
DB 2 PQQ 4

RESULT 12  
US-10-467-657-9179  
; Sequence 9179, Application US/10467657

Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SPA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; PRIOR FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 9179  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-9179

Query Match 30.0%; Score 3; DB 6; Length 7;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLV 5  
|||  
DB 3 YLV 5

RESULT 13  
US-10-485-788A-459  
; Sequence 459, Application US/10485788A  
; Publication No. US20050282743A1  
; GENERAL INFORMATION:  
; APPLICANT: Lu, Peter S.  
; APPLICANT: Rabinowitz, Joshua D.  
; APPLICANT: Schweitzer, Johannes  
; APPLICANT: Carrick, Deanna Marie  
; APPLICANT: Arbor Vita Corporation  
; TITLE OF INVENTION: Molecular Interactions in Cells  
; FILE REFERENCE: 20054-003320US  
; CURRENT APPLICATION NUMBER: US/10/485,788A  
; PRIOR FILING DATE: 2004-02-03  
; PRIOR APPLICATION NUMBER: US 60/309,841  
; PRIOR FILING DATE: 2001-08-03  
; PRIOR APPLICATION NUMBER: US 60/360,061  
; PRIOR FILING DATE: 2002-02-25  
; PRIOR APPLICATION NUMBER: WO PCT/US02/24655  
; PRIOR FILING DATE: 2002-08-02  
; NUMBER OF SEQ ID NOS: 841  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 459  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-485-788A-459

Query Match 30.0%; Score 3; DB 6; Length 7;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLV 5  
|||  
DB 2 YLV 4

RESULT 14  
US-10-880-238-133  
; Sequence 133, Application US/10880238  
; Publication No. US20050287538A1  
; GENERAL INFORMATION:  
; APPLICANT: Cheung, Wing-Tai

```

; APPLICANT: Cheng, Man
; TITLE OF INVENTION: FRAME-SHIFTING PCR FOR GERMLINE
; TITLE OF INVENTION: IMMUNOGLOBULIN GENES RETRIEVAL AND ANTIBODY ENGINEERING
; FILE REFERENCE: 17329-003001
; CURRENT APPLICATION NUMBER: US/10/880,238
; CURRENT FILING DATE: 2004-06-29
; NUMBER OF SEQ ID NOS: 214
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 133
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-880-238-133
```

```

Query Match 30.0%; Score 3; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 3 YLV 5
 |||
Db 2 YLV 4
```

```

RESULT 15
US-11-201-341-14
; Sequence 14, Application US/11201341
; Publication No. US20050287564A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: SECRETED PROTEINS ENCODED BY HUMAN
; TITLE OF INVENTION: CHROMOSOME 13
; FILE REFERENCE: 97-38C2
; CURRENT APPLICATION NUMBER: US/11/201,341
; CURRENT FILING DATE: 2005-08-10
; PRIOR APPLICATION NUMBER: US 10/010,050
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: US 09/122,383
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: US 60/053,613
; PRIOR FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Glu-Glu affinity tag peptide
US-11-201-341-14
```

```

Query Match 30.0%; Score 3; DB 7; Length 7;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 EEY 3
 |||
Db 1 EEY 3
```

```

RESULT 16
US-11-150-533-53
; Sequence 53, Application US/11150533
; Publication No. US20060002925A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Burkhead, Steven K.
; APPLICANT: Levin, Steven D.
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Gao, Zeren
; APPLICANT: Jaspers, Stephen R.
```

```

; APPLICANT: Bilsborough, Janine
; TITLE OF INVENTION: SOLUBLE ZCYTOR14, ANTI-ZCYTOR14
; TITLE OF INVENTION: ANTIBODIES AND BINDING PARTNERS AND METHODS OF USING IN
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 04-06P1
; CURRENT APPLICATION NUMBER: US/11/150,533
; CURRENT FILING DATE: 2005-06-10
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Glu-Glu tag
US-11-150-533-53
```

```

Query Match 30.0%; Score 3; DB 7; Length 7;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 EEY 3
 |||
Db 1 EEY 3
```

```

RESULT 17
US-10-485-788A-370
; Sequence 370, Application US/10485788A
; Publication No. US20050282743A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter S.
; APPLICANT: Rabinowitz, Joshua D.
; APPLICANT: Schweitzer, Johannes
; APPLICANT: Carrick, Deanna Marie
; APPLICANT: Arbor Vita Corporation
; TITLE OF INVENTION: Molecular Interactions in Cells
; FILE REFERENCE: 20054-00320US
; CURRENT APPLICATION NUMBER: US/10/485,788A
; CURRENT FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: US 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/360,061
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: WO PCT/US02/24655
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 370
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-485-788A-370
```

```

Query Match 30.0%; Score 3; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 6 PQQ 8
 |||
Db 2 PQQ 4
```

```

RESULT 18
US-10-485-788A-460
; Sequence 460, Application US/10485788A
; Publication No. US20050282743A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter S.
; APPLICANT: Rabinowitz, Joshua D.
; APPLICANT: Schweitzer, Johannes
; APPLICANT: Carrick, Deanna Marie
; APPLICANT: Arbor Vita Corporation
```



```
/ TITLE OF INVENTION: Molecular Interactions in Cells
/ FILE REFERENCE: 20054-003320US
/ CURRENT APPLICATION NUMBER: US/10/485,788A
/ CURRENT FILING DATE: 2004-02-03
/ PRIOR APPLICATION NUMBER: US 60/309,841
/ PRIOR FILING DATE: 2001-08-03
/ PRIOR APPLICATION NUMBER: US 60/360,061
/ PRIOR FILING DATE: 2002-02-25
/ PRIOR APPLICATION NUMBER: WO PCT/US02/24655
/ PRIOR FILING DATE: 2002-08-02
/ NUMBER OF SEQ ID NOS: 841
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 460
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-485-788A-460

Query Match
Best Local Similarity 30.0%; Score 3; DB 6; Length 8;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLV 5
DB 3 YLV 5

RESULT 19
US-11-044-051-91
/ Sequence 91, Application US/11044051
/ Publication No. US2005025553A1
/ GENERAL INFORMATION:
/ APPLICANT: VAN PEL, Aline
/ APPLICANT: GODELAINE, Daniel
/ APPLICANT: BRASSEUR, Francis
/ APPLICANT: BOON-FALEUR, Thierry
/ TITLE OF INVENTION: MAGE C2 ANTIGENIC PEPTIDES AND USES THEREOF
/ FILE REFERENCE: LUD 5888 US
/ CURRENT APPLICATION NUMBER: US/11/044,051
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 60/459,263
/ PRIOR FILING DATE: 2004-02-09
/ NUMBER OF SEQ ID NOS: 111
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 91
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-044-051-91

Query Match
Best Local Similarity 30.0%; Score 3; DB 7; Length 8;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLV 5
DB 5 YLV 7

RESULT 20
US-11-044-051-92
/ Sequence 92, Application US/11044051
/ Publication No. US2005025553A1
/ GENERAL INFORMATION:
/ APPLICANT: VAN PEL, Aline
/ APPLICANT: GODELAINE, Daniel
/ APPLICANT: BRASSEUR, Francis
/ APPLICANT: BOON-FALEUR, Thierry
/ TITLE OF INVENTION: MAGE C2 ANTIGENIC PEPTIDES AND USES THEREOF
/ FILE REFERENCE: LUD 5888 US
/ CURRENT APPLICATION NUMBER: US/11/044,051
```

```
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 60/459,263
/ PRIOR FILING DATE: 2004-02-09
/ NUMBER OF SEQ ID NOS: 111
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 92
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-044-051-92
```

```
Query Match
Best Local Similarity 30.0%; Score 3; DB 7; Length 8;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 3 YLV 5
DB 6 YLV 8
```

```
RESULT 21
US-11-045-024-189
/ Sequence 189, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chennut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Esteban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: Epimmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 189
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-189
```

```
Query Match
Best Local Similarity 30.0%; Score 3; DB 7; Length 8;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 8 QGF 10
DB 6 QGF 8
```

```
RESULT 22
US-11-045-024-1573
; Sequence 1573, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; PRIOR FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1573
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-1573

Query Match 30.0%; Score 3; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 QQG 9
 |||
Db 4 QQG 6

RESULT 23
US-11-045-024-3090
; Sequence 3090, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
```

```
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3090
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-3090

Query Match 30.0%; Score 3; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LVP 6
 |||
Db 2 LVP 4

RESULT 24
US-11-045-024-4235
; Sequence 4235, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4235
; LENGTH: 8
```

```
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-4235

Query Match 30.0%; Score 3; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 QGF 10
 |||
 5 QGF 7

Db

RESULT 25
US-11-045-024-4237
/ Sequence 4237, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Bstedan
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: EpiImmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 4237
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-4237

Query Match 30.0%; Score 3; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 QGF 10
 |||
 5 QGF 7

Db

RESULT 26
US-11-045-024-5505
/ Sequence 5505, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
```

```
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Bstedan
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: EpiImmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 5505
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-5505

Query Match 30.0%; Score 3; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 QGF 10
 |||
 6 QGF 8

Db

RESULT 27
US-11-045-024-7435
/ Sequence 7435, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Bstedan
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: EpiImmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
```

```

; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7435
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-7435

Query Match 30.0%; Score 3; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 QGF 10
Db 6 QGF 8

RESULT 28
US-11-045-024-7461
; Sequence 7461, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Cheesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; PRIOR FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7461
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-7461

Query Match 30.0%; Score 3; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 8 QGF 10
Db 2 QGF 4

RESULT 29
US-11-045-024-9375
; Sequence 9375, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Cheesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; PRIOR FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9375
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-9375

Query Match 30.0%; Score 3; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LVP 6
Db 2 LVP 4

RESULT 30
US-11-045-024-9399
; Sequence 9399, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Cheesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
```

```
APPLICANT: BpImmune Inc.
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
FILE REFERENCE: 2060.0040007
CURRENT APPLICATION NUMBER: US/11/045,024
PRIOR FILING DATE: 2005-01-28
PRIOR APPLICATION NUMBER: US 09/412,863
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/103,396
PRIOR FILING DATE: 1993-08-06
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/159,339
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/347,610
PRIOR FILING DATE: 1994-12-01
NUMBER OF SEQ ID NOS: 14528
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9399
LENGTH: 8
TYPE: PRT
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-9399
```

```
Query Match 30.0%; Score 3; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 8 QCG 10
Db 6 QCG 8
```

```
RESULT 31
US-11-045-024-9713
Sequence 9713, Application US/11045024
Publication No. US20050271676A1
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert
APPLICANT: Baker, Denise Marie
APPLICANT: Celis, Basteban
APPLICANT: Kado, Ralph
APPLICANT: Grey, Howard M.
APPLICANT: BpImmune Inc.
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
FILE REFERENCE: 2060.0040007
CURRENT APPLICATION NUMBER: US/11/045,024
PRIOR FILING DATE: 2005-01-28
PRIOR APPLICATION NUMBER: US 09/412,863
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/103,396
PRIOR FILING DATE: 1993-08-06
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/159,339
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
```

```
PRIOR APPLICATION NUMBER: US 08/347,610
PRIOR FILING DATE: 1994-12-01
NUMBER OF SEQ ID NOS: 14528
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9713
LENGTH: 8
TYPE: PRT
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-9713
```

```
Query Match 30.0%; Score 3; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 7 QCG 9
Db 4 QCG 6
```

```
RESULT 32
US-11-045-024-9714
Sequence 9714, Application US/11045024
Publication No. US20050271676A1
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert
APPLICANT: Baker, Denise Marie
APPLICANT: Celis, Basteban
APPLICANT: Kado, Ralph
APPLICANT: Grey, Howard M.
APPLICANT: BpImmune Inc.
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
FILE REFERENCE: 2060.0040007
CURRENT APPLICATION NUMBER: US/11/045,024
PRIOR FILING DATE: 2005-01-28
PRIOR APPLICATION NUMBER: US 09/412,863
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/103,396
PRIOR FILING DATE: 1993-08-06
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/159,339
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/347,610
PRIOR FILING DATE: 1994-12-01
NUMBER OF SEQ ID NOS: 14528
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9714
LENGTH: 8
TYPE: PRT
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-9714
```

```
Query Match 30.0%; Score 3; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 7 QCG 9
Db 3 QCG 5
```

```
RESULT 33
```

```
US-11-045-024-11467
; Sequence 11467, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Cells, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; PRIOR FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11467
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-11467

Query Match 30.0%; Score 3; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
US-11-045-024-11705
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11705
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-11705

Query Match 30.0%; Score 3; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
US-11-045-024-11705
; Sequence 11705, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Cells, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; PRIOR FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
```

```
US-11-045-024-12655
; Sequence 12655, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Cells, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; PRIOR FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12655
; LENGTH: 8
; TYPE: PRT
```

ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-11-045-024-12655

Query Match 30.0%; Score 3; DB 7; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 QCF 10  
DB 5 QCF 7

RESULT 36

US-11-041-270A-9  
Sequence 9, Application US/11041270A  
Publication No. US20050276854A1

GENERAL INFORMATION:  
APPLICANT: TRIGG, TIMOTHY ELLIOT  
APPLICANT: WALSH, JOHN DESMOND  
APPLICANT: RATHJEN, DEBORAH ANN  
TITLE OF INVENTION: BIOTRIMPLANT FORMULATION  
FILE REFERENCE: 4137-43  
CURRENT APPLICATION NUMBER: US/11/041,270A  
CURRENT FILING DATE: 2005-01-25  
PRIOR APPLICATION NUMBER: PCT/AU99/00585  
PRIOR FILING DATE: 1999-07-20  
PRIOR APPLICATION NUMBER: AU PP 4730  
PRIOR FILING DATE: 1998-07-20  
PRIOR APPLICATION NUMBER: AU PP 4731  
PRIOR FILING DATE: 1998-07-20  
PRIOR APPLICATION NUMBER: AU PP 0324  
PRIOR FILING DATE: 1999-05-13  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: PatentIn Ver. 3.3  
SEQ ID NO 9  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
FEATURE:  
OTHER INFORMATION: substance P antagonist  
US-11-041-270A-9

Query Match 30.0%; Score 3; DB 7; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PQQ 8  
DB 1 PQQ 3

RESULT 37

US-11-064-416-4  
Sequence 4, Application US/11064416  
Publication No. US20060080461A1

GENERAL INFORMATION:  
APPLICANT: Oregon Health & Science University  
APPLICANT: Vatelva, Milton B  
APPLICANT: Stowell, Michael HB  
APPLICANT: Gillicchio, Vincent S  
APPLICANT: Meredith, Michael J  
TITLE OF INVENTION: MICROPARTICLE-DRUG CONJUGATES FOR BIOLOGICAL TARGETING  
FILE REFERENCE: 899-71532  
CURRENT APPLICATION NUMBER: US/11/064,416  
CURRENT FILING DATE: 2005-02-22  
PRIOR APPLICATION NUMBER: 10/050,271  
PRIOR FILING DATE: 2002-01-15  
PRIOR APPLICATION NUMBER: 09/573,497  
PRIOR FILING DATE: 2000-05-16  
PRIOR APPLICATION NUMBER: 09/060,011

PRIOR FILING DATE: 1998-04-14  
PRIOR APPLICATION NUMBER: 08/691,891  
PRIOR FILING DATE: 1996-08-01  
PRIOR APPLICATION NUMBER: 08/441,770  
PRIOR FILING DATE: 1995-05-16  
PRIOR APPLICATION NUMBER: 08/246,941  
PRIOR FILING DATE: 1994-05-19  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 4  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: peptide linker  
US-11-064-416-4

Query Match 30.0%; Score 3; DB 7; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLV 5  
DB 5 YLV 7

RESULT 38

US-11-064-416-5  
Sequence 5, Application US/11064416  
Publication No. US20060080461A1

GENERAL INFORMATION:  
APPLICANT: Oregon Health & Science University  
APPLICANT: Vatelva, Milton B  
APPLICANT: Stowell, Michael HB  
APPLICANT: Gillicchio, Vincent S  
APPLICANT: Meredith, Michael J  
TITLE OF INVENTION: MICROPARTICLE-DRUG CONJUGATES FOR BIOLOGICAL TARGETING  
FILE REFERENCE: 899-71532  
CURRENT APPLICATION NUMBER: US/11/064,416  
CURRENT FILING DATE: 2005-02-22  
PRIOR APPLICATION NUMBER: 10/050,271  
PRIOR FILING DATE: 2002-01-15  
PRIOR APPLICATION NUMBER: 09/573,497  
PRIOR FILING DATE: 2000-05-16  
PRIOR APPLICATION NUMBER: 09/060,011  
PRIOR FILING DATE: 1998-04-14  
PRIOR APPLICATION NUMBER: 08/691,891  
PRIOR FILING DATE: 1996-08-01  
PRIOR APPLICATION NUMBER: 08/441,770  
PRIOR FILING DATE: 1995-05-16  
PRIOR APPLICATION NUMBER: 08/246,941  
PRIOR FILING DATE: 1994-05-19  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 5  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: peptide linker  
US-11-064-416-5

Query Match 30.0%; Score 3; DB 7; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLV 5  
DB 4 YLV 6

RESULT 39  
US-10-969-314-30

```
; Sequence 30, Application US/10969314
; Publication No. US20050249719A1
; GENERAL INFORMATION:
; APPLICANT: SHAN, LU
; APPLICANT: BETHUNE, MICHAEL
; APPLICANT: KHOSLA, CHAITAN
; APPLICANT: GASS, JONATHAN
; APPLICANT: PYLE, GAIL G.
; APPLICANT: GRAY, GARY
; APPLICANT: ISAACS, INDU
; APPLICANT: STROHMEIER, GREGG
; TITLE OF INVENTION: ENZYME TREATMENT OF FOODSTUFFS FOR
; FILE REFERENCE: STAN-361
; CURRENT APPLICATION NUMBER: US/10/969,314
; PRIOR FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: 60/565,668
; PRIOR FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 10/367,405
; PRIOR FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/357,238
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: 60/380,761
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 60/392,782
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 60/422,933
; PRIOR FILING DATE: 2002-10-31
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Trifolium aestivum
US-10-969-314-30
```

```
Query Match 30.0%; Score 3; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 6 PQQ 8
Db 3 PQQ 5
```

```
RESULT 40
US-10-969-314-31
; Sequence 31, Application US/10969314
; Publication No. US20050249719A1
; GENERAL INFORMATION:
; APPLICANT: SHAN, LU
; APPLICANT: BETHUNE, MICHAEL
; APPLICANT: KHOSLA, CHAITAN
; APPLICANT: GASS, JONATHAN
; APPLICANT: PYLE, GAIL G.
; APPLICANT: GRAY, GARY
; APPLICANT: ISAACS, INDU
; APPLICANT: STROHMEIER, GREGG
; TITLE OF INVENTION: ENZYME TREATMENT OF FOODSTUFFS FOR
; FILE REFERENCE: STAN-361
; CURRENT APPLICATION NUMBER: US/10/969,314
; PRIOR FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: 60/565,668
; PRIOR FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 10/367,405
; PRIOR FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/357,238
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: 60/380,761
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 60/392,782
; PRIOR FILING DATE: 2002-06-28
```

```
; PRIOR APPLICATION NUMBER: 60/422,933
; PRIOR FILING DATE: 2002-10-31
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Trifolium aestivum
US-10-969-314-31
```

```
Query Match 30.0%; Score 3; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 6 PQQ 8
Db 3 PQQ 5
```

```
RESULT 41
US-10-969-314-32
; Sequence 32, Application US/10969314
; Publication No. US20050249719A1
; GENERAL INFORMATION:
; APPLICANT: SHAN, LU
; APPLICANT: BETHUNE, MICHAEL
; APPLICANT: KHOSLA, CHAITAN
; APPLICANT: GASS, JONATHAN
; APPLICANT: PYLE, GAIL G.
; APPLICANT: GRAY, GARY
; APPLICANT: ISAACS, INDU
; APPLICANT: STROHMEIER, GREGG
; TITLE OF INVENTION: ENZYME TREATMENT OF FOODSTUFFS FOR
; FILE REFERENCE: STAN-361
; CURRENT APPLICATION NUMBER: US/10/969,314
; PRIOR FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: 60/565,668
; PRIOR FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 10/367,405
; PRIOR FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/357,238
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: 60/380,761
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 60/392,782
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 60/422,933
; PRIOR FILING DATE: 2002-10-31
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Trifolium aestivum
US-10-969-314-32
```

```
Query Match 30.0%; Score 3; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 6 PQQ 8
Db 3 PQQ 5
```

```
RESULT 42
US-10-969-314-33
; Sequence 33, Application US/10969314
; Publication No. US20050249719A1
; GENERAL INFORMATION:
; APPLICANT: SHAN, LU
; APPLICANT: BETHUNE, MICHAEL
```



APPLICANT: KHOSLA, CHAITAN  
APPLICANT: GASS, JONATHAN  
APPLICANT: FYLE, GAIL G.  
APPLICANT: GRAY, GARY  
APPLICANT: ISAACS, INDU  
APPLICANT: STROMMEIER, GREGG  
TITLE OF INVENTION: ENZYME TREATMENT OF FOODSTUFFS FOR  
FILE REFERENCE: STAN-361  
CURRENT APPLICATION NUMBER: US/10/969,314  
CURRENT FILING DATE: 2004-10-19  
PRIOR APPLICATION NUMBER: 60/565,668  
PRIOR FILING DATE: 2004-04-26  
PRIOR APPLICATION NUMBER: 10/367,405  
PRIOR FILING DATE: 2003-02-14  
PRIOR APPLICATION NUMBER: 60/357,238  
PRIOR FILING DATE: 2002-02-14  
PRIOR APPLICATION NUMBER: 60/380,761  
PRIOR FILING DATE: 2002-05-14  
PRIOR APPLICATION NUMBER: 60/392,782  
PRIOR FILING DATE: 2002-06-28  
PRIOR APPLICATION NUMBER: 60/422,933  
PRIOR FILING DATE: 2002-10-31  
NUMBER OF SEQ ID NOS: 46  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 33  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Trifolium aestivum  
US-10-969-314-33

Query Match 30.0%; Score 3; DB 6; Length 9;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PQQ 8  
Db 5 PQQ 7

RESULT 43  
US-10-925-366A-33  
Sequence 33, Application US/10925366A  
Publication No. US20050271663A1  
GENERAL INFORMATION:  
APPLICANT: Ignatovich, Olga  
APPLICANT: Demildt, Rudolph M.T.  
APPLICANT: Benjamin, Woolven  
APPLICANT: Grant, Steven  
APPLICANT: Jones, Phillip  
APPLICANT: Bastran, Amrik  
APPLICANT: Brewis, Neil  
TITLE OF INVENTION: Compositions and Methods for Treating Inflammatory Disorders  
FILE REFERENCE: 8039/2105  
CURRENT APPLICATION NUMBER: US/10/925,366A  
CURRENT FILING DATE: 2004-08-24  
PRIOR APPLICATION NUMBER: US 10/744,774  
PRIOR FILING DATE: 2003-12-23  
PRIOR APPLICATION NUMBER: PCT/GB2003/002804  
PRIOR FILING DATE: 2003-06-30  
PRIOR APPLICATION NUMBER: PCT/GB2002/03014  
PRIOR FILING DATE: 2002-06-28  
PRIOR APPLICATION NUMBER: GB 0230202.4  
PRIOR FILING DATE: 2002-12-27  
PRIOR APPLICATION NUMBER: GB 115841.9  
PRIOR FILING DATE: 2001-06-28  
PRIOR APPLICATION NUMBER: PCT/GB2004/002829  
PRIOR FILING DATE: 2004-06-30  
PRIOR APPLICATION NUMBER: US 60/535,076  
PRIOR FILING DATE: 2004-01-08  
PRIOR APPLICATION NUMBER: PCT/GB2003/005646  
PRIOR FILING DATE: 2003-12-24  
PRIOR APPLICATION NUMBER: GB 0327706.8

PRIOR FILING DATE: 2003-11-28  
PRIOR APPLICATION NUMBER: US 60/509,613  
PRIOR FILING DATE: 2003-10-08  
NUMBER OF SEQ ID NOS: 368  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 33  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Artificial CDR3 Sequence  
US-10-925-366A-33

Query Match 30.0%; Score 3; DB 6; Length 9;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 QQG 9  
Db 1 QQG 3

RESULT 44  
US-10-925-366A-72  
Sequence 72, Application US/10925366A  
Publication No. US20050271663A1  
GENERAL INFORMATION:  
APPLICANT: Ignatovich, Olga  
APPLICANT: Demildt, Rudolph M.T.  
APPLICANT: Benjamin, Woolven  
APPLICANT: Grant, Steven  
APPLICANT: Jones, Phillip  
APPLICANT: Bastran, Amrik  
APPLICANT: Brewis, Neil  
TITLE OF INVENTION: Compositions and Methods for Treating Inflammatory Disorders  
FILE REFERENCE: 8039/2105  
CURRENT APPLICATION NUMBER: US/10/925,366A  
CURRENT FILING DATE: 2004-08-24  
PRIOR APPLICATION NUMBER: US 10/744,774  
PRIOR FILING DATE: 2003-12-23  
PRIOR APPLICATION NUMBER: PCT/GB2003/002804  
PRIOR FILING DATE: 2003-06-30  
PRIOR APPLICATION NUMBER: PCT/GB2002/03014  
PRIOR FILING DATE: 2002-06-28  
PRIOR APPLICATION NUMBER: GB 0230202.4  
PRIOR FILING DATE: 2002-12-27  
PRIOR APPLICATION NUMBER: GB 115841.9  
PRIOR FILING DATE: 2001-06-28  
PRIOR APPLICATION NUMBER: PCT/GB2004/002829  
PRIOR FILING DATE: 2004-06-30  
PRIOR APPLICATION NUMBER: US 60/535,076  
PRIOR FILING DATE: 2004-01-08  
PRIOR APPLICATION NUMBER: PCT/GB2003/005646  
PRIOR FILING DATE: 2003-12-24  
PRIOR APPLICATION NUMBER: GB 0327706.8  
PRIOR FILING DATE: 2003-11-28  
PRIOR APPLICATION NUMBER: US 60/509,613  
PRIOR FILING DATE: 2003-10-08  
NUMBER OF SEQ ID NOS: 368  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 72  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Artificial CDR3 Sequence  
US-10-925-366A-72

Query Match 30.0%; Score 3; DB 6; Length 9;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 QQG 9

Db 1 CCG 3

## RESULT 45

US-10-966-483-8  
; Sequence 8, Application US/10966483  
; Publication No. US20050281783A1  
; GENERAL INFORMATION:  
; APPLICANT: Kinch, Michael S.  
; APPLICANT: Kienner, Peter A.  
; APPLICANT: Bruckheimer, Elizabeth  
; APPLICANT: Dubensky, Jr. Thomas W.  
; APPLICANT: Cook, David N.  
; TITLE OF INVENTION: LISTERIA-BASED BphA2 VACCINES  
; FILE REFERENCE: 10271-146  
; CURRENT APPLICATION NUMBER: US/10/966,483  
; PRIOR FILING DATE: 2004-10-15  
; PRIOR APPLICATION NUMBER: US 60/511,919  
; PRIOR FILING DATE: 2003-10-15  
; PRIOR APPLICATION NUMBER: US 60/511,719  
; PRIOR FILING DATE: 2003-10-15  
; PRIOR APPLICATION NUMBER: US 60/532,666  
; PRIOR FILING DATE: 2003-12-24  
; PRIOR APPLICATION NUMBER: US 60/556,631  
; PRIOR FILING DATE: 2004-03-26  
; PRIOR APPLICATION NUMBER:  
; PRIOR FILING DATE: 2004-10-01  
; PRIOR APPLICATION NUMBER:  
; PRIOR FILING DATE: 2004-10-07  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 8  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-966-483-8

## Query Match

Best Local Similarity 30.0%; Score 3; DB 6; Length 9;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LVP 6  
|||  
Db 2 LVP 4

## RESULT 46

US-10-859-643-19  
; Sequence 19, Application US/10859643  
; Publication No. US20060002993A1  
; GENERAL INFORMATION:  
; APPLICANT: Challita-Eid, Pia M.  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Morrison, Karen Jane Meyrick  
; APPLICANT: Jakobovits, Aya  
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein  
; TITLE OF INVENTION: Entitled 161p2f10B Useful in Treatment and Detection of  
; FILE REFERENCE: 511582006203  
; CURRENT APPLICATION NUMBER: US/10/859,643  
; PRIOR FILING DATE: 2004-06-02  
; PRIOR APPLICATION NUMBER: US 10/005,480  
; NUMBER OF SEQ ID NOS: 765  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 19  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-859-643-19

Query Match 30.0%; Score 3; DB 6; Length 9;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LVP 6  
|||  
Db 5 LVP 7

## RESULT 47

US-10-859-643-32  
; Sequence 32, Application US/10859643  
; Publication No. US20060002993A1  
; GENERAL INFORMATION:  
; APPLICANT: Challita-Eid, Pia M.  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Morrison, Karen Jane Meyrick  
; APPLICANT: Jakobovits, Aya  
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein  
; TITLE OF INVENTION: Entitled 161p2f10B Useful in Treatment and Detection of  
; FILE REFERENCE: 511582006203  
; CURRENT APPLICATION NUMBER: US/10/859,643  
; PRIOR FILING DATE: 2004-06-02  
; PRIOR APPLICATION NUMBER: US 10/005,480  
; PRIOR FILING DATE: 2001-11-07  
; NUMBER OF SEQ ID NOS: 765  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 32  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-859-643-32

Query Match 30.0%; Score 3; DB 6; Length 9;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LVP 6  
|||  
Db 2 LVP 4

## RESULT 48

US-10-859-643-271  
; Sequence 271, Application US/10859643  
; Publication No. US20060002993A1  
; GENERAL INFORMATION:  
; APPLICANT: Challita-Eid, Pia M.  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Morrison, Karen Jane Meyrick  
; APPLICANT: Jakobovits, Aya  
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein  
; TITLE OF INVENTION: Entitled 161p2f10B Useful in Treatment and Detection of  
; FILE REFERENCE: 511582006203  
; CURRENT APPLICATION NUMBER: US/10/859,643  
; PRIOR FILING DATE: 2004-06-02  
; PRIOR APPLICATION NUMBER: US 10/005,480  
; PRIOR FILING DATE: 2001-11-07  
; NUMBER OF SEQ ID NOS: 765  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 271  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-859-643-271

Query Match 30.0%; Score 3; DB 6; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LVP 6  
 |||  
 Db 1 LVP 3

RESULT 49  
 US-10-859-643-352

; Sequence 352, Application US/10859643  
 ; Publication No. US2006002993A1

; GENERAL INFORMATION:

; APPLICANT: Challita-Eld, Pia M.

; APPLICANT: Raitano, Arthur B.

; APPLICANT: Faris, Mary

; APPLICANT: Hubert, Rene S.

; APPLICANT: Morison, Karen Jane Meyrick

; APPLICANT: Jakobovits, Aya

; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein

; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of

; FILE REFERENCE: 511582006203

; CURRENT APPLICATION NUMBER: US/10/859,643

; PRIOR FILING DATE: 2004-06-02

; PRIOR FILING DATE: 2001-11-07

; NUMBER OF SEQ ID NOS: 765

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 352

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-859-643-352

Query Match 30.0%; Score 3; DB 6; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EYL 4  
 |||  
 Db 1 EYL 3

RESULT 50

US-10-859-643-487

; Sequence 487, Application US/10859643

; Publication No. US2006002993A1

; GENERAL INFORMATION:

; APPLICANT: Challita-Eld, Pia M.

; APPLICANT: Raitano, Arthur B.

; APPLICANT: Faris, Mary

; APPLICANT: Hubert, Rene S.

; APPLICANT: Morison, Karen Jane Meyrick

; APPLICANT: Jakobovits, Aya

; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein

; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of

; FILE REFERENCE: 511582006203

; CURRENT APPLICATION NUMBER: US/10/859,643

; PRIOR FILING DATE: 2004-06-02

; PRIOR FILING DATE: 2001-11-07

; NUMBER OF SEQ ID NOS: 765

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 487

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Homo Sapien

Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VPO 7  
 |||  
 Db 6 VPO 8

Search completed: January 18, 2006, 21:17:47  
 Job time : 32 secs

Query Match 30.0%; Score 3; DB 6; Length 9;

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 18, 2006, 20:45:40 ; Search time 72 Seconds  
(without alignments)  
2302.766 Million cell updates/sec

Title: US-09-930-125-2\_COPY\_975\_1209

Perfect score: 235  
Sequence: 1 EFSRMRARPPQRFVVIQNEIDL.....AVENPEVILPPGGAAPQHPH 235

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1027535

Minimum DB seq length: 0  
Maximum DB seq length: 235

Post-processing: Listing first 200 summaries

Database : UniProt 05.80:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID             | Description         |
|------------|-------|-------------|--------|----------------|---------------------|
| 1          | 8     | 3.4         | 95     | 1 ERBB4_MOUSE  | 061527 mus musculi  |
| 2          | 8     | 3.4         | 145    | 2 OMRP38_STRAW | 082438 streptomyces |
| 3          | 8     | 3.4         | 160    | 2 OMR427_RHOSH | 068227 rhodobacter  |
| 4          | 8     | 3.4         | 176    | 2 OMR5B5_MOUSE | 081505 mus musculus |
| 5          | 8     | 3.4         | 204    | 2 O5NL46_ZYMO  | 05n146 zymomonas m  |
| 6          | 8     | 3.4         | 232    | 2 O6W014_MAYDE | 06w014 mayetiola d  |
| 7          | 8     | 3.4         | 232    | 2 O6W015_MAYDE | 06w015 mayetiola d  |
| 8          | 8     | 3.4         | 234    | 2 O6W016_MAYDE | 06w016 mayetiola d  |
| 9          | 8     | 3.0         | 51     | 2 O5BXY8_SCHJA | 05bxy8 schistosoma  |
| 10         | 8     | 3.0         | 62     | 2 O5P2H2_AZOSE | 05p2h2 azoarcus sp  |
| 11         | 8     | 3.0         | 68     | 1 RL29_ARCFU   | 028361 archaeglob   |
| 12         | 8     | 3.0         | 75     | 2 O9TIV0_TRIVU | 09tivo trichosporus |
| 13         | 8     | 3.0         | 75     | 2 O88460_MOUSE | 088460 mus musculus |
| 14         | 8     | 3.0         | 84     | 2 O5BHP9_MACMU | 05bhp9 macaca mula  |
| 15         | 8     | 3.0         | 85     | 1 EGFR_MACMU   | 055245 macaca mula  |
| 16         | 8     | 3.0         | 85     | 2 O8A0I4_BACTN | 08a0i4 bacteroides  |
| 17         | 8     | 3.0         | 88     | 2 O8I012_PLAF7 | 08i012 plasmodium   |
| 18         | 8     | 3.0         | 90     | 2 O69V62_ORYSA | 069v62 oryza sativ  |
| 19         | 8     | 3.0         | 92     | 1 PETP_XANOR   | 059222 xanthomonas  |
| 20         | 8     | 3.0         | 93     | 2 O69W78_ORYSA | 069w78 oryza sativ  |
| 21         | 8     | 3.0         | 96     | 2 O9LJ15_ORYSA | 09lj15 oryza sativ  |
| 22         | 8     | 3.0         | 99     | 2 O4Q4G7_LEIMA | 04q4g7 leishmania   |
| 23         | 8     | 3.0         | 99     | 2 O7VUI9_BORPE | 07vui9 bordetella   |
| 24         | 8     | 3.0         | 105    | 1 NIFW_ANASP   | 044149 anabaena sp  |
| 25         | 8     | 3.0         | 114    | 2 O5Q2X0_IDILO | 05q2x0 idiomarina   |
| 26         | 8     | 3.0         | 115    | 2 O5JDA2_PYRO  | 05jda2 pyrococcus   |
| 27         | 8     | 3.0         | 117    | 2 O5JVO2_HUMAN | 05jvo2 homo sapien  |
| 28         | 8     | 3.0         | 120    | 2 O9ZB44_STRCO | 09zb44 streptomyces |
| 29         | 8     | 3.0         | 121    | 2 O8GSH5_ORYSA | 08gsh5 oryza sativ  |
| 30         | 8     | 3.0         | 125    | 2 O7PLP6_DROME | 07plp6 drosophila   |
| 31         | 8     | 3.0         | 128    | 2 O6BXP3_DEBHA | 06bxp3 debaromyces  |

|     |   |     |     |                 |                     |
|-----|---|-----|-----|-----------------|---------------------|
| 32  | 7 | 3.0 | 131 | 2 O6D9H7_ERWCT  | 06d9h7 erwintia car |
| 33  | 7 | 3.0 | 135 | 2 O6VY89_9CAUD  | 06vy89 bacteriophag |
| 34  | 7 | 3.0 | 135 | 2 O7UUR6_RHOBA  | 07uur6 rhodospirill |
| 35  | 7 | 3.0 | 136 | 2 O7ST02_RABIT  | 07st02 oryctolagus  |
| 36  | 7 | 3.0 | 136 | 2 O67TP2_ORYSA  | 067tp2 oryza sativ  |
| 37  | 7 | 3.0 | 137 | 2 O699F3_9HIV1  | 0699f3 human immun  |
| 38  | 7 | 3.0 | 138 | 2 O97JX6_CIOAB  | 097jx6 clostridium  |
| 39  | 7 | 3.0 | 140 | 2 O8I1Y7_PLAF7  | 08i1y7 plasmodium   |
| 40  | 7 | 3.0 | 142 | 2 O8XOM8_RALISO | 08xom8 ralsostoma s |
| 41  | 7 | 3.0 | 148 | 2 O511G9_ENTHI  | 0511g9 entamoeba s  |
| 42  | 7 | 3.0 | 155 | 2 O5WUT6_9ACTO  | 05wut6 streptomyces |
| 43  | 7 | 3.0 | 161 | 2 O5F4Y1_NEIG1  | 05f4y1 neisseria g  |
| 44  | 7 | 3.0 | 161 | 2 O65WU0_MANSM  | 065wuo mannheimia   |
| 45  | 7 | 3.0 | 164 | 2 O8B8T1_ORYSA  | 08b8t1 oryza sativ  |
| 46  | 7 | 3.0 | 165 | 2 O57ZP2_9TRYP  | 057zpz trypanosoma  |
| 47  | 7 | 3.0 | 167 | 2 O6NIG2_CORDI  | 06nig2 corynebacte  |
| 48  | 7 | 3.0 | 168 | 2 O6MNZ6_BDBRA  | 06mnz6 bdellovibri  |
| 49  | 7 | 3.0 | 175 | 2 O5W9T4_CHIRE  | 05w9t4 chlamydomon  |
| 50  | 7 | 3.0 | 176 | 2 O5B662_EMENT  | 05b662 aspergillus  |
| 51  | 7 | 3.0 | 182 | 1 NDOC2_RHIME   | 051793 cupriavidus  |
| 52  | 7 | 3.0 | 182 | 2 O64GB4_MUSAC  | 064gb4 mus acumin   |
| 53  | 7 | 3.0 | 191 | 2 O51793_9BURK  | 051793 cupriavidus  |
| 54  | 7 | 3.0 | 193 | 2 O7R316_GITAL  | 07r316 giardia lam  |
| 55  | 7 | 3.0 | 197 | 2 O8UDR2_AGRIS  | 08udr2 agrobacteri  |
| 56  | 7 | 3.0 | 198 | 2 O67VV2_ORYSA  | 067vv2 oryza sativ  |
| 57  | 7 | 3.0 | 201 | 2 O51Q66_MAGGR  | 051q66 magnaporthe  |
| 58  | 7 | 3.0 | 205 | 2 O5DC06_SCHJA  | 05dc06 schistosoma  |
| 59  | 7 | 3.0 | 206 | 2 O51SB7_MAGGR  | 051sb7 magnaporthe  |
| 60  | 7 | 3.0 | 206 | 2 O861F6_DROME  | 0861f6 drosophila   |
| 61  | 7 | 3.0 | 207 | 2 O5H5A0_XANOR  | 05h5a0 xanthomonas  |
| 62  | 7 | 3.0 | 211 | 2 O8L100_ORYSA  | 08l100 oryza sativ  |
| 63  | 7 | 3.0 | 211 | 2 O92SV6_RHIME  | 092sv6 rhizobium m  |
| 64  | 7 | 3.0 | 212 | 2 O59W49_CANAL  | 059w49 candida alb  |
| 65  | 7 | 3.0 | 212 | 2 O8UIY7_AGRIS  | 08uiy7 agrobacteri  |
| 66  | 7 | 3.0 | 212 | 2 O98GQ6_RHITO  | 098gq6 rhizobium l  |
| 67  | 7 | 3.0 | 213 | 2 O7PPG8_ANOGA  | 07ppg8 anopheles g  |
| 68  | 7 | 3.0 | 213 | 2 O7CXX1_AGRIS  | 07cxx1 agrobacteri  |
| 69  | 7 | 3.0 | 214 | 1 PPAX_CLOPE    | 044T44 tetraglo     |
| 70  | 7 | 3.0 | 214 | 2 O9NMT9_HUMAN  | 09nmt9 homo sapien  |
| 71  | 7 | 3.0 | 216 | 2 O57FK6_BRUAB  | 057fk6 brucella ab  |
| 72  | 7 | 3.0 | 218 | 2 O8G2Y7_BRUSU  | 08g2y7 brucella su  |
| 73  | 7 | 3.0 | 218 | 2 O9RIU2_STRCO  | 09riu2 streptomyces |
| 74  | 7 | 3.0 | 219 | 2 O926S7_LISIN  | 0926s7 listeria in  |
| 75  | 7 | 3.0 | 220 | 2 O4KRG5_9VIRU  | 04krg5 baculovirus  |
| 76  | 7 | 3.0 | 223 | 2 O6WQW6_9CALI  | 06wqw6 norwalk-lik  |
| 77  | 7 | 3.0 | 223 | 1 FOG1_BRARE    | 060622 brachydanio  |
| 78  | 7 | 3.0 | 224 | 1 O9YD60_AERPE  | 09yd60 aeropyrum p  |
| 79  | 7 | 3.0 | 224 | 2 O59W89_CANAL  | 059w89 candida alb  |
| 80  | 7 | 3.0 | 224 | 2 O6L1B8_PHOPR  | 06l1b8 photobacter  |
| 81  | 7 | 3.0 | 228 | 2 O7D232_AGRIS  | 07d232 agrobacteri  |
| 82  | 7 | 3.0 | 229 | 2 LBD40_ARATH   | 092w96 arabidopsis  |
| 83  | 7 | 3.0 | 233 | 1 O53XE6_ARATH  | 053xe6 arabidopsis  |
| 84  | 7 | 3.0 | 233 | 2 O8B1J4_PSEPK  | 08b1j4 pseudomonas  |
| 85  | 7 | 3.0 | 233 | 2 O8B1J4_PSEPK  | 08b1j4 pseudomonas  |
| 86  | 7 | 2.6 | 13  | 1 GER1_HORVU    | 028526 hordeum vul  |
| 87  | 6 | 2.6 | 13  | 1 GER2_HORVU    | 028526 hordeum vul  |
| 88  | 6 | 2.6 | 13  | 1 GER3_HORVU    | 028526 hordeum vul  |
| 89  | 6 | 2.6 | 20  | 2 P81896_SOLTU  | 07m1v0 oryza sativ  |
| 90  | 6 | 2.6 | 26  | 2 O7M1V0_ORYSA  | 07m1v0 oryza sativ  |
| 91  | 6 | 2.6 | 37  | 1 NLRP3_VITEX   | 080273 vitis sp. (  |
| 92  | 6 | 2.6 | 43  | 2 O9TXK3_CAREL  | 09txk3 caenorhabdi  |
| 93  | 6 | 2.6 | 45  | 2 O4TGH9_TETNG  | 04tgh9 tetraodon n  |
| 94  | 6 | 2.6 | 46  | 2 O4RDT8_TETNG  | 04rdt8 tetraodon n  |
| 95  | 6 | 2.6 | 47  | 2 O9N858_HUMAN  | 09n858 homo sapien  |
| 96  | 6 | 2.6 | 47  | 2 O90774_CHICK  | 090774 gallus gall  |
| 97  | 6 | 2.6 | 50  | 2 O716L2_9CAUD  | 0716l2 mycobacteri  |
| 98  | 6 | 2.6 | 51  | 2 O26905_TRICO  | 026905 trichospor   |
| 99  | 6 | 2.6 | 52  | 2 O96GJ3_HUMAN  | 096gj3 homo sapien  |
| 100 | 6 | 2.6 | 53  | 2 O63WD5_BURPS  | 063wds burholderi   |
| 101 | 6 | 2.6 | 54  | 2 O91KM9_9HSPC  | 091km9 hepatitis c  |
| 102 | 6 | 2.6 | 54  | 2 O4FE54_HUMAN  | 04fes4 homo sapien  |
| 103 | 6 | 2.6 | 54  | 2 O9BBJ2_RHITO  | 09bbj2 rhizobium l  |
| 104 | 6 | 2.6 | 57  | 2 O725W9_DESYA  | 0725w9 desulfovib   |
|     |   |     |     |                 | 0725w9 oryza sativ  |

|     |     |     |    |               |                     |                    |     |     |     |    |               |                     |                    |
|-----|-----|-----|----|---------------|---------------------|--------------------|-----|-----|-----|----|---------------|---------------------|--------------------|
| 105 | 6   | 2.6 | 58 | 2             | 064HJ5_MERVL        | 064HJ5_meleagrid h | 178 | 6   | 2.6 | 88 | 2             | Q7M1S4_CHLVU        | Q7M1S4_chlorella v |
| 106 | 2.6 | 61  | 2  | 06K8S7_ORRSA  | 06K8S7_oryza sativ  | 179                | 6   | 2.6 | 88  | 2  | Q4RC42_TETNG  | Q4RC42_tetradon n   |                    |
| 107 | 2.6 | 61  | 2  | 065583_9ALPH  | 065583_bovine hecp  | 180                | 6   | 2.6 | 89  | 2  | 0657A8_ORRSA  | 0657A8_oryza sativ  |                    |
| 108 | 2.6 | 61  | 2  | 04SX62_TETNG  | 04SX62_tetradon n   | 181                | 6   | 2.6 | 89  | 2  | 058PV5_BRWMA  | 058PV5_erwinia amy  |                    |
| 109 | 2.6 | 62  | 2  | 096FS0_HUMAN  | 096FS0_homo sapien  | 182                | 6   | 2.6 | 89  | 2  | 0924E3_SALTY  | 0924E3_salmonella   |                    |
| 110 | 2.6 | 62  | 2  | 04XD34_PLACH  | 04XD34_plasmodium   | 183                | 6   | 2.6 | 89  | 2  | 06NH88_CORDI  | 06NH88_corymbace    |                    |
| 111 | 2.6 | 63  | 2  | 08EN91_OCBRH  | 08EN91_oceanobacill | 184                | 6   | 2.6 | 89  | 2  | 098HY8_RHILLO | 098HY8_rhizobium l  |                    |
| 112 | 2.6 | 66  | 2  | 06AV31_ORRSA  | 06AV31_oryza sativ  | 185                | 6   | 2.6 | 89  | 2  | Q7DJY7_9Z2ZZ  | Q7DJY7_plasmod col  |                    |
| 113 | 2.6 | 66  | 2  | 08AV72_HUMAN  | 08AV72_homo sapien  | 186                | 6   | 2.6 | 89  | 2  | 011332_MCVI   | 011332_molnucleum c |                    |
| 114 | 2.6 | 67  | 2  | 07X3M1_PSEPU  | 07X3M1_pseudomonas  | 187                | 6   | 2.6 | 90  | 2  | 05OJJO_SALTY  | 05OJJO_salmonella   |                    |
| 115 | 2.6 | 67  | 2  | 07X3M1_PSEPU  | 07X3M1_pseudomonas  | 188                | 6   | 2.6 | 90  | 2  | 09ZGS5_ECO57  | 09ZGS5_escherichia  |                    |
| 116 | 2.6 | 68  | 2  | 05XNQ4_MANES  | 05XNQ4_manihot esc  | 189                | 6   | 2.6 | 90  | 2  | 08VAS5_MSCV   | 08VAS5_white spot   |                    |
| 117 | 2.6 | 68  | 2  | 075HL5_ORRSA  | 075HL5_oryza sativ  | 190                | 6   | 2.6 | 91  | 2  | TM10_DEBHA    | TM10_debaryomyce    |                    |
| 118 | 2.6 | 69  | 2  | 05ZSR0_ORRSA  | 05ZSR0_oryza sativ  | 191                | 6   | 2.6 | 91  | 2  | 096U75_NEUCR  | 096U75_neurospora   |                    |
| 119 | 2.6 | 69  | 2  | 06J913_LYCES  | 06J913_lycopersico  | 192                | 6   | 2.6 | 92  | 2  | 09HP62_HALSA  | 09HP62_halobacteri  |                    |
| 120 | 2.6 | 69  | 2  | 083HD7_TROW8  | 083HD7_tropheryma   | 193                | 6   | 2.6 | 92  | 2  | 056ZY0_ARATH  | 056ZY0_arabidopsis  |                    |
| 121 | 2.6 | 70  | 2  | 05CTC6_ORRSA  | 05CTC6_oryza sativ  | 194                | 6   | 2.6 | 92  | 2  | Q9KM34_PSEAB  | Q9KM34_pseudomonas  |                    |
| 122 | 2.6 | 70  | 2  | 09RPS5_SALTY  | 09RPS5_salmomella   | 195                | 6   | 2.6 | 93  | 1  | YGJG_ERWCH    | YGJG_erwinia chr    |                    |
| 123 | 2.6 | 71  | 2  | 09JMA4_BORPE  | 09JMA4_bordecella   | 196                | 6   | 2.6 | 93  | 2  | 064BZ1_9ARCH  | 064BZ1_uncultured   |                    |
| 124 | 2.6 | 72  | 2  | 07U685_SYMPX  | 07U685_synchococc   | 197                | 6   | 2.6 | 93  | 2  | 064DI6_9ARCH  | 064DI6_uncultured   |                    |
| 125 | 2.6 | 72  | 2  | 04V2C5_BURMA  | 04V2C5_burkholderi  | 198                | 6   | 2.6 | 93  | 2  | 069TI9_ORRSA  | 069TI9_oryza sativ  |                    |
| 126 | 2.6 | 72  | 2  | 07TDM6_SVIRU  | 07TDM6_haloavirus h | 199                | 6   | 2.6 | 94  | 2  | 084DW8_TROWH  | 084DW8_tropheryma   |                    |
| 127 | 2.6 | 72  | 2  | 08V6U1_SVIRU  | 08V6U1_haloavirus h | 200                | 6   | 2.6 | 94  | 1  | VIXS_BRAPS    | VIXS_bacteriophba   |                    |
| 128 | 2.6 | 73  | 2  | 05TVJ9_ANGGA  | 05TVJ9_anopheles g  |                    |     |     |     |    |               |                     |                    |
| 129 | 2.6 | 73  | 2  | 09KBP1_BACHD  | 09KBP1_bacillus ha  |                    |     |     |     |    |               |                     |                    |
| 130 | 2.6 | 73  | 2  | 09RCA0_BACHD  | 09RCA0_bacillus ha  |                    |     |     |     |    |               |                     |                    |
| 131 | 2.6 | 74  | 2  | 0949H1_HORVU  | 0949H1_hordeum vul  |                    |     |     |     |    |               |                     |                    |
| 132 | 2.6 | 75  | 2  | 08RZS5_ORRSA  | 08RZS5_oryza sativ  |                    |     |     |     |    |               |                     |                    |
| 133 | 2.6 | 75  | 2  | 090160_NPYBM  | 090160_bombyx mori  |                    |     |     |     |    |               |                     |                    |
| 134 | 2.6 | 76  | 2  | 094Q10_SOLTU  | 094Q10_solanum tub  |                    |     |     |     |    |               |                     |                    |
| 135 | 2.6 | 76  | 2  | 04RWD3_TETNG  | 04RWD3_tetradodon n |                    |     |     |     |    |               |                     |                    |
| 136 | 2.6 | 77  | 2  | 096WMD3_9HYPO | 096WMD3_akanthomyce |                    |     |     |     |    |               |                     |                    |
| 137 | 2.6 | 77  | 2  | 096WFB_9HYPO  | 096WFB_polyccephalo |                    |     |     |     |    |               |                     |                    |
| 138 | 2.6 | 77  | 2  | 09NRK3_HUMAN  | 09NRK3_homo sapien  |                    |     |     |     |    |               |                     |                    |
| 139 | 2.6 | 77  | 2  | 06L006_XENLA  | 06L006_xenopus lae  |                    |     |     |     |    |               |                     |                    |
| 140 | 2.6 | 78  | 2  | 094Q10_SOLTU  | 094Q10_solanum tub  |                    |     |     |     |    |               |                     |                    |
| 141 | 2.6 | 78  | 2  | 04ZV49_PSESY  | 04ZV49_pseudomonas  |                    |     |     |     |    |               |                     |                    |
| 142 | 2.6 | 78  | 2  | 083EUT_COXBU  | 083EUT_coxiella bu  |                    |     |     |     |    |               |                     |                    |
| 143 | 2.6 | 80  | 1  | CX7A1_MOUSE   | P56392_mus musculu  |                    |     |     |     |    |               |                     |                    |
| 144 | 2.6 | 80  | 2  | 08J2W6_PYPAB  | 08J2W6_pyrococcus   |                    |     |     |     |    |               |                     |                    |
| 145 | 2.6 | 80  | 2  | 04LSC7_9BORR  | 04LSC7_burkholderi  |                    |     |     |     |    |               |                     |                    |
| 146 | 2.6 | 80  | 2  | 08VH90_MASHI  | 08VH90_maecomyx hi  |                    |     |     |     |    |               |                     |                    |
| 147 | 2.6 | 80  | 2  | 08VH91_HYLA1  | 08VH91_hyalomycus   |                    |     |     |     |    |               |                     |                    |
| 148 | 2.6 | 80  | 2  | 08VH92_MUSMI  | 08VH92_mus minutol  |                    |     |     |     |    |               |                     |                    |
| 149 | 2.6 | 80  | 2  | 08VH94_MUSPA  | 08VH94_mus pahari   |                    |     |     |     |    |               |                     |                    |
| 150 | 2.6 | 80  | 2  | 08VH95_MUSCO  | 08VH95_mus cookii   |                    |     |     |     |    |               |                     |                    |
| 151 | 2.6 | 80  | 2  | 08VH96_MUSCR  | 08VH96_mus caroli   |                    |     |     |     |    |               |                     |                    |
| 152 | 2.6 | 80  | 2  | 08VH97_MUSCE  | 08VH97_mus cervico  |                    |     |     |     |    |               |                     |                    |
| 153 | 2.6 | 80  | 2  | 08VH98_MUSSE  | 08VH98_mus spretus  |                    |     |     |     |    |               |                     |                    |
| 154 | 2.6 | 80  | 2  | 08VH99_MUSSI  | 08VH99_mus spicile  |                    |     |     |     |    |               |                     |                    |
| 155 | 2.6 | 80  | 2  | 08VHA0_MUSMA  | 08VHA0_mus macedon  |                    |     |     |     |    |               |                     |                    |
| 156 | 2.6 | 80  | 2  | 08VHA1_MOUSE  | 08VHA1_mus musculu  |                    |     |     |     |    |               |                     |                    |
| 157 | 2.6 | 80  | 2  | 08VHA2_MUSNM  | 08VHA2_mus musculu  |                    |     |     |     |    |               |                     |                    |
| 158 | 2.6 | 80  | 2  | 08VHA3_MUSMC  | 08VHA3_mus musculu  |                    |     |     |     |    |               |                     |                    |
| 159 | 2.6 | 80  | 2  | 08VHA4_MOUSE  | 08VHA4_mus musculu  |                    |     |     |     |    |               |                     |                    |
| 160 | 2.6 | 80  | 2  | 0792A4_MOUSE  | 0792A4_mus musculu  |                    |     |     |     |    |               |                     |                    |
| 161 | 2.6 | 81  | 2  | 06YWG7_ORRSA  | 06YWG7_oryza sativ  |                    |     |     |     |    |               |                     |                    |
| 162 | 2.6 | 81  | 2  | 05KTV8_GROXA  | 05KTV8_geobacillus  |                    |     |     |     |    |               |                     |                    |
| 163 | 2.6 | 83  | 2  | 05W399_9BACT  | 05W399_uncultured   |                    |     |     |     |    |               |                     |                    |
| 164 | 2.6 | 83  | 2  | 06X3H1_PSEAB  | 06X3H1_pseudomonas  |                    |     |     |     |    |               |                     |                    |
| 165 | 2.6 | 83  | 2  | 09AK32_STRCO  | 09AK32_streptomyces |                    |     |     |     |    |               |                     |                    |
| 166 | 2.6 | 83  | 2  | 092KCS_RHIME  | 092KCS_rhizobium m  |                    |     |     |     |    |               |                     |                    |
| 167 | 2.6 | 85  | 2  | 09HBZ3_HUMAN  | 09HBZ3_homo sapien  |                    |     |     |     |    |               |                     |                    |
| 168 | 2.6 | 85  | 2  | 016Z75_HUMAN  | 016Z75_homo sapien  |                    |     |     |     |    |               |                     |                    |
| 169 | 2.6 | 85  | 2  | 09ZTV5_9ASPA  | 09ZTV5_phalaenopel  |                    |     |     |     |    |               |                     |                    |
| 170 | 2.6 | 85  | 2  | 073KKS_TREDE  | 073KKS_treponeuma d |                    |     |     |     |    |               |                     |                    |
| 171 | 2.6 | 86  | 2  | 052PU3_FELCA  | 052PU3_felis silve  |                    |     |     |     |    |               |                     |                    |
| 172 | 2.6 | 86  | 2  | 07XEE5_ORRSA  | 07XEE5_oryza sativ  |                    |     |     |     |    |               |                     |                    |
| 173 | 2.6 | 86  | 2  | 06XN61_RHOER  | 06XN61_rhodococcus  |                    |     |     |     |    |               |                     |                    |
| 174 | 2.6 | 87  | 2  | 07XCL3_ORRSA  | 07XCL3_oryza sativ  |                    |     |     |     |    |               |                     |                    |
| 175 | 2.6 | 87  | 2  | 09FWF6_ORRSA  | 09FWF6_oryza sativ  |                    |     |     |     |    |               |                     |                    |
| 176 | 2.6 | 87  | 2  | 09FV03_PHYIN  | 09FV03_phytophthor  |                    |     |     |     |    |               |                     |                    |
| 177 | 2.6 | 87  | 2  | 075NQ7_HRSV   | 075NQ7_human respi  |                    |     |     |     |    |               |                     |                    |

## ALIGNMENTS

RESULT 1  
 ERBB4\_MOUSE STANDARD; PRT; 95 AA.  
 ID ERBB4\_MOUSE  
 AC Q61527;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Receptor tyrosine-protein kinase erbB-4 (EC 2.7.1.112) (fragments).  
 GN Name=Erbb4; Synonyms=Mert4;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Mus.  
 NCBI\_TaxId=10090;  
 [1]  
 NUCLEOTIDE SEQUENCE OF 1-27 (ISOPFORMS JM-A AND JM-B).  
 RP TISSUE=Heart, and Kidney;  
 RC MEDLINE=97476287; PubMed=9334263; DOI=10.1074/jbc.272.42.26761;  
 RA Elenius K., Corfas G., Paul S., Choi C.J., Rio C., Plowman G.D.,  
 "A novel juxtamembrane domain isoform of HER4/Erbb4. Isoform-specific  
 tissue distribution and differential processing in response to phorbol  
 ester.";  
 J. Biol. Chem. 272:26761-26766(1997).  
 [2]  
 NUCLEOTIDE SEQUENCE OF 28-95.  
 RP STRAIN=C57BL/6; TISSUE=Brain;  
 RC MEDLINE=96069911; PubMed=7589796; DOI=10.1006/dbio.1995.0012;  
 RA Moscoso I.M., Chu G.C., Gautam M., Noakes P.G., Merlie J.P.,  
 Sane J.R.;  
 "Synapse-associated expression of an acetylcholine receptor-inducing  
 protein, ARIA/heretulin, and its putative receptors, Erbb2 and Erbb3,  
 in developing mammalian muscle.";  
 Dev. Biol. 172:158-169(1995).  
 -1- FUNCTION: Specifically binds and is activated by neuregulin, NRG-  
 2, NRG-3, heparin-binding EGF-like growth factor, betacellulin and  
 NTAK. Interaction with these factors induces cell differentiation.  
 Not activated by EGF, TGF-A, and amphiregulin (By similarity).  
 -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein  
 tyrosine phosphate.  
 -1- SUBUNIT: Homodimer or heterodimer with each of the other ERBB  
 receptors. Interacts with PDZ domains of DLG2, DLG3, DLG4 and the  
 synrophin SNTB2 (By similarity).  
 -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 -1- ALTERNATIVE PRODUCTS:

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CC Event=Alternative splicing; Named Isoforms=2;
CC Comment=The 2 isoforms differ functionally in their response to
CC photol ester: Isoform JM-A is processed but not isoform JM-B.
CC So, they respectively represent cleavable and noncleavable forms
CC of the receptor. Both isoforms are expressed in cerebellum,
CC cerebral cortex, spinal cord, medulla oblongata and eye, but the
CC kidney expresses solely isoform JM-A and the heart solely
CC isoform JM-B;
CC Name=JM-A;
CC IsoId=Q61527-1; Sequence=Displayed;
CC Name=JM-B;
CC IsoId=Q61527-2; Sequence=VSP_002896;
CC -1- PTM: Ligand-binding increases phosphorylation on tyrosine
CC residues
CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. EGF receptor
CC subfamily.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL: I47241; AAA3534.1; -; mRNA.
CC DR Ensembl: ENSMUSG0000062209; Mus musculus.
CC MGI: MGI:104771; ErbB4.
CC DR GO: GO:0045165; P:cell fate commitment; IDA.
CC DR GO: GO:0007507; P:heart development; IMP.
CC DR GO: GO:0007399; P:neurogenesis; IMP.
CC DR InterPro: IPR000719; Prot kinase.
CC DR InterPro: IPR008266; Tyr kinase AS.
CC DR PROSITE: PS00107; PROTEIN_KINASE_ATP; PARTIAL.
CC DR PROSITE: PS00011; PROTEIN_KINASE_DOM; PARTIAL.
CC DR PROSITE: PS00109; PROTEIN_KINASE_TYR; PARTIAL.
CC DR Alternative splicing; ATP-binding; Kinase; Multigene family;
CC Nucleotide-binding; Phosphorylation; Receptor; Transferase;
CC KM Transmembrane; Tyrosine-protein kinase.
CC PT VARSPUBLIC 3 25 NCPSTSHDCIYPWTGHTLPQHA -> IGSIRDCIGLTD
CC (in isoform JM-B).
CC /FTid=VSP_002896.
CC FT NON CONS 27 28
CC FT NON TER 1 1
CC FT NON TER 95 95
CC SO SEQUENCE 95 AA; 10524 MW; BA3D0B99591744D8 CRC64;

Query Match 3.4%; Score 8; DB 1; Length 95;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 AERYLVPO 53
DB 28 AERYLVPO 35

RESULT 2
082F38_STRAW PRELIMINARY; PRT; 145 AA.
ID 082F38_STRAW PRELIMINARY; PRT; 145 AA.
AC 082F38;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative RNA polymerase BCF-subfamily sigma factor.
GN Name=61938; OrderedLocustNames=SAV4425;
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxId=33903;
RN [1]
RZ NOCLEOTIDE SEQUENCE.
RP STRAIN=NA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RC MEDLINE=22608306; PubMed=12692562; DOI=10.1073/pnas.211433198;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sekaki Y., Hattori M., Omura S.;

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RT *Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermitilis.";
RT Nat. Biotechnol. 21:526-531(2003).
RN [2]
RP NOCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=NA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RA MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RT *Genome sequence of an industrial microorganism Streptomyces
RT avermitilis: deducing the ability of producing secondary
RT metabolites.";
RT Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
RL EMBL: BA000030; BAC72137.1; -; Genomic DNA.
DR HSSP: P34086; 1OR7.
DR GO: GO:0016987; P:sigma factor activity; IEA.
DR GO: GO:0003700; P:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription; IEA.
DR GO: GO:0006350; P:transcription; IEA.
DR GO: GO:0006352; P:transcription initiation; IEA.
DR InterPro: IPR007630; Sigma70_r4.
DR InterPro: IPR011991; Wing_hlx_DNA_bd.
DR Pfam: PF04545; Sigma70_r4; 1.
KM Complete proteome; DNA-binding; Transcription;
KM Transcription regulation.
SO SEQUENCE 145 AA; 15792 MW; 81AF896072574B55 CRC64;

Query Match 3.4%; Score 8; DB 2; Length 145;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 173 POPPSPRE 180
DB 3 POPPSPRE 10

RESULT 3
06SA27_RHOSH PRELIMINARY; PRT; 160 AA.
ID 06SA27_RHOSH PRELIMINARY; PRT; 160 AA.
AC 06SA27;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE R. Real endonuclease.
GN Name=rsair;
OS Rhodospirillum rubrum (Rhodospirillum rubrum sphaeroides).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacteriales;
OC Rhodobacteraceae; Rhodobacter.
OX NCBI_TaxId=1063;
RN [1]
RZ NOCLEOTIDE SEQUENCE.
RP Luunen K.D., Wilson G.G.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY461516; AA19437.1; -; Genomic DNA.
DR GO: GO:0004519; P:endonuclease activity; IEA.
KM Endonuclease.
SO SEQUENCE 160 AA; 18649 MW; 665D7EABEBB10CFC CRC64;

Query Match 3.4%; Score 8; DB 2; Length 160;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAPSEGAG 108
DB 52 LAPSEGAG 59

RESULT 4
08R5B5_MOUSE PRELIMINARY; PRT; 176 AA.
ID 08R5B5_MOUSE PRELIMINARY; PRT; 176 AA.
AC 08R5B5;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)

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DT 01-JUN-2002 (TREMBlrel. 21, last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, last annotation update)
DE Tor2a protein (Fragment).
GN Name=tor2a.
OC Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RX MEDLINE=22388557; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Struhsberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carinci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Boeak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gumaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzywinski M.T., Skalska U., Smalhus D.E.,
RA Scheraga A., Schin J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RA Struhsberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC023085; AAH23085.1; -; mRNA.
DR MGI; MGI:1335596; Tor2a.
DR GO; GO:0005615; Cytoplasmic space; TMS.
DR InterPro; IPR010448; Torsin.
DR Pfam; PF06309; Torsin; 1.
DR NON TER
SQ SEQUENCE 176 AA; 19940 MW; 404F703101F4B64 CRC64;

Query Match 3.4%; Score 8; DB 2; Length 176;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 LGLEPSEE 94
DB 134 LGLEPSEE 141

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RA Hong J.H., Kim H., Kim J.-H., Kil J.-I., Park C.J., Oh H.-M.,
RA Lee J.-S., Jin S.-Y., Um H.-W., Lee H.-J., Oh S.-D., Kim J.Y.,
RA Kang H.L., Lee S.Y., Lee K.J., Kang H.S.;
RT "The genome sequence of the ethanologenic bacterium Zymomonas mobilis
RT ZM4."
RL Nat. Biotechnol. 23:63-68(2005).
DR EMBL; AB008692; AAY90564.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 204 AA; 22120 MW; 5876D500A2D3C1A CRC64;

Query Match 3.4%; Score 8; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 184 PAAAPAGA 191
DB 46 PAAAPAGA 53

RESULT 6
ID 06W014 MAYDE PRELIMINARY; PRT; 232 AA.
AC 06W014;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Salivary secreted protein.
OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Sciaroidea;
OC Cecidomyiidae; Mayetiola.
OX NCBI_TaxID=39758;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14871619; DOI=10.1016/j.jmb.2003.10.008;
RA Liu X., Fellers J.P., Wilde G.B., Stuart J.J., Chen M.S.;
RT "Characterization of two genes expressed in the salivary glands of the
RL Hessian fly, Mayetiola destructor (Say).";
RL Insect Biochem. Mol. Biol. 34:229-237(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Chen M.-S., Fellers J.P.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY318788; AAC08248.1; -; mRNA.
SQ SEQUENCE 232 AA; 25436 MW; 1A732E80010DAC7 CRC64;

Query Match 3.4%; Score 8; DB 2; Length 232;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 RSSSTRSG 81
DB 104 RSSSTRSG 111

RESULT 7
ID 06W015 MAYDE PRELIMINARY; PRT; 232 AA.
AC 06W015;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Salivary secreted protein.
OS Mayetiola destructor (Hessian fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Sciaroidea;
OC Cecidomyiidae; Mayetiola.
OX NCBI_TaxID=39758;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14871619; DOI=10.1016/j.jmb.2003.10.008;
RA Liu X., Fellers J.P., Wilde G.B., Stuart J.J., Chen M.S.;
RT "Characterization of two genes expressed in the salivary glands of the

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RT Hessian fly, Mayetiola destructor (Say).";  
 RL Insect Biochem. Mol. Biol. 34:229-237(2004).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Chen M.-S., Fellers J.P.;  
 DR Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
 EMBL: AY18187; AAC08247.1; -; mRNA.  
 SO SEQUENCE 232 AA; 25419 MW; 4F2FC5386601056A CRC64;

Query Match 3.4%; Score 8; DB 2; Length 232;  
 Best Local Similarity 100.0%; Pred. No. 38;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 RSSSTRSG 81  
 DB 104 RSSSTRSG 111

## RESULT 8

Q6W016\_MAYDE PRELIMINARY; PRT; 234 AA.  
 AC Q6W016;  
 DT 05-JUL-2004 (TREMBlrel. 27, Created)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
 DE Salivary secreted protein.  
 OS Mayetiola destructor (Hessian fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Nematocera; Sciaroidea;  
 OC Cecidomyiidae; Mayetiola.  
 OX NCBI\_TaxId=39758;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Published=14871619; DOI=10.1016/j.jmb.2003.10.008;  
 RL Liu X., Fellers J.P., Wilde G.E., Stuart J.J., Chen M.S.;  
 RT "Characterization of two genes expressed in the salivary glands of the  
 Hessian fly, Mayetiola destructor (Say).";  
 RL Insect Biochem. Mol. Biol. 34:229-237(2004).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Chen M.-S., Fellers J.P.;  
 DR Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
 EMBL: AY181876; AAC08246.1; -; Genomic DNA.  
 SO SEQUENCE 234 AA; 25664 MW; 9764921336ED706C CRC64;

Query Match 3.4%; Score 8; DB 2; Length 234;  
 Best Local Similarity 100.0%; Pred. No. 38;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 RSSSTRSG 81  
 DB 104 RSSSTRSG 111

## RESULT 9

OSBX18\_SCHJA PRELIMINARY; PRT; 51 AA.  
 AC OSBX18;  
 DT 10-MAY-2005 (TREMBlrel. 30, Created)  
 DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)  
 DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)  
 DE Hypothetical protein.  
 OS Schistosoma japonicum (Blood fluke).  
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeiida;  
 OC Schistosomatoidea; Schistosomatidae; Schistosoma.  
 OX NCBI\_TaxId=6182;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.

RA Han Z.;  
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AY81148; AAX2737.1; -; mRNA.  
 KW Hypothetical protein.  
 SO SEQUENCE 51 AA; 5540 MW; 1E27BAB016CB973B CRC64;

Query Match 3.0%; Score 7; DB 2; Length 51;  
 Best Local Similarity 100.0%; Pred. No. 97;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 PASPLDS 28  
 DB 5 PASPLDS 11

## RESULT 10

Q5P2H2\_AZOSE PRELIMINARY; PRT; 62 AA.  
 AC Q5P2H2;  
 DT 01-FEB-2005 (TREMBlrel. 29, Created)  
 DT 01-FEB-2005 (TREMBlrel. 29, Last sequence update)  
 DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)  
 DE Hypothetical protein.  
 GN OrderedLocustNames=AZOSEA23670; ORFNames=eba4183;  
 OS Azoarcus sp. (strain BbN1).  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Rhodocyclales;  
 OC Rhodocyclaceae; Azoarcus.  
 OX NCBI\_TaxId=76114;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=BbN1;  
 RX PubMed=15551059; DOI=10.1007/s00203-004-0742-9;  
 RA Rabus R., Kube M., Heider J., Beck A., Heilmann K., Widdel F.,  
 RA Reinhardt R.;  
 RT "The genome sequence of an anaerobic aromatic-degrading denitrifying  
 bacterium, strain BbN1.";  
 RL Arch. Microbiol. 183:27-36(2005).  
 DR EMBL: CR55306; CA108492.1; -; Genomic DNA.  
 KW Complete proteome; Hypothetical protein.  
 SO SEQUENCE 62 AA; 7272 MW; 194B330C3A5F5B1A CRC64;

Query Match 3.0%; Score 7; DB 2; Length 62;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 RSSSTRS 80  
 DB 17 RSSSTRS 23

## RESULT 11

RL29\_ARCFU STANDARD; PRT; 68 AA.  
 ID RL29\_ARCFU  
 AC 028361;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE 50S ribosomal protein L29P.  
 GN Name=rp129p; OrderedLocustNames=AF1918;  
 OS Archaeoglobus fulgidus.  
 OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;  
 OC Archaeoglobaceae; Archaeoglobus.  
 OX NCBI\_TaxId=2234;  
 RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;  
 RX MEDLINE=98049343; PubMed=9389475; DOI=10.1038/37052;  
 RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,  
 RA Richardson D.L., Kiehl J., Gwinn M.L., Hickey E.K., Peterson J.D.,  
 RA Ketchum K.A., Dodson R.J., Gwinn M.L., Hickey E.K., Peterson J.D.,  
 RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.R.,  
 RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.J.,  
 RA Peterson S.N., Reich C.I., McNeil L.K., Badger J.H., Glodek A.,  
 RA Zhou L., Overbeek R., Gocayne J.D., Spriggs T., Artiach P., Kaine B.P.,  
 RA Uitterback T.R., Cotton M.D., Spilligs T., Artiach P., Fujii C.,  
 RA Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C.,  
 RA Garland S.A., Mason T.M., Olsen G.V., Frazer C.M., Smith H.O.,  
 RA Woese C.R., Venter J.C.;

RT "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon *Archaeoglobus fulgidus*.";  
RL Nature 390:364-370(1997).  
CC -1- SIMILARITY: Belongs to the ribosomal protein L29P family.  
CC -----  
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CC -----  
CC EMBL; AE000971; AAB89356.1; -; Genomic\_DNA.  
DR PIR; E69489; E69489.  
DR TIGR; AF1918; -.  
DR HAMAP; MF\_00374; -; 1.  
DR InterPro; IPR001854; Ribosomal\_L29.  
DR Pfam; PF00831; Ribosomal\_L29; 1.  
DR TIGRFAMs; TIGR00012; L29; 1.  
DR PROSITE; PS00579; RIBOSOMAL\_L29; 1.  
KW Complete proteome; Ribonucleoprotein; Ribosomal protein.  
SQ SEQUENCE 68 AA; 8010 MW; BF962BB601FF3A9 CRC64;  
  
Query Match 3.0%; Score 7; DB 1; Length 68;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 214 GGAVERN 220  
DB 38 GGAVERN 44  
|||||  
Q9TVV0; TRIVU PRELIMINARY; PRT; 75 AA.  
  
RESULT 12  
Q9TVV0; TRIVU PRELIMINARY; PRT; 75 AA.  
AC Q9TVV0;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE Type II gonadotrophin releasing hormone.  
OS *Trichosurus vulpecula* (Brush-tailed possum).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Metatheria; Diprotodontia; Phalangeridae; Trichosurus.  
OX NCBI\_TaxID=9337;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Lawrence S.B., McNally K.P., Fidler A.E.;  
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF193516; AAF07190.1; -; mRNA.  
DR GO; GO:0005576; Extracellular region; IEA.  
DR GO; GO:0005179; P.hormone activity; IEA.  
DR GO; GO:0007275; P.development; IEA.  
DR InterPro; IPR002012; GNRH.  
DR Pfam; PF00446; GNRH; 1.  
DR PROSITE; PS00473; GNRH; 1.  
KW Hormone.  
SQ SEQUENCE 75 AA; 8381 MW; 1C0E324492CA4283 CRC64;  
  
Query Match 3.0%; Score 7; DB 2; Length 75;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 88 GLEPSEE 94  
DB 42 GLEPSEE 48  
|||||  
O88460; MOUSE PRELIMINARY; PRT; 75 AA.  
  
RESULT 13  
O88460; MOUSE PRELIMINARY; PRT; 75 AA.  
AC O88460;  
DT 01-NOV-1998 (TREMBlrel. 08, Created)  
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE EGF-like growth factor receptor ErbB4 intracellular domain  
DE (Fragment).  
GN Name=ErbB4;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=CD-1; TISSUE=Uterus;  
RA Lim H., Das S.K., Dey S.K.;  
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF059177; AAC28334.1; -; mRNA.  
DR MGI; MGI:104771; ErbB4.  
DR GO; GO:0045165; P:cell fate commitment; IDA.  
DR GO; GO:0007507; P:heart development; IMP.  
DR GO; GO:007399; P:neurogenesis; IMP.  
KW Receptor.  
FT NON\_TER 1 1  
FT NON\_TER 75 75  
SQ SEQUENCE 75 AA; 8371 MW; 718C044B67673A70 CRC64;  
  
Query Match 3.0%; Score 7; DB 2; Length 75;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 47 BEYLVPO 53  
DB 2 BEYLVPO 8  
|||||  
O58HP9; MACMU PRELIMINARY; PRT; 84 AA.  
  
RESULT 14  
O58HP9; MACMU PRELIMINARY; PRT; 84 AA.  
AC O58HP9;  
DT 10-MAY-2005 (TREMBlrel. 30, Created)  
DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)  
DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)  
DE Cut-like 1 (Fragment).  
OS *Macaca mulatta* (rhesus macaque).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; OC Cercopitheidae; Cercopitheciinae; Macaca.  
OX NCBI\_TaxID=9544;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Roth C.L., Mastroianni C.A., Cabrera R., Mungenast A., Heger S., Jung H., Dubay C., Ojeda S.R.;  
RL "Gene Expression Profiling of the Nonhuman Primate Hypothalamus at the Time of Female Puberty Reveals Activation of Tumor Suppressor.";  
RT Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY950560; AAX44002.1; -; mRNA.  
FT NON\_TER 1 1  
FT NON\_TER 84 84  
SQ SEQUENCE 84 AA; 9190 MW; 57C48FE764827B20 CRC64;  
  
Query Match 3.0%; Score 7; DB 2; Length 84;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 102 APSEGAG 108  
DB 38 APSEGAG 44  
|||||  
EGFR; MACMU STANDARD; PRT; 85 AA.  
  
RESULT 15  
EGFR; MACMU STANDARD; PRT; 85 AA.  
AC P55245;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Epidermal growth factor receptor (EC 2.7.1.112) (Fragment).  
 GN Name:EGFR;  
 OS Macaca mulatta (Rhesus macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 OC Cercopithecoidea; Cercopithecinae; Macaca.  
 NCBI\_TaxID=9544;  
 [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Hypothalamus;  
 RX MEDLINE=95124501; PubMed=7545971;  
 RA Ma Y.J., Costa M.E., Ojeda S.R.;  
 RT "developmental expression of the genes encoding transforming growth  
 factor alpha and its receptor in the hypothalamus of female rhesus  
 macaques";  
 RL Neuroendocrinology 60:346-359(1994).  
 CC -1- FUNCTION: The EGF receptor mediates the biological signal of EGF,  
 and also of TGF-alpha, amphiregulin, heparin-binding EGF, GP30 and  
 vaccinia virus growth factor.  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein  
 tyrosine phosphate.  
 CC -1- SUBUNIT: Binds RPR1. Part of a complex with ERBB2 and either  
 PIK3C2A or PIK3C2B. The autophosphorylated form interacts with  
 PIK3C2B, maybe indirectly (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- TISSUE SPECIFICITY: Hypothalamus.  
 CC -1- DEVELOPMENTAL STAGE: Levels in the medial basal hypothalamus and  
 preoptic area are elevated during neonatal life (1 week-6 months),  
 decrease during juvenile development (8-18 months) and markedly  
 increase during the expected time of puberty (30-36 months).  
 CC -1- MISCELLANEOUS: Binding of EGF to the receptor leads to  
 dimerization, internalization of the EGF-receptor complex,  
 induction of the tyrosine kinase activity, stimulation of cell DNA  
 synthesis, and cell proliferation.  
 CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. EGF receptor  
 subfamily.  
 -----  
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 use as long as its content is in no way modified and this statement is not  
 removed.  
 -----  
 DR EMBL: S75916; AAB33095.1; -; mRNA.  
 DR F1R: I78540; I78540.  
 DR HSP: Q9H2C9; I14.  
 DR SW: P55245; 1-85.  
 DR InterPro: IPR000719; Prot\_kinase.  
 DR InterPro: IPR001245; Tyr\_kinase.  
 DR InterPro: IPR008266; Tyr\_kinase\_AS.  
 DR PRINTS: PR00109; TYRKINASE.  
 DR ProDom: PD000001; Prot\_kinase; 1.  
 DR PROSITE: PS00107; PROTEIN KINASE ATP; PARTIAL.  
 DR PROSITE: PS50011; PROTEIN KINASE DOM; 1.  
 DR PROSITE: PS00109; PROTEIN KINASE TYR; PARTIAL.  
 KW ATP-binding; Kinase; Nucleotide-Binding; Receptor; Transferase;  
 KW Tyrosine-protein kinase.  
 FT DOMAIN 1 77 Protein kinase.  
 FT NON\_TER 1 1  
 FT NON\_TER 85 85  
 SQ SEQUENCE 85 AA; 9866 MW; D812DF47C23B3C18 CRC64;  
 Query Match 3.0%; Score 7; DB 1; Length 85;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 MARDPDR 11  
 DB 79 MARDPDR 85

RESULT 16  
 Q8A014\_BACTN

ID Q8A014\_BACTN PRELIMINARY; PRT; 85 AA.  
 AC Q8A014;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 GN OrderedLocustNames=BT4037;  
 OS Bacteroides thetaiotaomicron.  
 OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;  
 OC Bacteroidaceae; Bacteroides.  
 NCBI\_TaxID=818;  
 [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=VPI-5482 / ATCC 29148;  
 RX MEDLINE=22550858; PubMed=1263928; DOI=10.1126/science.1080029;  
 RA Xu J., Bjurell M.K., Hamrod J., Deng S., Carmichael L.K.,  
 RA Chiang H.C., Hooper L.V., Gordon J.I.;  
 RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis";  
 RL Science 299:2074-2076(2003).  
 DR EMBL: AS016943; AA079142.1; -; Genomic\_DNA.  
 KW Complete proteome.  
 SQ SEQUENCE 85 AA; 9534 MW; 3A8BA1F1084BCA03 CRC64;  
 Query Match 3.0%; Score 7; DB 2; Length 85;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 23 ASPLDST 29  
 DB 56 ASPLDST 62

RESULT 18

QY 121 AKGIQSL 127  
 DB 73 AKGIQSL 79  
 Query Match 3.0%; Score 7; DB 2; Length 88;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,  
 RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,  
 RA Hijiya S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,  
 RA Ikono M., Itoh S., Itoh T., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K.,  
 RA Katsawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,  
 RA Machida K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,  
 RA Nagasaki H., Nakashima M., Nakama Y., Nakemichi Y., Nakamura M.,  
 RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,  
 RA Shimokawa T., Shomura A., Song J., Takazaki Y., Teresawa K., Tsuji K.,  
 RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshinaka R., Yukawa K.,  
 RA Yano M., Jiang J., Gojobori T., Ito H., Hahn J.H., Kim H.T., Eun M.Y.,  
 RA "The genome sequence and structure of rice chromosome 1.";  
 RT Nature 420:312-316(2002).  
 RL EMBL: AB001073; BAA89575.1; -; Genomic\_DNA.  
 DR Gramene; O9LJ15; -;  
 KW Hypothetical protein.  
 SQ SEQUENCE 96 AA; 9606 MW; 2AC6441717D52FP CRC64;  
 Query Match 3.0%; Score 7; DB 2; Length 96;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 77 STRSGG 83  
 DB 59 STRSGG 65  
 RESULT 22  
 Q0404G7 LEIMA PRELIMINARY; PRT; 99 AA.  
 AC Q0404G7;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DE Hypothetical protein.  
 GN ORFNames=lmfj3.0420;  
 OS Leishmania major.  
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.  
 OX NCBI\_TaxID=5664;  
 RX (1)  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Frledlin;  
 RA Beacock C.S., Murphy L., Ivens A.C., Bertman M., Blackwell J.,  
 RA Smith D., Collins M., Foster N., Harris D., Oliver K., O'Neill S.,  
 RA Saunders D., Seeger K., Warren T., Rajandream M., and Barrett B.G.;  
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.  
 RM EMBL: CT005270; CAJ05987.1; -; Genomic\_DNA.  
 KW Hypothetical protein.  
 SQ SEQUENCE 99 AA; 10713 MW; 82F2A39B24975BB4 CRC64;  
 Query Match 3.0%; Score 7; DB 2; Length 99;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 225 POGGAAP 231  
 DB 87 POGGAAP 93  
 RESULT 23  
 Q7VU19 BORPE PRELIMINARY; PRT; 99 AA.  
 AC Q7VU19;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Putative exported protein.  
 GN OrderedLocustNames=BP3099;  
 OS Bordetella pertussis.  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
 OC Alcaligenaceae; Bordetella.  
 OX NCBI\_TaxID=520;

RN [1]  
 RC STRAIN=Tohama I / ATCC BAA-589 / NCTC 13251;  
 RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;  
 RA Parkhill J., Sebatia M.T., Preston A., Murphy L.D., Thomson N.R.,  
 RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,  
 RA Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,  
 RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,  
 RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,  
 RA Felstead T., Goble A., Hamlin N., Hauser H., Holtroyd S., Jagsels K.,  
 RA Leather S., Mole S., Nobereczak H., O'Neill S., Ormond D., Price C.,  
 RA Rabbintowitach B., Rutter S., Sanders S., Saunders D., Seeger K.,  
 RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,  
 RA Unwin L., Whitehead S., Barrall B.G., Masekell D.J.;  
 RT "Comparative analysis of the genome sequences of Bordetella pertussis,  
 RT Bordetella parapertussis and Bordetella bronchiseptica.";  
 RL Nat. Genet. 35:32-40(2003).  
 DR EMBL: BX640420; CAB43367.1; -; Genomic\_DNA.  
 KW Complete proteome.  
 SQ SEQUENCE 99 AA; 9995 MW; 7F3C417E0B36BA25 CRC64;  
 Query Match 3.0%; Score 7; DB 2; Length 99;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 184 PAARPAG 190  
 DB 64 PAARPAG 70  
 RESULT 24  
 N1FW ANASP STANDARD; PRT; 105 AA.  
 AC Q441I9;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Nitrogenase stabilizing/protective protein n1fw.  
 GN Name=n1fw; OrderedLocustNames=all11433;  
 OS Anabaena sp. (strain PCC 7120).  
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.  
 OX NCBI\_TaxID=103690;  
 RX (1)  
 RP NUCLEOTIDE SEQUENCE.  
 RC Bulkema W.J., Scappino L.A., Haselkorn R.;  
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RX MEDLINE=21595285; PubMed=11759840;  
 RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,  
 RA Watanabe A., Iriuguchi M., Ishikawa A., Kawashima K., Kimura T.,  
 RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,  
 RA Nakazaki N., Shibata S., Sugimoto M., Takazawa M., Yamada M.,  
 RA Yasuda M., Tabata S.;  
 RT "Complete genomic sequence of the filamentous nitrogen-fixing  
 RT cyanobacterium Anabaena sp. strain PCC 7120.";  
 RL DNA Res. 8:205-213(2001).  
 CC -1- FUNCTION: May protect the nitrogenase Fe-Mo protein from oxidative  
 CC damage (By similarity).  
 CC -1- SUBUNIT: Homotrimer; associates with n1fd (By similarity).  
 CC -1- SIMILARITY: Belongs to the n1fw family.  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC EMBL: U47055; AA87952.1; -; Genomic\_DNA.  
 CC EMBL: BA000019; BAB73390.1; -; Genomic\_DNA.  
 CC PIR: AFI985; AFI985.  
 CC HAMAP: MF\_00529; -; 1.  
 DR InterPro: IPR004893; N1FW.

DR Pfam; PF03206; Nifw; 1.  
KM Complete proteome; Nitrogen fixation.  
SQ SEQUENCE 105 AA; 12262 MW; 496DF9B8ADB9B95F CRC64;  
Query Match 3.0%; Score 7; DB 1; Length 105;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 43 LVDAREY 49  
DB 11 LVDAREY 17  
RESULT 25  
OSQZX0 IDILO PRELIMINARY; PRT; 114 AA.  
ID OSQZX0 IDILO PRELIMINARY; PRT; 114 AA.  
AC OSQZX0;  
DT 01-FEB-2005 (TREMBlrel. 29, Created)  
DT 01-FEB-2005 (TREMBlrel. 29, Last sequence update)  
DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)  
DE Transposase Tra5 related protein.  
DE Name=tra5\_2; OrderedlocusNames=IL0051;  
OS Idiomarina lothiensis.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;  
OC Idiomarinaceae; Idiomarina.  
OX NCBI\_TaxId=135577;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=L2-TR / DSM 15497 / ATCC BAA-735;  
RX PubMed=15596722; DOI=10.1073/pnas.0407638102;  
RA Hou S., Saw J.H., Lee K.S., Freitas T.A., Belisle C., Kawarabayasi Y.,  
RA Domachke S.P., Pltkin A., Galperin M.Y., Koonin E.V., Makarova K.S.,  
RA Omelchenko M.V., Sorokin A., Wolf Y.I., Li Q.X., Krum Y.S.,  
RA Campbell S., Denery J., Aizawa S.-I., Shibata S., Malhotra A.,  
RA Alam M.;  
RT "Genome sequence of the deep-sea gamma-proteobacterium Idiomarina  
RT lothiensis reveals amino acid fermentation as a source of carbon and  
RT energy.";  
RU Proc. Natl. Acad. Sci. U.S.A. 101:18036-18041 (2004).  
DR EMBL; AF017340; AAV80895.1; -, Genomic\_DNA.  
KM Complete proteome.  
SQ SEQUENCE 114 AA; 12952 MW; 1C31899E1841D187 CRC64;  
Query Match 3.0%; Score 7; DB 2; Length 114;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 184 PAARPAG 190  
DB 83 PAARPAG 89  
RESULT 26  
OSJDA2 PYRKO PRELIMINARY; PRT; 115 AA.  
ID OSJDA2 PYRKO PRELIMINARY; PRT; 115 AA.  
AC OSJDA2;  
DT 10-MAY-2005 (TREMBlrel. 30, Created)  
DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)  
DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)  
DE SnorNP component, Garl homolog.  
DE OrderedlocusNames=TK2286;  
GN Pyrococcus kodakarensis (Thermococcus kodakarensis).  
OS Pyrococcus kodakarensis (Thermococcus kodakarensis).  
OC Archaea; Euryarchaeota; Thermococci; Thermococcaceae;  
OC Thermococcus.  
OX NCBI\_TaxId=69014;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=KOD1;  
RX PubMed=15710748; DOI=10.1101/gr.3003105;  
RA Fukui T., Atomi H., Kanai T., Matsumi R., Fujiwara S., Imanaka T.;  
RT "Complete genome sequence of the hyperthermophilic archaeon  
RT Thermococcus kodakarensis KOD1 and comparison with Pyrococcus  
RT genomes.";

RL Genome Res. 15:352-363 (2005).  
DR EMBL; AP006878; BAD86475.1; -, Genomic\_DNA.  
KM Complete proteome.  
SQ SEQUENCE 115 AA; 12737 MW; AA2ED15F21ACTD84 CRC64;  
Query Match 3.0%; Score 7; DB 2; Length 115;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 205 GVMKDV 211  
DB 39 GVMKDV 45  
RESULT 27  
OSJVO2 HUMAN PRELIMINARY; PRT; 117 AA.  
ID OSJVO2 HUMAN PRELIMINARY; PRT; 117 AA.  
AC OSJVO2;  
DT 10-MAY-2005 (TREMBlrel. 30, Created)  
DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)  
DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)  
DE OTTHUMP0000000474 (Fragment).  
GN ORNames=RP11-176F3.6-003;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;  
OC Homo.  
OX NCBI\_TaxId=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC Tacey A.;  
RA Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL139113; CA139660.1; -, Genomic\_DNA.  
FT NON TER 1  
SQ SEQUENCE 117 AA; 12034 MW; DA7B8F90E5ACEF0B CRC64;  
Query Match 3.0%; Score 7; DB 2; Length 117;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 173 POPSPR 179  
DB 93 POPSPR 99  
RESULT 28  
OSZBP4 STRCO PRELIMINARY; PRT; 120 AA.  
ID OSZBP4 STRCO PRELIMINARY; PRT; 120 AA.  
AC OSZBP4;  
DT 01-MAY-1999 (TREMBlrel. 10, Created)  
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)  
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)  
DE Putative regulatory protein.  
DE OrderedlocusNames=SC06459; ORNames=SC9B5.26c;  
GN Streptomyces coelicolor.  
OS Streptomyces coelicolor.  
OC Bacteria; Actinobacteria; Actinobacteriales;  
OC Streptomyces; Streptomyces.  
OX NCBI\_TaxId=1902;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=A3(2) / M145;  
RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;  
RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,  
RA Thomson N.R., James K.D., Harris D.B., Quail M.A., Kieser H.,  
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,  
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,  
RA Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neil S.,  
RA Rabinovitch E., Rajandream M.A., Rutherford K.M., Rutter S.,  
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,  
RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,  
RA Hopwood D.A.;  
RT "Complete genome sequence of the model actinomycete Streptomyces  
RT coelicolor A3(2).";

RL Nature 417:141-147(2002).  
DR EMBL: AL939127; CAA22768.1; -; Genomic\_DNA.  
DR F01; T35946; T35946.  
DR HSP; P30340; ISMT.  
DR GO; GO:0005622; C:intracellular; IEA.  
DR GO; GO:0003700; P:transcription factor activity; IEA.  
DR GO; GO:006355; P:regulation of transcription, DNA-dependent; IEA.  
DR GO; GO:0006350; P:transcription; IEA.  
DR InterPro; IPR001845; HTH\_Arse.  
DR InterPro; IPR011991; Wing\_hlx\_DNA\_bd.  
DR Pfam; PF01022; HTH\_5; 1.  
DR PRINTS; PRO0778; HTHARSR.  
DR SMART; SM00418; HTH\_Arse\_2; 1.  
DR PROSITE; PSS0987; HTH\_Arse\_2; 1.  
DR Cadmus; resistance; Complete proteome; DNA-binding; Transcription;  
KW Transcription regulation.  
SQ SEQUENCE 120 AA; 12840 MW; C345598BB098D423 CRC64;  
  
Query Match 3.0%; Score 7; DB 2; Length 120;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 179 PRSPLP 185  
DB 46 PRSPLP 52  
  
RESULT 29  
QSGSH5 ORYSA PRELIMINARY; PRT; 121 AA.  
ID QSGSH5 ORYSA PRELIMINARY; PRT; 121 AA.  
AC QSGSH5;  
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 29, Last annotation update)  
DE Hypothetical protein P0418E08.129 (Hypothetical protein  
DE C01341 A08.107).  
GN Name:P0418E08.129; Synonyms:C01341 A08.107;  
OS Oryza sativa (Japonica cultivar-group).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzaceae; Oryza.  
OX NCBI\_TaxID=39947;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Sasaki T., Matsumoto T., Yamamoto K.;  
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RA Sasaki T., Matsumoto T., Yamamoto K.;  
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RA Sasaki T., Matsumoto T., Yamamoto K.;  
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, BAC  
RT clone:OJ1341 A08.";  
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AP004382; BAC16086.1; -; Genomic DNA.  
DR EMBL; AP003754; BAC30199.1; -; Genomic DNA.  
DR Gramene; QSGSH5; -;  
KW Hypothetical protein.  
SQ SEQUENCE 121 AA; 12512 MW; 1E104206D3A7FDB8 CRC64;  
  
Query Match 3.0%; Score 7; DB 2; Length 121;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 97 PRSPLP 103  
DB 72 PRSPLP 78  
  
RESULT 30  
Q7PLP6 DROME PRELIMINARY; PRT; 125 AA.  
AC Q7PLP6;  
DT 01-MAR-2004 (TREMBlrel. 26, Created)  
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)

DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
DE CG40207-PA.3.  
GN ORFNames=CG40207;  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22426065; PubMed=12537568;  
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,  
RA Patel S., Adams M., Champagne M., Dugan S.P., Friese E., Hodgson A.,  
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,  
RA Pacile J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
RA Svirskae R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
RA Weinstein G., Scherer S.B., Myers E.W., Gibbs R.A., Rubin G.M.,  
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila  
RT melanogaster euchromatic genome sequence."  
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22426071; PubMed=12537574;  
RA Hoskins R.A., Smith C.D., Carlson J.W., Carvalho A.B., Halpern A.,  
RA Kaminker J.S., Kennedy C., Mungall C.J., Sullivan B.A., Sutton G.G.,  
RA Yasuhara J.C., Wakimoto B.T., Myers E.W., Celniker S.E., Rubin G.M.,  
RA Karpen G.H.;  
RT "Heterochromatic sequences in a Drosophila whole-genome shotgun  
RT assembly."  
RL Genome Biol. 3:RESEARCH0085.1-RESEARCH0085.16 (2002).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RA Adams M.D., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G.,  
RA Li P.W., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D.,  
RA Zhang Q., Chen L.X., Brandon R.C., Rogers Y.H., An H.J., Baxendale J.,  
RA Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J.,  
RA Beasley E.M., Beeson K.Y., Bhandari D., Bolanos R.A., Busam D.A.,  
RA Center A., Chandra I., Dahlke C., Davenport L.B., Davies P.,  
RA Delcher A., Deng Z., Dove D., Dew I., Dietz S.M., Dodson K.,  
RA Doup L.E., Dunn P., Evangelista C.C., Ferrieres S., Flanagan M.J.,  
RA Foster C., Gabrielian A.B., Gary N.S., Glasser K., Glodek A., Gong F.,  
RA Gu Z., Guan P., Halpern A.L., Harris M., Heiman T.J., Houck J.,  
RA Hostin D., Howland T.J., Wei M.H., Ibegwan C., Jalili M., Kalish F.,  
RA Ke Z., Ketchum K.A., Kodira C.D., Kraft C., Kravitz S., Lai Z.,  
RA Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X.,  
RA Maizels B., McIntosh T.C., McPherson D., Merkulov G., Miller J.R.,  
RA Milshina N.V., Mobarry C., Moy M., Murphy B., Nelson K.A.,  
RA Nuskern D.R., Pittman G.S., Pan S., Pollard J., Puri V., Reinert K.,  
RA Remington K., Scheeler F., Shue B.C., Siden-Kiamos I., Simpson M.,  
RA Skupski M.P., Smith T., Spier E., Strong R., Sun B., Tector C.,  
RA Turner R., Venter E., Wang A.H., Wang X., Wang Z.Y., Williams S.M.,  
RA Woodage T., Wu D., Yao Q.A., Ye J., Zaveri J.S., Zhan M., Zhang G.,  
RA Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhu S., Zhu X.,  
RA Smith H.O., Myers E.W., Venter J.C.;  
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RA Smith C.D., Acevedo D., Carlson J.W., Hoskins R.A., Kennedy C.,  
RA Mungall C.J., Yandell M.D., Celniker S.E., Karpen G.H.;  
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB001002422; EAA46276.1; -; Genomic DNA.  
DR Ensembl; CG40207; Drosophila melanogaster.  
SQ SEQUENCE 125 AA; 13549 MW; A574074BB2A1B54 CRC64;  
  
Query Match 3.0%; Score 7; DB 2; Length 125;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 182 PLPAP 188  
DB 29 PLPAP 35

```

RESULT 31
O6BXP3 DEBHA PRELIMINARY; PRT; 128 AA.
ID O6BXP3 DEBHA PRELIMINARY; PRT; 128 AA.
AC O6BXP3 DEBHA PRELIMINARY; PRT; 128 AA.
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Debaryomyces hanseii chromosome B of strain CBS767 of Debaryomyces
DE hanseii.
GN Ordered locus names=DEHA0B013649;
OS Debaryomyces hanseii (yeast) (Torulaepora hanseii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Debaryomycetes.
OX NCBI_TaxID=4959;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 36239 / CBS 767;
RX PubMed=1529592; DOI=10.1038/nature02579;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
RA Goffard N., Frangoul L., Aigle M., Anthonard V., Babour A., Barde V.,
RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
RA Boissarie A., Boyer J., Cattoir L., Confanier F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Gropi A.,
RA Hantreya F., Heneguin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerret A., Koszul R., Lemaire M., Lesur I., Ma L., Müller H.,
RA Nicoud J.-M., Nikolaki M., Ozias S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Sureau A.,
RA Sennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zenou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudon B., Scarpelli C., Gallardin C., Weissenbach J.,
RA Wincker P., Souciet J.-L.;
RT "Genome evolution in yeasts.";
RU Nature 430:35-44(2004)
DR EMBL; CR382134; CNG85011.1; -; Genomic_DNA.
DR InterPro; IPR005341; UPF0108.
DR Pfam; PF03656; Paml6; 1.
DR ProDom; PD311402; UPF0108; 1.
KM Complete proteome.
SQ SEQUENCE 128 AA; 13894 MW; D2844494C5E1BD35 CRC64;

Query Match 3.0%; Score 7; DB 2; Length 128;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 TPOGGA 230
DB 35 TPOGGA 41

RESULT 32
O6D9H7 ERWCT PRELIMINARY; PRT; 131 AA.
ID O6D9H7 ERWCT PRELIMINARY; PRT; 131 AA.
AC O6D9H7 ERWCT PRELIMINARY; PRT; 131 AA.
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Putative membrane protein.
GN Ordered locus names=ECAD0638;
OS Erwinia carotovora (bubsp. atroseptica) (Pectobacterium atrosepticum).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Pectobacterium.
OX NCBI_TaxID=29471;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=SCRI 1043 / ATCC BAA-672;
RX PubMed=1523089; DOI=10.1073/pnas.0402424101;
RA Bell K.S., Sebahia M., Pritchard L., Holden M.T.G., Hyman L.J.,
RA Holava M.C., Thomson N.R., Bentley S.D., Churcher L.J.C., Mungall K.,
RA Atkin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.,
RA Frazer A., Hance Z., Hauser H., Jagels K., Moule S., Norbertcak H.,
RA Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
RA Salmond G.P.C., Birch P.R.J., Parkhill J., Toth I.K.;

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RT "Genome sequence of the enterobacterial phytopathogen Erwinia
RT carotovora subsp. atroseptica and characterization of virulence
RT factors.";
RU Proc. Natl. Acad. Sci. U.S.A. 101:11105-11110(2004).
DR EMBL; BX950851; CAG73553.1; -; Genomic_DNA.
DR InterPro; IPR011309; UCP009726.
DR PIRSF; PIRSF009726; UCP009726; 1.
KM Complete proteome.
SQ SEQUENCE 131 AA; 14322 MW; 4A94397D34B150A7 CRC64;

Query Match 3.0%; Score 7; DB 2; Length 131;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 RSLLED 38
DB 123 RSLLED 129

RESULT 33
O6YV89 9CAUD PRELIMINARY; PRT; 135 AA.
ID O6YV89 9CAUD PRELIMINARY; PRT; 135 AA.
AC O6YV89 9CAUD PRELIMINARY; PRT; 135 AA.
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE InterPro; IPR011309; UCP009726.
DE Hypothetical protein.
OS Bacteriophage VMB.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
OC Lambda-like viruses.
OX NCBI_TaxID=10702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=9536309; PubMed=7611876;
RA Anne J., Piten P., Van Mellaert L., Joris B., Opdenakker G.,
RA Eysen H.;
RT "Analysis of the open reading frames of the main capsid proteins of
RT actinophage VMB.";
RU Arch. Virol. 140:1033-1047(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=9908696; PubMed=9884227;
RA Van Mellaert L., Mel L., Lammerlyn E., Schacht S., Anne J.;
RT "Site-specific integration of bacteriophage VMB genome into
RT Streptomyces venezuelae and construction of a VMB-based integrative
RT vector.";
RU Microbiology 144:3351-3358(1998).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=91037942; PubMed=2230721;
RA Anne J., Van Mellaert L., Decock B., Van Damme J., Van Aerschoot A.,
RA Herdewijn P., Eysen H.;
RT "Further biological and molecular characterization of actinophage
RT VMB.";
RU J. Gen. Microbiol. 136:1365-1372(1990).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15629775; DOI=10.1016/j.virol.2004.10.028;
RA Van Dessel W., Van Mellaert L., Liesegang H., Raasch C.,
RA De Keersmaeker S., Geukens N., Lammerlyn E., Streit W., Anne J.;
RT "Complete genomic nucleotide sequence and analysis of the temperate
RT bacteriophage VMB.";
RU Virology 331:325-337(2005).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RA Van Dessel W., Van Mellaert L., Raasch C., Liesegang H., Streit W.,
RA Anne J.;
RT "Nucleotide sequence analysis of Streptomyces venezuelae bacteriophage
RT VMB.";
RU (in) Unknown A. (eds.);
MICROBIAL IMMUNE EVASION STRATEGIES: MEETING OF THE BELGIAN SOCIETY
RU FOR MICROBIOLOGY, pp.30-30, Unknown Publisher (2003).
RN [6]

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RP NUCLEOTIDE SEQUENCE.  
 RA Anne J.F.C.;  
 RL Submitted (MAY-1993) to the EMBL/GenBank/DBJ databases.  
 RN [7]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Van Meillaert L.M.G.;  
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.  
 RN [8]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Van Dessel W., Van Meillaert L., Raasch C., Liesegang H., Streit W.,  
 RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY320035; AAR29748.1; -; Genomic\_DNA.  
 KW Hypothetical protein.  
 SQ SEQUENCE 135 AA; 14696 MW; 40B13987CA4DD477 CRC64;

Query Match 3.0%; Score 7; DB 2; Length 135;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 PASPLDS 28  
 DB 60 PASPLDS 66

RESULT 34  
 Q7UR6\_RHOBA  
 ID Q7UR6\_RHOBA PRELIMINARY; PRT; 135 AA.  
 AC Q7UR6;  
 DT 01-OCT-2003 (TREMBlrel. 25, Created)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 GN OrderedLocustNames=RB3125;  
 OS Rhodospirillum rubrum.  
 OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;  
 OC Planctomycetaceae; Pirellula.  
 NCBI\_TaxId=117;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=1;  
 RX MEDLINE=2735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;  
 RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardoc T.,  
 RA Ludwig W., Gade D., Beck A., Borzym K., Heltmann K., Rabus R.,  
 RA Schiesner H., Mann R., Reinhardt R.;  
 RT "Complete genome sequence of the marine planctomycete Pirellula sp.  
 RT strain 1.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303 (2003).  
 DR EMBL; BX294138; CAD73011.1; -; Genomic\_DNA.  
 KW Complete proteome; Hypothetical protein.  
 SQ SEQUENCE 135 AA; 14862 MW; 83B9F9FCBA53DPF2 CRC64;

Query Match 3.0%; Score 7; DB 2; Length 135;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 RSGGCDL 85  
 DB 108 RSGGCDL 114

RESULT 35  
 Q75T02\_RABIT  
 ID Q75T02\_RABIT PRELIMINARY; PRT; 136 AA.  
 AC Q75T02;  
 DT 05-JUL-2004 (TREMBlrel. 27, Created)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
 DE Interleukin 1 receptor molecule-1 (Fragment).  
 GN Name=ICAM-1;  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;

OC Oryctolagus.  
 OX NCBI\_TaxId=9986;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Murata T.;  
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB128157; BAD04920.1; -; mRNA.  
 FT NON TER 1 136  
 SQ SEQUENCE 136 AA; 14755 MW; 42EC3FPA18CB2B23 CRC64;

Query Match 3.0%; Score 7; DB 2; Length 136;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 SSSTRSG 81  
 DB 108 SSSTRSG 114

RESULT 36  
 O67TP2\_ORYSA  
 ID O67TP2\_ORYSA PRELIMINARY; PRT; 136 AA.  
 AC O67TP2;  
 DT 25-OCT-2004 (TREMBlrel. 28, Created)  
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)  
 DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)  
 DE Hypothetical protein B1342C04.50 (Hypothetical protein  
 DE B1045B05.3).  
 GN Name=B1342C04.50; Synonym=B1045B05.3;  
 OS Oryza sativa (Japanese cultivar-group).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Rharotideae; Oryzaceae; Oryza.  
 NCBI\_TaxId=39947;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Sasaki T., Matsumoto T., Katayose Y.;  
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 9, BAC  
 RT clone:B1342C04.50";  
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Sasaki T., Matsumoto T., Katayose Y.;  
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 9, BAC  
 RT clone:B1045B05.3";  
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AP006057; BAD38479.1; -; Genomic\_DNA.  
 DR EMBL; AP005891; BAD38365.1; -; Genomic\_DNA.  
 DR Gramene; O67TP2;  
 KW Hypothetical protein.  
 SQ SEQUENCE 136 AA; 14817 MW; CF4D7ACADA37386 CRC64;

Query Match 3.0%; Score 7; DB 2; Length 136;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 185 AARPAGA 191  
 DB 32 AARPAGA 38

RESULT 37  
 O699F3\_9HIV1  
 ID O699F3\_9HIV1 PRELIMINARY; PRT; 137 AA.  
 AC O699F3;  
 DT 25-OCT-2004 (TREMBlrel. 28, Created)  
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)  
 DE Gag protein (Fragment).  
 GN Name=gag;  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;

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OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=01CM2213;
RX PubMed=15577423;
RA Ndembi N., Takehisa J., Zekeng L., Kobayashi E., Nganop C.,
 Songok E.M., Kageyama S., Takemura T., Ido E., Hayami M., Kapteue L.,
 Ichimura H.;
RA "Genetic Diversity of HIV Type 1 in Rural Eastern Cameroon.";
RT J. Acquir. Immune Defic. Syndr. 37:1641-1650(2004).
RL EMBL; AY535583; AAT1000.1; -; Genomic_DNA.
DR SMR; O699F3; 3-81.
DR GO; GO:0019013; C:Viral nucleocapsid; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0016032; F:viral life cycle; IEA.
DR InterPro; IPR00721; Gag_p24.
DR InterPro; IPR01878; Znf_CCHC.
DR Pfam; PF00607; Gag_p24; 1.
DR Pfam; PF00098; zf-CCHC; 1.
DR PRINTS; PR00939; C2HCZNRNGR.
DR SMART; SM00343; Znf_C2HC; 1.
DR PROSITE; PS50158; ZF_CCHC; 1.
KM Core protein; Metal-binding; Zinc; Zinc-finger.
PT NON_TER
SQ SEQUENCE 137 AA; 15329 MW; 21BB33CEDC893BE CRC64;

Query Match 3.0%; Score 7; DB 2; Length 137;
Best Local Similarity 100.0%; Pred.No.2.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 189 AGATLIER 195
DB 69 AGATLIER 75

RESULT 38
Q97JX6_CLOAB
AC Q97JX6;
ID Q97JX6_CLOAB PRELIMINARY; PRT; 138 AA.
DT 01-OCT-2001 (TREMBlrel. 18, Created)
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Hypothetical protein CAC1147.
GN OrderedLocNames=CAC1147;
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 Clostridium.
OX NCBI_TaxID=1488;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=1466286;
RX DOI=10.1128/JB.183.16.4823-4838.2001;
RA Gsellling J., Breton G., Omeichenko M.V., Makarova K.S., Zeng Q.,
 Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
 Tatusov R.L., Sabathe F., Doucette-Stamm L.A., Soucille F.,
 Dally M.J., Bennett G.N., Koonin E.V., Smith D.R.;
RT "Genome sequence and comparative analysis of the solvent-producing
 bacterium Clostridium acetobutylicum.";
RL J. Bacteriol. 183:4823-4838(2001).
DR EMBL; AE007631; AAK79119.1; -; Genomic_DNA.
KM Complete proteome; Hypothetical protein.
SQ SEQUENCE 138 AA; 16453 MW; 99A7841D39ADE687 CRC64;

Query Match 3.0%; Score 7; DB 2; Length 138;
Best Local Similarity 100.0%; Pred.No.2.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 LGLPSE 93

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DB 37 LGLPSE 43

RESULT 39
Q81Y7_PLAF7
ID Q81Y7_PLAF7 PRELIMINARY; PRT; 140 AA.
AC Q81Y7;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical protein.
GN ORENAMES=PF11_0015;
OS Plasmodium falciparum (Isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22255705; PubMed=12368864; DOI=10.1038/nature01097;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
 Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
 Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
 Chan M.-S., Nene V., Shallow S.J., Sub B., Peterson J., Angiuoli S.,
 Pereira M., Allen J., Selengut J., Hart D., Mather M.W., Vaidya A.B.,
 Martin D.M.A., Fairlamb A.H., Fraunholz M.U., Roos D.S., Ralph S.A.,
 McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
 Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
 Fraser C.M., Barrett B.G.;
RA "Genome sequence of the human malaria parasite Plasmodium
 falciparum.";
RT Nature 419:498-511(2002).
RL EMBL; AE014836; AAN35612.1; -; Genomic_DNA.
KM Hypothetical protein.
SQ SEQUENCE 140 AA; 16578 MW; 1B1CF83FDB15EAF6 CRC64;

Query Match 3.0%; Score 7; DB 2; Length 140;
Best Local Similarity 100.0%; Pred.No.2.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 AKGLQSL 127
DB 125 AKGLQSL 131

RESULT 40
O8XOM8_RALSO
ID O8XOM8_RALSO PRELIMINARY; PRT; 142 AA.
AC O8XOM8;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE PROBABLE PROLINE RICH TRANSMEMBRANE PROTEIN.
GN OrderedLocNames=RSpl194; ORFNAMES=RS03138;
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 Burkholderia; megaplasmid.
OX NCBI_TaxID=305;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GM1100;
RX MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangot S.,
 Arlat M., Billault A., Broctier P., Camus J.C., Cartolico L.,
 Chandler M., Choisme N., Claudel-Renard C., Cunac S., Demange N.,
 Gaspin C., Lavie M., Moisan A., Robert C., Sautin W., Schlex T.,
 Sigister P., Trebault P., Whalen M., Wincker P., Levy M.,
 Weisenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
DR EMBL; AL646083; CAD18345.1; -; Genomic_DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR005590; DUF333.

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DR Pfam; PF03691; DUF333; 1.  
 KW Complete proteome; Plasmid; Transmembrane.  
 SO SEQUENCE 142 AA; 14319 MW; 7A55E24890DF441 CRC64;

Query Match 3.0%; Score 7; DB 2; Length 142;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 77 TRSGGG 83  
 DB 111 TRSGGG 117

## RESULT 41

OS11G9\_ENTH1 PRELIMINARY; PRT; 148 AA.  
 AC OS11G9;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Hypothetical protein.  
 OS Entamoeba histolytica HM-1:IMSS.  
 GN ORFNames=102.t00008;  
 OC Eukaryota; Entamoebidae; Entamoeba.  
 NCBI\_TaxId=294381;

## NUCLEOTIDE SEQUENCE.

RP STRAIN=HM-1:IMSS;  
 RX PubMed=15729342; DOI=10.1038/nature03291;  
 RA Lofthus B., Anderson I., Davies R., Almark U.C., Samuelson J.,  
 RA Amedeo P., Roncaglia P., Bertman M., Hirt R.P., Mann B.J., Nozaki T.,  
 RA Suh B., Pop M., Duchene M., Ackers J., Tannich E., Leippe M.,  
 RA Chillingworth T., Churche K., Hance Z., Harris B., Harris D.,  
 RA Jagella K., Moule S., Mungall K., Ormond D., Squares R., Whitehead S.,  
 RA Quail M.A., Rabinowitch E., Norbertczak H., Price C., Wang Z.,  
 RA Guillen N., Glickstein C., Stroup S.E., Bhattacharya S., Lohia A.,  
 RA Foster P.G., Sticheritz-Ponten T., Weber C., Singh U., Mukherjee C.,  
 RA El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M., Barrett B.,  
 RA Fraser C.M., Hall N.;  
 RT "The genome of the protist parasite Entamoeba histolytica.";  
 RL Nature 433:865-868(2005).  
 CC -1- CAUTION: The sequence shown here is derived from an  
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 preliminary data.  
 CC EMBL; GenBank; DBJ  
 CC EMBL; AAFB01000364; EAL47492.1; -; Genomic\_DNA.  
 DR EMBL; AAFB01000364;  
 KW Hypothetical protein.  
 SO SEQUENCE 148 AA; 17319 MW; 6D0803B90F057FDE CRC64;

Query Match 3.0%; Score 7; DB 2; Length 148;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 TRSGGG 84  
 DB 22 TRSGGG 28

## RESULT 42

OSNUT6\_9ACTO PRELIMINARY; PRT; 155 AA.

AC OSNUT6;  
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)  
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)  
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)  
 DE Hypothetical protein ORF15.  
 GN Name=ORF15;  
 OS Streptomyces albulus.  
 CC Plasmid pNO33.  
 CC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 CC Streptomycineae; Streptomycetaceae; Streptomycetes.  
 NCBI\_TaxId=68570;  
 RN [1]

## NUCLEOTIDE SEQUENCE.

RP STRAIN=IFO 14147;  
 RA Kawai T., Inoue S.;  
 RT "Complete Sequence of the Plasmid pNO33 from Streptomyces albulus  
 RT IFO14147.";  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB058947; BAD80773.1; -; Genomic\_DNA.  
 DR GO; GO:0003677; P:DNA binding; IEA.  
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro; IPR001187; HTH\_3.  
 DR Pfam; PF01381; HTH\_3; 2.  
 DR SMART; SM00530; HTH\_XRB; 2.  
 DR PROSITE; PS00943; HTH\_CROCI; 2.  
 KW Hypothetical protein; Plasmid.  
 SO SEQUENCE 155 AA; 16884 MW; 5687DEB1FE53DC2F CRC64;

Query Match 3.0%; Score 7; DB 2; Length 155;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAPSGA 107  
 DB 68 LAPSGA 74

## RESULT 43

OSF4Y1\_NEIG1 PRELIMINARY; PRT; 161 AA.  
 AC OSF4Y1;  
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
 DE Hypothetical protein.  
 GN OrderedCusNames=NGO2162;  
 OS Neisseria gonorrhoeae (strain ATCC 700825 / FA 1090).  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
 OC Neisseriaceae; Neisseria.  
 NCBI\_TaxId=242231;

## NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RP Lewis L.A., Gillaspay A.F., McLaughlin R.E., Gipson M., Ducey T.F.,  
 RA Ombey T., Hartman K., Nydick C., Carson M.B., Vaughn J., Thomson C.,  
 RA Song L., Lin S., Yuan X., Najaf F., Zhan F., Ren Q., Zhu H., Qi S.,  
 RA Kenion S.M., Lai H., White J.D., Clifton S., Roe B.A., Dyer D.W.;  
 RT "The complete genome sequence of Neisseria gonorrhoeae.";  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB004969; AAW90756.1; -; Genomic\_DNA.  
 DR InterPro; IPR004027; SEC\_C\_motif.  
 DR Pfam; PF02810; SEC-C; 2.  
 KW Complete proteome; Hypothetical protein.  
 SO SEQUENCE 161 AA; 18035 MW; ACFB74F0A12B5877 CRC64;

Query Match 3.0%; Score 7; DB 2; Length 161;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 141 DPTVPLP 147  
 DB 129 DPTVPLP 135

## RESULT 44

OS65MNO\_MANSN PRELIMINARY; PRT; 161 AA.

AC OS65MNO;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Hypothetical protein  
 GN OrderdCusNames=MS0033;  
 OS Mannheimia succiniciproducens (strain MBE155E).  
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
 OC Pasteurellaceae; Mannheimia.

OK NCBI\_TaxID=221988;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=15378067; DOI=10.1038/nbt1010;  
RA Hong S.H., Kim J.S., Lee S.Y., In Y.H., Choi S.S., Rih J.-K.,  
RA Kim C.H., Jeong H., Hur C.G., Kim J.U.,  
RT "The genome sequence of the capnophilic rumen bacterium Mannheimia  
RT succiniciproducens".  
RL Nat. Biotechnol. 22:1275-1281(2004).  
DR EMBL, AB016827; AAU36640.1; -; Genomic\_DNA.  
DR InterPro, IPR004027; SEC\_C\_motif.  
DR Pfam; PF02810; SEC\_C\_2.  
DR Complete proteome; Hypothetical protein.  
SQ SEQUENCE 161 AA; 18249 MW; B371B2C548B9DE91 CRC64;  
  
Query Match 3.0%; Score 7; DB 2; Length 161;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 141 DPTVPLP 147  
DB 133 DPTVPLP 139  
  
RESULT 45  
OBH8T1 ORYSA PRELIMINARY; PRT; 164 AA.  
ID OBH8T1 ORYSA PRELIMINARY;  
AC OBH8T1  
DT 01-MAR-2003 (TRENBLrel. 23, Created)  
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)  
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
DE Hypothetical protein OJ1523\_A02.9.  
GN Name=OJ1523\_A02.9;  
OS Oryza sativa (japonica cultivar-group).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzaceae; Oryza.  
OX NCBI\_TaxID=39947;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,  
RA Overton I.L., Talcott T., Kim M.W., Bera J.U., Jin S.S.,  
RA Vanden D.W., Tallon L.J., Koo H., Ziemann V., Haiso J., Blunt S.,  
RA Fankesh S.S., Riedmuller S.B., Ulterback T.T., Feldblyum T.V.,  
RA Yang Q.O., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,  
RA White O., Salzberg S.L., Fraser C.M.,  
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RA Buell R.;  
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL, AC090874; AAN08215.1; -; Genomic\_DNA.  
DR Gramene; OBH8T1; -;  
DR GO; GO:0005489; F:electron transporter activity; IEA.  
DR GO; GO:0006118; P:electron transport; IEA.  
KW Hypothetical protein.  
SQ SEQUENCE 164 AA; 17643 MW; 0932D550E724E717 CRC64;  
  
Query Match 3.0%; Score 7; DB 2; Length 164;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 72 RHRSSST 78  
DB 120 RHRSSST 126  
  
RESULT 46  
OS7P2\_9TRYP PRELIMINARY; PRT; 165 AA.  
ID OS7P2\_9TRYP PRELIMINARY;  
AC OS7P2\_9TRYP PRELIMINARY;  
DT 10-MAY-2005 (TRENBLrel. 30, Created)  
DT 10-MAY-2005 (TRENBLrel. 30, Last sequence update)



DT 10-MAY-2005 (TRENBLrel. 30, Last annotation update)  
DE Ecotin, putative.  
GN ORFNames=TB927.5.1730;  
OS Trypanosoma brucei.  
OC Eukaryota; Eukaryota; Kinetoplastida; Trypanosomatidae; Trypanosoma.  
OX NCBI\_TaxID=5691;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=GUrat10.1;  
RA Ghedin E., Blandin G., Bartholomeu D., Caler E., Haas B., Hannick L.,  
RA Shalom U., Hou L., Djikeng A., Feldblyum T., Hostetler J.,  
RA Johnson J., Jones K., Koo H.L., Larkin C., Pai G., Peterson J.,  
RA Khalak H.G., Salzberg S., Simpson A.J., Tallon L., Van Aken S.,  
RA Wamless D., White O., Wortman J., Fraser C.M., El-Sayed N.M.A.;  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=GUrat10.1;  
RA El-Sayed N.M., Khalak H., Adams M.D.;  
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=GUrat10.1;  
RA Haas B., Blandin G., El-Sayed N.;  
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.  
EMBL, AC104617; AAX79124.1; -; Genomic\_DNA.  
SQ SEQUENCE 165 AA; 19342 MW; EE06716BBE515476 CRC64;  
  
Query Match 3.0%; Score 7; DB 2; Length 165;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 175 PPSPPREG 181  
DB 33 PPSPPREG 39  
  
RESULT 47  
OENIG2 CORDI PRELIMINARY; PRT; 167 AA.  
ID OENIG2 CORDI PRELIMINARY;  
AC OENIG2  
DT 05-JUL-2004 (TRENBLrel. 27, Created)  
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
GN OrderedLocNames=DIP0813;  
OS Corynebacterium diptheriae.  
OC Bacteria; Actinobacteria; Actinobacteriales;  
OC Corynebacteriaceae; Corynebacteriaceae; Corynebacterium.  
OX NCBI\_TaxID=1717;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Biotype graveis / NCTC 13129;  
RX MEDLINE=22965443; PubMed=14602910; DOI=10.1093/nar/gkg874;  
RA Cerdeno-Tarraga A.-M., Bistratou A., Dover L.G., Holden M.T.G.,  
RA Pallen M.J., Bentley S.D., Beera G.S., Church C.M., James K.D.,  
RA De Zuyva A., Chillingworth T., Cronin A., Dowd L., Feldblyum T.,  
RA Hamlin N., Holtroyd S., Jagels K., Moule S., Quail M.A.,  
RA Rabinowitch E., Rutherford K.M., Thomson N.R., Unwin L.,  
RA Whitehead S., Barrett B.G., Parkhill J.,  
RT "The complete genome sequence and analysis of Corynebacterium  
RT diptheriae NCTC13129".  
RL Nucleic Acids Res. 31:6516-6523(2003).  
DR EMBL, BX248356; CAB49331.1; -; Genomic\_DNA.  
KW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 167 AA; 18627 MW; 48F57F331105DCD0 CRC64;  
  
Query Match 3.0%; Score 7; DB 2; Length 167;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 101 LAPSEGA 107

Db 53 LAPSEGA 59

## RESULT 48

ID Q6NMZ6\_BDEBA PRELIMINARY; PRT; 168 AA.

AC Q6NMZ6;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Flagellar protein FlL.

GN Name=flL; OrderedlocusNames=Bd1076;

OS Bdellovibrio bacteriovorus.

OC Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;

OC Bdellovibrionaceae; Bdellovibrio.

NCBI\_TaxID=959;

OK NCB1\_TaxID=959;

RN NUCLEOTIDE SEQUENCE.

RC STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;

RX PubMed=14752164; DOI=10.1126/science.1093027;

RA Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,

RA Keller H., Lambert C., Evans K.J., Goessmann A., Meyer F.,

RA Sockert R.E., Schuster S.C.;

RT "A predator unmasked: life cycle of Bdellovibrio bacteriovorus from a

RT genomic perspective.";

RL Science 303:689-692(2004).

EMBL BX4248; CAB79003.1; -; Genomic DNA.

DR GO; GO:0009425; C:flagellar basal body (sensu Bacteria); IEA.

DR GO; GO:0006935; P:chemotaxis; IEA.

DR GO; GO:0001539; P:ciliary or flagellar motility; IEA.

DR InterPro: IPR005503; FlL.

DR Pfam PF03748; FlL; 1.

KM Complete proteome; Flagellum.

SQ SEQUENCE 168 AA; 18796 MW; 23B42DC5E920E15 CRC64;

Query Match 3.0%; Score 7; DB 2; Length 168;

Best Local Similarity 100.0%; Pred. No. 2, 9e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 205 GVYKDV 211

DB 155 GVYKDV 161

## RESULT 49

ID Q5W9T4\_CHLRE PRELIMINARY; PRT; 175 AA.

AC Q5W9T4;

DT 01-FEB-2005 (TrEMBLrel. 29, Created)

DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)

DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)

DE Lhc-like protein Lh1.

GN Name=Lh1;

OS Chlamydomonas reinhardtii.

OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae;

OC Chlamydomonadales; Chlamydomonadales; Chlamydomonas.

NCBI\_TaxID=3055;

OK NCB1\_TaxID=3055;

RN NUCLEOTIDE SEQUENCE.

RP PubMed=15509845; DOI=10.1093/pcp/pch157;

RX Teramoto H., Itoh T., Ono T.;

RT "High-Intensity-Light-Dependent and Transient Expression of New Genes

RT Encoding Distant Relatives of Light-Harvesting Chlorophyll-a/b

RT Proteins in Chlamydomonas reinhardtii.";

RL Plant Cell Physiol. 45:1221-1232(2004).

EMBL AB159046; BAB67134.1; -; mRNA.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0009765; P:photosynthesis light harvesting; IEA.

DR InterPro: IPR001344; Chlora\_Abblnd.

DR Pfam PF00504; Chloroa\_b-bind; 1.

SQ SEQUENCE 175 AA; 18747 MW; 2EE5EBE33614851 CRC64;

Query Match 3.0%; Score 7; DB 2; Length 175;

Best Local Similarity 100.0%; Pred. No. 3e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 209 DVYAFGG 215

DB 51 DVYAFGG 57

## RESULT 50

ID Q5BG62\_EMENI PRELIMINARY; PRT; 176 AA.

AC Q5BG62;

DT 10-MAY-2005 (TrEMBLrel. 30, Created)

DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)

DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)

DE Hypothetical protein.

GN ORFNames=AN0468.2;

OS Aspergillus nidulans FGSC A4.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

OC Eurotiiales; Trichocomaceae; Emericella.

NCBI\_TaxID=227321;

OK NCB1\_TaxID=227321;

RN NUCLEOTIDE SEQUENCE.

RC STRAIN=FGSC A4;

RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,

RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavsky L.,

RA Bouhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,

RA Choepel Y., Collymore A., Cook A., Cooke P., Conum B., Dearellano K.,

RA Diaz J.S., Dodge S., Dooley K., Dorris L., Ekins T., Engels R.,

RA Erickson J., Fairo S., Ferreira P., Fitzgerald N., Gage D., Galagan J.,

RA Gardy A.S., Gierke S., Graham L., Grand-Pierre N., Haez N.,

RA Hagopian D., Hages B., Hall J., Horton L., Hulme W., Iliev I.,

RA Jaffe D., Johnson R., Jones C., Kamat M., Kamat A., Karatas A.,

RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Liu A.,

RA Ma L.-J., Mabbitt R., Maclean C., MacDonald P., Major J., Manning J.,

RA Matthews C., Mauceli B., McCarthy M., Meldrum J., Menes L.,

RA Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,

RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,

RA Oliver J., Peterson K., Phunhng P., Pierre N., Purcell S.,

RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,

RA Roman U., Schauer S., Schupack R., Seaman S., Severy P., Smirnov S.,

RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,

RA Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,

RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wagers S., Wilson B.,

RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,

RA Zander E.,

RT "Genome Sequence of Aspergillus nidulans.";

RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.

CC -1- CAUTION: The sequence shown here is derived from an

CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is

CC preliminary data.

DR EMBL; AACD01000007; EAA66567.1; -; Genomic DNA.

KM Hypothetical protein.

SQ SEQUENCE 176 AA; 18926 MW; 98BC9B122419DEA3 CRC64;

Query Match 3.0%; Score 7; DB 2; Length 176;

Best Local Similarity 100.0%; Pred. No. 3e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 GDLTGL 89

DB 169 GDLTGL 175

Search completed: January 18, 2006, 20:49:10  
Job time: 83 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 18, 2006, 20:43:47 ; Search time 76 Seconds  
(without alignments)  
1358.605 Million cell updates/sec

Title: US-09-930-125-2\_COPY\_975\_1209

Perfect score: 235  
Sequence: 1 EFSRRARDPQRVYIGNEDL.....AVENPEYLPGGAAPQHP 235

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1763552

Minimum DB seq length: 0  
Maximum DB seq length: 235

Post-processing: Listing first 200 summaries

Database :

A\_Geneseq\_21:.\*  
1: geneseqp19808:.\*  
2: geneseqp19908:.\*  
3: geneseqp20008:.\*  
4: geneseqp20018:.\*  
5: geneseqp20028:.\*  
6: geneseqp20038:.\*  
7: geneseqp20048:.\*  
8: geneseqp20058:.\*  
9: geneseqp20068:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 178   | 75.7        | 224    | 7     | ABR82073    |
| 2          | 168   | 71.5        | 214    | 8     | ADP80499    |
| 3          | 132   | 56.2        | 217    | 4     | AAE13121    |
| 4          | 84    | 35.7        | 88     | 8     | ABO55591    |
| 5          | 65    | 27.7        | 162    | 8     | ADT50881    |
| 6          | 65    | 27.7        | 164    | 8     | ADT50880    |
| 7          | 59    | 25.1        | 59     | 3     | AAE21202    |
| 8          | 59    | 25.1        | 59     | 5     | AAE51147    |
| 9          | 39    | 16.6        | 135    | 3     | AAE43787    |
| 10         | 38    | 16.2        | 103    | 9     | ADY30516    |
| 11         | 37    | 15.7        | 221    | 7     | ABR82070    |
| 12         | 15    | 6.4         | 15     | 3     | AAE98969    |
| 13         | 15    | 6.4         | 15     | 3     | AAE98875    |
| 14         | 15    | 6.4         | 15     | 3     | AAE98965    |
| 15         | 15    | 6.4         | 15     | 3     | AAE98970    |
| 16         | 15    | 6.4         | 15     | 3     | AAE98973    |
| 17         | 15    | 6.4         | 15     | 3     | AAE98975    |
| 18         | 15    | 6.4         | 15     | 3     | AAE98967    |
| 19         | 15    | 6.4         | 15     | 3     | AAE98972    |
| 20         | 15    | 6.4         | 15     | 3     | AAE98874    |
| 21         | 15    | 6.4         | 15     | 3     | AAE98971    |
| 22         | 15    | 6.4         | 15     | 3     | AAE98968    |
| 23         | 15    | 6.4         | 15     | 3     | AAE98974    |
| 24         | 15    | 6.4         | 15     | 4     | AAE88728    |

|    |    |     |    |   |           |           |           |
|----|----|-----|----|---|-----------|-----------|-----------|
| 25 | 15 | 6.4 | 15 | 4 | AAE89108  | AAE89108  | HER2/neu  |
| 26 | 15 | 6.4 | 15 | 4 | AAE88326  | AAE88326  | HER2/neu  |
| 27 | 15 | 6.4 | 15 | 4 | AAE88362  | AAE88362  | HER2/neu  |
| 28 | 15 | 6.4 | 15 | 4 | AAE89099  | AAE89099  | HER2/neu  |
| 29 | 15 | 6.4 | 15 | 4 | AAE88294  | AAE88294  | HER2/neu  |
| 30 | 15 | 6.4 | 15 | 4 | AAE88474  | AAE88474  | HER2/neu  |
| 31 | 15 | 6.4 | 15 | 4 | AAE88720  | AAE88720  | HER2/neu  |
| 32 | 15 | 6.4 | 15 | 4 | AAE89046  | AAE89046  | HER2/neu  |
| 33 | 15 | 6.4 | 15 | 4 | AAE88360  | AAE88360  | HER2/neu  |
| 34 | 15 | 6.4 | 15 | 4 | AAE88518  | AAE88518  | HER2/neu  |
| 35 | 15 | 6.4 | 15 | 4 | AAE88590  | AAE88590  | HER2/neu  |
| 36 | 15 | 6.4 | 15 | 4 | AAE88514  | AAE88514  | HER2/neu  |
| 37 | 15 | 6.4 | 15 | 4 | AAE88540  | AAE88540  | HER2/neu  |
| 38 | 15 | 6.4 | 15 | 4 | AAE88558  | AAE88558  | HER2/neu  |
| 39 | 15 | 6.4 | 15 | 4 | AAE88672  | AAE88672  | HER2/neu  |
| 40 | 15 | 6.4 | 15 | 4 | AAE88684  | AAE88684  | HER2/neu  |
| 41 | 15 | 6.4 | 15 | 4 | AAE88566  | AAE88566  | HER2/neu  |
| 42 | 15 | 6.4 | 15 | 4 | AAE88682  | AAE88682  | HER2/neu  |
| 43 | 15 | 6.4 | 15 | 4 | AAE88336  | AAE88336  | HER2/neu  |
| 44 | 15 | 6.4 | 15 | 4 | AAE89045  | AAE89045  | HER2/neu  |
| 45 | 15 | 6.4 | 15 | 4 | AAE89109  | AAE89109  | HER2/neu  |
| 46 | 15 | 6.4 | 15 | 4 | AAE89100  | AAE89100  | HER2/neu  |
| 47 | 15 | 6.4 | 15 | 4 | AAE89101  | AAE89101  | HER2/neu  |
| 48 | 15 | 6.4 | 15 | 4 | AAE89105  | AAE89105  | HER2/neu  |
| 49 | 15 | 6.4 | 15 | 4 | AAE88346  | AAE88346  | HER2/neu  |
| 50 | 15 | 6.4 | 15 | 4 | AAE89104  | AAE89104  | HER2/neu  |
| 51 | 15 | 6.4 | 15 | 4 | AAE88330  | AAE88330  | HER2/neu  |
| 52 | 15 | 6.4 | 15 | 4 | AAE888436 | AAE888436 | HER2/neu  |
| 53 | 15 | 6.4 | 15 | 4 | AAE88700  | AAE88700  | HER2/neu  |
| 54 | 15 | 6.4 | 15 | 4 | AAE88718  | AAE88718  | HER2/neu  |
| 55 | 15 | 6.4 | 15 | 4 | AAE89103  | AAE89103  | HER2/neu  |
| 56 | 15 | 6.4 | 15 | 4 | AAE89107  | AAE89107  | HER2/neu  |
| 57 | 15 | 6.4 | 15 | 4 | AAE888476 | AAE888476 | HER2/neu  |
| 58 | 15 | 6.4 | 15 | 4 | AAE88866  | AAE88866  | HER2/neu  |
| 59 | 15 | 6.4 | 15 | 4 | AAE88714  | AAE88714  | HER2/neu  |
| 60 | 15 | 6.4 | 15 | 4 | AAE888570 | AAE888570 | HER2/neu  |
| 61 | 15 | 6.4 | 15 | 4 | AAE88614  | AAE88614  | HER2/neu  |
| 62 | 15 | 6.4 | 15 | 4 | AAE89106  | AAE89106  | HER2/neu  |
| 63 | 15 | 6.4 | 15 | 4 | AAE88696  | AAE88696  | HER2/neu  |
| 64 | 15 | 6.4 | 15 | 4 | AAE88738  | AAE88738  | HER2/neu  |
| 65 | 15 | 6.4 | 15 | 4 | AAE89044  | AAE89044  | HER2/neu  |
| 66 | 15 | 6.4 | 15 | 4 | AAE88328  | AAE88328  | HER2/neu  |
| 67 | 15 | 6.4 | 15 | 4 | AAE88388  | AAE88388  | HER2/neu  |
| 68 | 15 | 6.4 | 15 | 4 | AAE89102  | AAE89102  | HER2/neu  |
| 69 | 15 | 6.4 | 15 | 7 | ADN23119  | ADN23119  | Breast ca |
| 70 | 15 | 6.4 | 15 | 8 | ADN12610  | ADN12610  | MHC class |
| 71 | 15 | 6.4 | 15 | 8 | ADN65253  | ADN65253  | HLA bindi |
| 72 | 15 | 6.4 | 15 | 8 | ADN65253  | ADN65253  | HLA bindi |
| 73 | 13 | 5.5 | 13 | 2 | AAE52923  | AAE52923  | TK-SH2 as |
| 74 | 13 | 5.5 | 13 | 7 | ABO07317  | ABO07317  | Human HER |
| 75 | 13 | 5.5 | 13 | 7 | ABO00329  | ABO00329  | HER-2 D10 |
| 76 | 13 | 5.5 | 13 | 8 | ADN64691  | ADN64691  | HLA bindi |
| 77 | 13 | 5.5 | 13 | 8 | ADP80312  | ADP80312  | Human HLA |
| 78 | 13 | 5.5 | 13 | 9 | ADZ38289  | ADZ38289  | Human kin |
| 79 | 12 | 5.1 | 12 | 8 | ADN12603  | ADN12603  | MHC class |
| 80 | 12 | 5.1 | 12 | 8 | ADN64682  | ADN64682  | HLA bindi |
| 81 | 12 | 5.1 | 12 | 8 | ADN38834  | ADN38834  | Human HER |
| 82 | 12 | 5.1 | 12 | 8 | ADP80211  | ADP80211  | Human HLA |
| 83 | 12 | 5.1 | 12 | 8 | ADN64690  | ADN64690  | HLA bindi |
| 84 | 12 | 5.1 | 13 | 8 | ADP80187  | ADP80187  | Human HLA |
| 85 | 12 | 5.1 | 13 | 8 | AAE98876  | AAE98876  | HLA class |
| 86 | 12 | 5.1 | 21 | 2 | AAW05679  | AAW05679  | Peptide c |
| 87 | 11 | 4.7 | 11 | 2 | AAE52915  | AAE52915  | TK-SH2 as |
| 88 | 11 | 4.7 | 11 | 4 | AAU26877  | AAU26877  | Human Leu |
| 89 | 11 | 4.7 | 11 | 4 | AAU26875  | AAU26875  | Human Leu |
| 90 | 11 | 4.7 | 11 | 5 | ABJ00203  | ABJ00203  | HER2/neu  |
| 91 | 11 | 4.7 | 11 | 5 | ABJ00204  | ABJ00204  | HER2/neu  |
| 92 | 11 | 4.7 | 11 | 6 | ABO01068  | ABO01068  | B7-like s |
| 93 | 11 | 4.7 | 11 | 6 | ABO01069  | ABO01069  | B7-like s |
| 94 | 11 | 4.7 | 11 | 8 | ADN64665  | ADN64665  | HLA bindi |
| 95 | 11 | 4.7 | 11 | 8 | ADN64667  | ADN64667  | HLA bindi |
| 96 | 11 | 4.7 | 11 | 8 | ADN64669  | ADN64669  | HLA bindi |
| 97 | 11 | 4.7 | 11 | 8 | ADN64671  | ADN64671  | HLA bindi |





PT against cancer cells expressing Her2/neu, and for vaccination strategies.  
XX  
XX Example 1; Fig 7B; 83pp; English.  
XX  
XX The present invention describes a recombinant polynucleotide (I)  
CC comprising a first nucleotide sequence encoding a Her2/neu target antigen  
CC consisting of an amino acid sequence corresponding to: (a) amino acid  
CC residues 634-683 or 606-683 operatively linked to amino acid residues  
CC 1035-1255 of human Her2/neu (SEQ ID NO:1, ABR82066); or (b) amino acid  
CC residues 635-685 or 608-685 operatively linked to amino acid residues  
CC 1037-1257 of rat Her2/neu (SEQ ID NO:2, ABR82067). (I) has cytoskeletal and  
CC immunostimulant activities, and can be used in vaccines. The  
CC polynucleotide encoding a Her2/neu target antigen can be used for  
CC stimulating immunoeffector cells or an immune response in a subject  
CC against cancer cells expressing Her2/neu. The encoded Her2/neu target  
CC antigen polypeptide is useful as a tag to detect or isolate the fusion  
CC protein containing the Her2/neu target an immune response stimulated by  
CC the Her2/neu target antigen. The Her2/neu target antigen polynucleotides  
CC and polypeptides are useful in genetic or polypeptide vaccination  
CC strategies. The present sequence represents distal human Her2/neu, which  
CC is used in the exemplification of the present invention  
XX  
SQ Sequence 224 AA;  
Query Match 75.7%; Score 178; DB 7; Length 224;  
Best Local Similarity 100.0%; Pred. No. 8.5e-157; Indels 0; Gaps 0;  
Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 58 CPDPAPAGAGMVMHRRSSSTRSGGDLTLGLEPSEBEAPRSPPLAPSEAGSDVFPDGLG 117  
DB 1 CPDPAPAGAGMVMHRRSSSTRSGGDLTLGLEPSEBEAPRSPPLAPSEAGSDVFPDGLG 60  
QY 118 MGAAGLQSLPTHTDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNOQPVRRQPPS 177  
DB 61 MGAAGLQSLPTHTDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNOQPVRRQPPS 120  
QY 178 PRGGPLPARPAGATLERPKTLSPGKNGVVKDVFARFGAVENBEYLTPOGGAAPQPHP 235  
DB 121 PRGGPLPARPAGATLERPKTLSPGKNGVVKDVFARFGAVENBEYLTPOGGAAPQPHP 178  
RESULT 2  
ADP80499  
ID ADP80499 standard; protein; 214 AA.  
XX  
XX ADP80499;  
XX  
XX 18-NOV-2004 (first entry)  
XX  
XX Human epitope vaccine-related Her2/neu protein SeqID758.  
XX  
XX epitope; HLA-A1; HLA-A2; HLA-A3; HLA-A24; HLA-B7; HLA-B44;  
XX tumour associated antigen peptide; cytoskeletal; vaccine; human.  
XX  
XX Homo sapiens.  
OS  
XX WO2004052917-A2.  
XX  
XX 24-JUN-2004.  
XX  
XX 10-DEC-2003; 2003WO-US038949.  
XX  
XX 10-DEC-2002; 2002US-0432017P.  
XX  
XX (EPIM-) EPIMMUNE INC.  
XX  
XX Keogh EA, Southwood S, Fikes JD, Sette A;  
XX WPI, 2004-468809/44.  
XX  
XX New HLA-A1, A2, A3, A24, B7 or B44 tumor associated antigen peptides,  
XX useful in preparing a composition for diagnosing or treating tumor  
XX associated antigen-related disease.  
PT

XX  
XX Disclosure; SEQ ID NO 758; 24pp; English.  
XX  
XX This invention relates to a novel isolated peptide which comprises at  
CC least 1, 2, 3, 4, 5, 6 or 7 epitopes or analogues of the epitopes given  
CC in the specification. The peptide comprises HLA-A1, A2, A3, A24, B7 or  
CC B44 tumor associated antigen peptide. The invention may be useful for  
CC the production of compounds with a cytoskeletal activity or for the  
CC production of a vaccine. The peptide is useful in preparing a composition  
CC diagnosing or treating tumor associated antigen-related disease. The  
CC present sequence is that of a protein which may be used to derive epitope  
CC peptides for use in the peptide of the invention.  
XX  
SQ Sequence 214 AA;  
Query Match 71.5%; Score 168; DB 8; Length 214;  
Best Local Similarity 100.0%; Pred. No. 1.6e-147; Indels 0; Gaps 0;  
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 68 MYHHRSSSTRSGGDLTLGLEPSEBEAPRSPPLAPSEAGSDVFPDGLGMGAAGLQSL 127  
DB 1 MYHHRSSSTRSGGDLTLGLEPSEBEAPRSPPLAPSEAGSDVFPDGLGMGAAGLQSL 60  
QY 128 PTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNOQPVRRQPPSPPRGPPLPAR 187  
DB 61 PTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNOQPVRRQPPSPPRGPPLPAR 120  
QY 188 PAGATLERPKTLSPGKNGVVKDVFARFGAVENBEYLTPOGGAAPQPHP 235  
DB 121 PAGATLERPKTLSPGKNGVVKDVFARFGAVENBEYLTPOGGAAPQPHP 168  
RESULT 3  
AAE13121  
ID AAE13121 standard; protein; 217 AA.  
XX  
XX AAE13121;  
XX  
XX 28-JAN-2002 (first entry)  
XX  
XX Mature human HER-2 membrane distal intracellular domain.  
XX  
XX Immunostimulatory fusion protein; IFP; antigen component; therapy;  
XX immunostimulatory component; T-cell mediated immune response; DC;  
XX dendritic cell; colon cancer; breast carcinoma; ovarian cancer; human;  
XX HER-2 membrane distal intracellular domain.  
XX  
XX Homo sapiens.  
OS  
XX WO200174855-A2.  
XX  
XX 11-OCT-2001.  
XX  
XX 30-MAR-2001; 2001WO-US010515.  
XX  
XX 30-MAR-2000; 2000US-0193504P.  
XX  
XX (DENB-) DENDREON CORP.  
XX  
XX Laus R, Vidovic D, Graddie T;  
XX WPI, 2001-662965/76.  
XX  
XX N-PSDB; AAD21572.  
XX  
XX An immunostimulatory fusion protein comprising the intracellular domain  
XX of HER-2 and an antigen elicits an immune response to the antigen and is  
XX useful for the treatment of associated cancer associated.  
XX  
XX Claim 2; Page 31; 59pp; English.  
XX  
XX The invention relates to immunostimulatory fusion proteins (IFP) and  
XX nucleic acid molecules encoding such proteins. The IFPs comprise a  
XX polypeptide antigen component and an immunostimulatory component derived  
CC

CC from the intracellular domain of HER-2 protein which is effective to  
CC elicit a protective dendritic cell (DC)-induced T-cell mediated cellular  
CC immune response to the antigen. IIP or superactivated dendritic cells are  
CC used to treat cancer e.g. breast carcinoma, ovarian and colon cancer  
CC associated with a particularly antigen. The present sequence is mature  
CC human HER-2 membrane distal intracellular domain. This sequence is used  
CC in the HER500 and HER300 GM-CSF fusion constructs of the invention  
XX  
SQ Sequence 217 AA;  
  
Query Match 56.2%; Score 132; DB 4; Length 217;  
Best Local Similarity 100.0%; Pred. No. 4.8e-114;  
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 64 GAGGVNHRHRSSTRRSGGDLTLGLPSEERAPRPLAPSGAGSDVFDGLGMAKKG 123  
DB 1 GAGGVNHRHRSSTRRSGGDLTLGLPSEERAPRPLAPSGAGSDVFDGLGMAKKG 60  
QY 124 LQSLPTHDPSPLOKRSDEPTVPLPSETDGYVAPLTCSPQPEYVNPDPVAPQPPSPREGPL 183  
DB 61 LQSLPTHDPSPLOKRSDEPTVPLPSETDGYVAPLTCSPQPEYVNPDPVAPQPPSPREGPL 120  
QY 184 PAARPAGATLER 195  
DB 121 PAARPAGATLER 132  
  
RESULT 4  
ABO55591  
ID ABO55591 standard; protein; 88 AA.  
XX  
AC ABO55591;  
XX  
DT 29-JUL-2004 (first entry)  
XX  
DE Human genome derived single exon protein #1825.  
XX  
KW Human; gene expression; single exon probe; microarray;  
XX alternative splicing event; genomic alteration.  
XX  
OS Homo sapiens.  
XX  
PN US2003194704-A1.  
XX  
PD 16-OCT-2003.  
XX  
PF 03-APR-2002; 2002US-00029386.  
XX  
PR 03-APR-2002; 2002US-00029386.  
XX  
PA (PENN/) PENN S G.  
XX (RANK/) RANK D R.  
XX (HANZ/) HANZEL D K.  
XX  
PI Penn SG, Rank DR, Hanzel DK;  
XX  
DR WPI; 2004-119264/12.  
XX  
PT New human genome-derived single exon nucleic acid probes useful for human  
PT gene expression analysis, for identifying or characterizing alternative  
PT splicing events, for assessing genomic alterations or as tools for  
PT surveying tissues.  
XX  
PS Claim 45; SEQ ID NO 29225; 80pp; English.  
XX  
XX The invention relates to a nucleic acid probe for measuring human gene  
XX expression, comprising any of the 27,400 fully defined nucleotide  
XX sequences in the specification, or their complements or fragments, and  
XX encoding at least 8 amino acids of any of the 688 amino acid sequences  
XX fully defined in the specification. The probe is a single exon probe that  
XX hybridises under high stringency conditions to a nucleic acid molecule  
XX expressed in human cells or tissues. Also included are a spatially-  
XX addressable set of single exon nucleic acid probes for measuring human

CC gene expression (comprising a plurality of single exon nucleic acid  
CC probes cited above, where each of the plurality of probes is separately  
CC and addressably isolatable or amplifiable from the plurality), a single  
CC exon microarray for measuring human gene expression, a method of  
CC measuring human gene expression, a vector comprising the single exon  
CC probe cited above, an ORF-encoded peptide comprising at least 8  
CC contiguous amino acids of any of the above-mentioned amino acid  
CC sequences (optionally with conservative amino acid substitutions), an  
CC isolated antibody that binds specifically to a peptide cited above,  
CC a method of selling and/or licensing single exon probes or microarrays to  
CC a customer desiring to measure gene expression, a method of providing  
CC human gene expression data by subscription, and a computer-readable  
CC storage medium which contains a database having a plurality of records  
CC (each record including data on the expression of a single exon probe  
CC cited above. The probe, methods and apparatus are useful in gene  
CC expression analysis. The probes may be used as tools for surveying  
CC tissues to detect the presence of expressed messages that contain their  
CC specific exon, or in constructing genome-derived single exon microarrays.  
CC In addition, the probes are used in identifying and characterising  
CC alternative splicing events, in detecting and characterising gross  
CC alterations in the genomic locus that includes their exon, in assessing  
CC smaller genomic alterations, in priming the synthesis of nucleic acids,  
CC or in expressing the ORF-encoded peptide. The present sequence data for  
CC single exon probe protein of the invention. Note: The sequence data for  
CC this patent did not form part of the printed specification, but was  
CC obtained in electronic format directly from USPTO at  
CC seqdata.uspto.gov/sequence.html?docid=20030194704  
XX  
SQ Sequence 88 AA;  
  
Query Match 35.7%; Score 84; DB 8; Length 88;  
Best Local Similarity 100.0%; Pred. No. 8.7e-70;  
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 80 SGGGDLTLGLPSEERAPRPLAPSGAGSDVFDGLGMAKKGSLPTHDPSPLOKRS 139  
DB 3 SGGGDLTLGLPSEERAPRPLAPSGAGSDVFDGLGMAKKGSLPTHDPSPLOKRS 62  
QY 140 EDPYVPLPSETDGYVAPLTCSPQP 163  
DB 63 EDPYVPLPSETDGYVAPLTCSPQP 86  
  
RESULT 5  
ADT50881  
ID ADT50881 standard; protein; 162 AA.  
XX  
AC ADT50881;  
XX  
DT 13-JAN-2005 (first entry)  
XX  
DE Cancer related protein sequence #44.  
XX  
KW cytostatic; gene therapy; vaccine; diagnosis; breast; colon; lung;  
KW ovarian; prostate; cancer.  
XX  
OS Homo sapiens.  
XX  
PN WO2004092338-A2.  
XX  
PD 28-OCT-2004.  
XX  
PF 12-APR-2004; 2004WO-US011104.  
XX  
PR 11-APR-2003; 2003US-0462399P.  
XX  
PR 01-JUL-2003; 2003US-0484333P.  
XX  
PA (DIAD-) DIADEXUS INC.  
XX  
PI Macina RA, Turner LR, Sun Y, Tam A;  
XX  
DR WPI; 2004-766851/75.  
XX

PT New cancer specific nucleic acid (CasNA) molecules, useful for  
PT diagnosing, monitoring the presence of, or treating a patient with  
PT breast, colon, lung, ovarian, or prostate cancer.

PS Claim 12; SEQ ID NO 185; 891bp; English.

XX The invention relates to an isolated nucleic acid molecule (1)  
CC selectively hybridizing to, or comprising at least 95% sequence identity  
CC to, any of the 362 nucleotide sequences fully defined in the  
CC specification. The nucleic acid molecules and polypeptides are useful for  
CC diagnosing, monitoring the presence of, or treating a patient with  
CC breast, colon, lung, ovarian, or prostate cancer. This sequence  
CC corresponds to a protein of the invention.

XX Sequence 162 AA;

Query Match 27.7%; Score 65; DB 8; Length 162;  
Best Local Similarity 100.0%; Pred. No. 7.1e-52;  
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 DSPPLQRYSEDPVPLPSETDGYVAPLTCSPPQEVYNQDPVRPQPPSPREGPLPAAPAG 190  
DB 12 DSPPLQRYSEDPVPLPSETDGYVAPLTCSPPQEVYNQDPVRPQPPSPREGPLPAAPAG 71

QY 191 ATLER 195  
DB 72 ATLER 76

RESULT 6

ADTS0880  
ID ADTS0880 standard; protein; 164 AA.

AC ADTS0880;

XX 13-JAN-2005 (first entry)

XX Cancer related protein sequence #43.

XX cytosolic; gene therapy; vaccine; diagnosis; breast; colon; lung;  
KW ovarian; prostate; cancer.

OS Homo sapiens.

XX MO2004092338-A2.

XX 28-OCT-2004.

PF 12-APR-2004; 2004MO-US011104.

XX 11-APR-2003; 2003US-0462399P.

PR 01-JUL-2003; 2003US-0484333P.

PA (DIAD-) DIADEXUS INC.

XX Macina RA, Turner LR, Sun Y, Tam A;

XX MPI; 2004-766851/75.

XX New cancer specific nucleic acid (CasNA) molecules, useful for  
PT diagnosing, monitoring the presence of, or treating a patient with  
PT breast, colon, lung, ovarian, or prostate cancer.

PS Claim 12; SEQ ID NO 184; 891bp; English.

XX The invention relates to an isolated nucleic acid molecule (1)  
CC selectively hybridizing to, or comprising at least 95% sequence identity  
CC to, any of the 362 nucleotide sequences fully defined in the  
CC specification. The nucleic acid molecules and polypeptides are useful for  
CC diagnosing, monitoring the presence of, or treating a patient with  
CC breast, colon, lung, ovarian, or prostate cancer. This sequence  
CC corresponds to a protein of the invention.

SQ Sequence 164 AA;

Query Match 27.7%; Score 65; DB 8; Length 164;  
Best Local Similarity 100.0%; Pred. No. 7.2e-52;  
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 DSPPLQRYSEDPVPLPSETDGYVAPLTCSPPQEVYNQDPVRPQPPSPREGPLPAAPAG 190  
DB 14 DSPPLQRYSEDPVPLPSETDGYVAPLTCSPPQEVYNQDPVRPQPPSPREGPLPAAPAG 73

QY 191 ATLER 195  
DB 74 ATLER 78

RESULT 7

AAB21202  
ID AAB21202 standard; protein; 59 AA.

AC AAB21202;

XX 12-JAN-2001 (first entry)

DE Human HER-2/neu protein phosphorylation domain partial sequence.

XX Human; HER-2/neu; oncogene; tyrosine kinase; cytosolic; vaccine;  
KW breast cancer; prostate cancer; ovarian cancer; lung cancer;  
KW colon cancer.

OS Homo sapiens.

XX MO200044899-A1.

XX 03-AUG-2000.

PF 28-JAN-2000; 2000MO-US02164.

PR 29-JAN-1999; 99US-0117976P.

PA (CORI-) CORIXA CORP.

XX (SMIK) SMITHKLINE BEECHAM.

XX Cheever MA, Gheysen D;

XX MPI; 2000-505976/45.

XX HER-2/neu extracellular domain/phosphorylation domain fusion proteins  
PT useful for vaccinating against breast, ovarian, colon, lung and prostate  
PT cancers.

PS Claim 27; Fig 11; 128bp; English.

XX The present sequence is a preferred portion of the phosphorylation domain  
CC of the HER-2/neu protein. HER-2/neu is a member of the tyrosine kinase  
CC family of receptor-like glycoproteins and shows homology to the epidermal  
CC growth factor receptor (EGFR). It probably plays a part in cell growth  
CC and/or differentiation. The HER-2/neu gene is an oncogene. An HER-2/neu  
CC fusion protein comprising a HER-2/neu extracellular domain fused to a HER  
CC -2/neu phosphorylation domain may be used to treat or prevent cancer by  
CC eliciting or enhancing an immune response to the HER-2/neu protein. It  
CC may be used to treat malignancies such as breast, ovarian, colon, lung  
CC and prostate cancers, and may be used as an antigen to vaccinate against  
CC these neoplasias

XX Sequence 59 AA;

Query Match 25.1%; Score 59; DB 3; Length 59;  
Best Local Similarity 100.0%; Pred. No. 1e-46;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 QNEDLGPASPLDSTFRSLLEDMDGLVDAEYLVPOGFFCPDDAPAGGVHHRH 74  
DB 1 QNEDLGPASPLDSTFRSLLEDMDGLVDAEYLVPOGFFCPDDAPAGGVHHRH 59

## RESULT 8

AA051147  
ID AA051147 standard; protein; 59 AA.  
XX  
AC AA051147;  
XX  
DT 17-JUN-2002 (first entry)  
XX  
DE Human Her-2/neu oncoprotein phosphorylation domain fragment.  
XX  
KW Her-2/neu; oncogene; cancer; tumour; vaccine; human; p185;  
KW tyrosine kinase; receptor; c-erbB2; gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN WO200212341-A2.  
XX  
PD 14-FEB-2002.  
XX  
PF 03-AUG-2001; 2001WO-US024283.  
XX  
PR 03-AUG-2000; 2000US-00632507.  
XX  
PA (CORI-) CORIXA CORP.  
XX  
PA (SMK) SMITHKLINE BEECHAM BIOLOGICALS.  
XX  
PI Cheever MA, Gheyssen D;  
XX  
DR WPI; 2002-241743/29.  
XX  
PT Her-2/neu fusion protein for treating or preventing cancer by eliciting  
PT or enhancing an immune response to the protein, has Her-2/neu  
PT extracellular domain fused to Her-2/neu intracellular or phosphorylation  
PT domain.  
XX  
PS Disclosure; Fig 11; 141pp; English.  
XX  
CC The present sequence is that of a fragment (Delta9D) of the  
CC phosphorylation domain of human Her-2/neu (p185 glycoprotein, c-erbB2),  
CC an oncogenic self-protein and target for anti-cancer vaccines. The Her-  
CC 2/neu gene is amplified and p185 is overexpressed in breast, ovarian,  
CC colon, lung and prostate cancer. Her-2/neu (see AA051143) is a member of  
CC the tyrosine kinase family of receptor-like glycoproteins. It comprises  
CC an extracellular domain with homology to the epidermal growth factor  
CC receptor (EGFR), a highly hydrophobic transmembrane domain and a C-  
CC terminal intracellular domain that also shows homology to EGFR. Its  
CC overexpression correlates with a poor prognosis in breast and ovarian  
CC cancers. The invention provides Her-2/neu fusion proteins, nucleic acids  
CC encoding them, viral vectors, and vaccines comprising the fusion proteins  
CC or nucleic acid molecules. In preferred fusion proteins, the  
CC extracellular domain of a Her-2/neu protein is fused to a Her-2/neu  
CC intracellular domain or phosphorylation domain (or the Delta9D fragment).  
CC An immune response to Her-2/neu protein is elicited or enhanced by  
CC administering the fusion protein in the form of a vaccine, or by  
CC transfecting cells of an animal *ex vivo* with a nucleic acid encoding the  
CC fusion protein, and delivering the transfected cells to the animal. The  
CC fusion proteins, nucleic acids, and isolated specific T-cells are useful  
CC for inhibiting the development of a cancer, especially breast, ovarian,  
CC colon, lung or prostate cancer in a patient. T cells that specifically  
CC react with a Her-2/neu fusion protein can be used to remove tumour cells  
CC from a sample in order to inhibit the development of cancer in a patient  
XX  
SQ Sequence 59 AA;

Query Match 25.1%; Score 59; DB 5; Length 59;  
Best Local Similarity 100.0%; Pred. No. 1e-46;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 QNEDIGPASPPLDSTFYRSLLEDMDGLVDAERYLVPOGFCPPDPAAGGVHRRHR 74  
DB 1 QNEDIGPASPPLDSTFYRSLLEDMDGLVDAERYLVPOGFCPPDPAAGGVHRRHR 59

## RESULT 9

AA043787  
ID AA043787 standard; protein; 135 AA.  
XX  
AC AA043787;  
XX  
DT 08-FEB-2001 (first entry)  
XX  
DE Human cancer associated protein sequence SEQ ID NO:1232.  
XX  
KW Human; cancer associated gene; cancer antigen; detection; cancer;  
KW diagnosis; cytostatic; proliferative; vulnery; immunomodulator;  
KW antidiabetic; antiaesthetic; antirheumatic; antithyroid; cardiac;  
KW antinflammatory; antichryoid; antiallergic; antibacterial; cardiac;  
KW dermatologic; neuroprotective; thrombolytic; coagulant; nocotropic;  
KW vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation;  
KW immune disorder; haematopoietic cell disorder; autoimmune disorder;  
KW allergic reaction; graft versus host disease; organ rejection;  
KW haemostatic; thrombolytic; cardiovascular disorder; infection;  
KW neurological disease; drug screening.  
XX  
OS Homo sapiens.  
XX  
PN WO200055350-A1.  
XX  
PD 21-SEP-2000.  
XX  
PF 08-MAR-2000; 2000WO-US005882.  
XX  
PR 12-MAR-1999; 99US-0124270P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Rosen CA, Ruben SM;  
XX  
DR WPI; 2000-587533/55.  
XX  
DR N-PSDB; AAC77996.  
XX  
PT Novel isolated nucleic acids comprising sequences encoding peptides  
PT useful for treating or diagnosing e.g. cancer.  
XX  
PS Claim 11; Page 1864; 2352pp; English.  
XX  
CC AAC7607 to AAC7848 encode the human cancer associated proteins given in  
CC AA043398 to AA044239. The proteins can have activities based on the  
CC tissues and cells the genes are expressed in. Example of activities  
CC include: cytostatic; proliferative; vulnery; immunomodulator;  
CC antidiabetic; antiaesthetic; antirheumatic; antithyroid; cardiac;  
CC antinflammatory; antichryoid; antiallergic; antibacterial; antiviral;  
CC dermatologic; neuroprotective; cardiac; thrombolytic; coagulant;  
CC nocotropic; vasotropic; antipsoriatic and antiangiogenic. The  
CC polynucleotides and polypeptides can be used for preventing, treating or  
CC ameliorating medical conditions and diagnosing pathological conditions.  
CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from  
CC or inhibiting the proliferation, differentiation or mobilisation of  
CC immune cells, to treat disorders of haematopoietic cells, autoimmune  
CC disorders, allergic reactions, graft versus host disease and organ  
CC rejection, modulate haemostatic or thrombolytic activity, modulate  
CC inflammation, cancers, cardiovascular disorders, neurological disease and  
CC bacterial or viral infections. The peptides, nucleotides, antibodies,  
CC agonists and antagonists may be also be used in drug screens. AAC7849 to  
CC AAC78457 and AA044240 represent sequences used in the exemplification of  
CC the present invention  
XX  
SQ Sequence 135 AA;

Query Match 16.6%; Score 39; DB 3; Length 135;  
Best Local Similarity 100.0%; Pred. No. 8.9e-26;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 197 KTLSFGKNGVVKDVPFARFGAVENPEYLTPOGGAAPQPH 235
DB 51 KTLSFGKNGVVKDVPFARFGAVENPEYLTPOGGAAPQPH 89

RESULT 10
ID ADY30516 standard; protein; 103 AA.
AC ADY30516;
AD ADY30516;
DE 05-MAY-2005 (first entry)
KW Human splice variant protein expressed in ovary cells DEX0487_002.aa.5.
XX ovarian tumor; diagnosis; prognosis; vaccine; cytostatic; gene therapy.
XX Homo sapiens.
XX MO2005017102-A2.
XX 24-FEB-2005.
XX 01-JUN-2004; 2004MO-US017156.
XX 30-MAY-2003; 2003JUS-0474856P.
XX (DIAD-) DIADEXUS INC.
XX Macina RA, Turner LR, Sun Y;
XX WPI; 2005-182347/19.
XX DR N-PSDB; ADY30412.
XX PT New ovarian specific nucleic acid (OSNA) molecules and polypeptides,
XX useful for diagnosing, monitoring or treating, and detecting the presence
XX of, ovarian cancer in a subject.
XX Claim 12; SEQ ID NO 111; 834bp; English.
XX This invention relates to novel isolated nucleic acid molecules and the
XX encoding polypeptides thereof that are present in normal and neoplastic
XX ovarian cells. Specifically, it refers to splice variants of these
XX polynucleotides. The present invention describes generating antibodies,
XX as well as agonists and antagonists of the polypeptides that can be used
XX in the diagnosis, monitoring, staging, imaging and treatment of ovarian
XX cancer and non-cancerous disease states of the ovary. Furthermore, it
XX provides a kit for detecting the risk of cancer or the presence of cancer
XX in patient that comprises a means for determining the presence of a
XX nucleic acid or protein as given in the specification. These nucleic acid
XX and protein molecules can also be used to induce an immune response and
XX hence be useful in the development of a vaccine for the treatment of
XX ovarian cancer. Accordingly, compositions derived thereof exhibit
XX cytostatic activity and can be used for gene therapy purposes. This
XX polypeptide is encoded by a human splice variant DNA sequence that is
XX expressed in ovarian cells, given in an exemplification of the invention.
XX Sequence 103 AA;

Query Match 16.2%; Score 38; DB 9; Length 103;
Best Local Similarity 100.0%; Pred. No. 5, 8e-27;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 198 TLSFGKNGVVKDVPFARFGAVENPEYLTPOGGAAPQPH 235
DB 20 TLSFGKNGVVKDVPFARFGAVENPEYLTPOGGAAPQPH 57

RESULT 11
ID ABR82070 standard; protein; 221 AA.
AC ABR82070;
AD ABR82070;
XX ABR82070;

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XX 23-SBP-2003 (first entry)
DT Terminal rat Her2/neu amino acid sequence SEQ ID NO:7.
XX DE
XX Rat; Her2/neu; Her2/neu target antigen; immune response; cytostatic;
XX immunostimulant; vaccine; cancer.
XX OS
XX Rattus norvegicus.
XX PN WO2003055439-A2.
XX PD 10-JUL-2003.
XX PF 18-JUL-2002; 2002MO-US022975.
XX PR 18-JUL-2001; 2001JUS-0306250P.
XX PA (REGC) UNIV CALIFORNIA.
XX PI Nelson BL;
XX DR WPI; 2003-569400/53.
XX DR N-PSDB; ACF06076.
XX PT New Her2/neu target antigens and polynucleotides encoding them, useful
XX for stimulating immunoeffector cells or an immune response in a subject
XX against cancer cells expressing Her2/neu, and for vaccination strategies.
XX Example 1; Fig 6B; 83bp; English.
XX The present invention describes a recombinant polynucleotide (I)
XX comprising a first nucleotide sequence encoding a Her2/neu target antigen
XX consisting of an amino acid sequence corresponding to: (a) amino acid
XX residues 634-683 or 606-683 operatively linked to amino acid residues
XX 1035-1255 of human Her2/neu (SEQ ID NO:1; ABR82066); or (b) amino acid
XX residues 635-685 or 608-685 operatively linked to amino acid residues
XX 1037-1257 of rat Her2/neu (SEQ ID NO:2; ABR82067). (I) has cytostatic and
XX immunostimulant activities, and can be used in vaccines. The
XX polynucleotide encoding a Her2/neu target antigen can be used for
XX stimulating immunoeffector cells or an immune response in a subject
XX against cancer cells expressing Her2/neu. The encoded Her2/neu target
XX antigen polypeptide is useful as a tag to detect or isolate the fusion
XX protein containing the Her2/neu target an immune response stimulated by
XX the Her2/neu target antigen. The Her2/neu target antigen polynucleotides
XX and polypeptides are useful in genetic or polypeptide vaccination
XX strategies. The present sequence represents terminal rat Her2/neu, which
XX is used in the exemplification of the present invention
XX Sequence 221 AA;

Query Match 15.7%; Score 37; DB 7; Length 221;
Best Local Similarity 100.0%; Pred. No. 1e-25;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 187 RPAQATLERPKTSLSPGKNGVVKDVPFARFGAVENPEYL 223
DB 127 RPAQATLERPKTSLSPGKNGVVKDVPFARFGAVENPEYL 163

RESULT 12
ID AAY98969 standard; peptide; 15 AA.
AC AAY98969;
AD 07-AUG-2000 (first entry)
DE HLA class II binding antigen epitope peptide #158.
XX Human leucocyte antigen; HLA class II; antigen epitope; pharmaceutical;
XX immune response; chronic viral disease; cancer; autoimmune disease;
XX rheumatoid arthritis; multiple sclerosis; myasthenia gravis; AIDS;
XX

```

KW allograft rejection; allergy; lyme disease; hepatitis; prostate cancer;  
KW glomerulonephritis; food hypersensitivity; malaria.  
XX  
XX Unidentified.  
XX  
XX W09961916-A1.  
XX  
XX 02-DEC-1999.  
XX  
XX 28-MAY-1999; 99WO-US012066.  
XX  
XX 29-MAY-1998; 98US-0087192P.  
XX  
XX (EPIM-) EPIMUNE INC.  
XX  
XX Sette A, Southwood S, Sidney J;  
XX  
XX WPI; 2000-097143/08.  
XX  
XX  
XX New compositions containing immunogenic peptide epitopes for various HLA  
XX class II DR molecules useful for inducing helper T cell response.  
XX  
XX  
XX Claim 1; Page 42; 60pp; English.  
XX  
XX The present invention relates to a new pharmaceutical composition  
XX comprising a unit dose form of a peptide, or analogue, comprising an  
XX epitope selected from those represented by peptides AAY98812-Y99339 which  
XX are derived from various antigens for various human leucocyte antigen  
XX class DR molecules, representative of the world wide population. The  
XX peptide/analogue binds to an HLA class II molecule at an IC-50 of less  
XX than or equal to 1,000 nM. The pharmaceutical can be used to induce a  
XX helper T cell response. The pharmaceutical focuses the immune response  
XX towards selected determinants and could therefore be used in cases of  
XX chronic viral diseases and cancer. Examples of diseases that can be  
XX treated using the peptide containing pharmaceutical include autoimmune  
XX diseases (rheumatoid arthritis, multiple sclerosis, and myasthenia  
XX gravis), allograft rejection, allergies, lyme disease, hepatitis, post-  
XX streptococcal endocarditis or glomerulonephritis and food  
XX hypersensitivities. The peptide epitopes can be used to enhance immune  
XX responses against other immunogens administered with the peptides.  
XX Diseases which can be treated using immunogenic mixtures include prostate  
XX cancer, hepatitis B, hepatitis C, AIDS, renal carcinoma, cervical  
XX carcinoma, lymphoma, and condyloma acuminatum. The peptides may also be  
XX used to make monoclonal antibodies useful as potential diagnostic or  
XX therapeutic agents. The peptides may also be useful as diagnostic  
XX reagents, for example, to determine the susceptibility of an individual  
XX to a treatment regimen. Also, the peptides may be used to predict which  
XX individuals will be at substantial risk of developing chronic infection.  
XX The selection of appropriate T and B cell epitopes should allow the  
XX development of epitope based vaccines particularly towards conserved  
XX epitopes of pathogens which are characterized by high sequence  
XX variability such as HIV, HCV and Malaria  
XX  
XX Sequence 15 AA;  
SQ  
Query Match 6.4%; Score 15; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 41 GDLVDAEYLVPOQG 55  
DB 1 GDLVDAEYLVPOQG 15  
RESULT 13  
AAY98875  
ID AAY98875 standard; peptide; 15 AA.  
XX  
XX AAY98875;  
AC  
XX 07-AUG-2000 (first entry)  
DT  
XX  
XX HLA class II binding antigen epitope peptide #64.

XX Human leucocyte antigen; HLA class II; antigen epitope; pharmaceutical;  
XX immune response; chronic viral disease; cancer; autoimmune disease;  
XX rheumatoid arthritis; multiple sclerosis; myasthenia gravis; AIDS;  
KW allograft rejection; allergy; lyme disease; hepatitis; prostate cancer;  
KW glomerulonephritis; food hypersensitivity; malaria.  
XX  
XX Unidentified.  
XX  
XX W09961916-A1.  
XX  
XX 02-DEC-1999.  
XX  
XX 28-MAY-1999; 99WO-US012066.  
XX  
XX 29-MAY-1998; 98US-0087192P.  
XX  
XX (EPIM-) EPIMUNE INC.  
XX  
XX Sette A, Southwood S, Sidney J;  
XX  
XX WPI; 2000-097143/08.  
XX  
XX  
XX New compositions containing immunogenic peptide epitopes for various HLA  
XX class II DR molecules useful for inducing helper T cell response.  
XX  
XX  
XX Claim 1; Page 41; 60pp; English.  
XX  
XX The present invention relates to a new pharmaceutical composition  
XX comprising a unit dose form of a peptide, or analogue, comprising an  
XX epitope selected from those represented by peptides AAY98812-Y99339 which  
XX are derived from various antigens for various human leucocyte antigen  
XX class DR molecules, representative of the world wide population. The  
XX peptide/analogue binds to an HLA class II molecule at an IC-50 of less  
XX than or equal to 1,000 nM. The pharmaceutical can be used to induce a  
XX helper T cell response. The pharmaceutical focuses the immune response  
XX towards selected determinants and could therefore be used in cases of  
XX chronic viral diseases and cancer. Examples of diseases that can be  
XX treated using the peptide containing pharmaceutical include autoimmune  
XX diseases (rheumatoid arthritis, multiple sclerosis, and myasthenia  
XX gravis), allograft rejection, allergies, lyme disease, hepatitis, post-  
XX streptococcal endocarditis or glomerulonephritis and food  
XX hypersensitivities. The peptide epitopes can be used to enhance immune  
XX responses against other immunogens administered with the peptides.  
XX Diseases which can be treated using immunogenic mixtures include prostate  
XX cancer, hepatitis B, hepatitis C, AIDS, renal carcinoma, cervical  
XX carcinoma, lymphoma, and condyloma acuminatum. The peptides may also be  
XX used to make monoclonal antibodies useful as potential diagnostic or  
XX therapeutic agents. The peptides may also be useful as diagnostic  
XX reagents, for example, to determine the susceptibility of an individual  
XX to a treatment regimen. Also, the peptides may be used to predict which  
XX individuals will be at substantial risk of developing chronic infection.  
XX The selection of appropriate T and B cell epitopes should allow the  
XX development of epitope based vaccines particularly towards conserved  
XX epitopes of pathogens which are characterized by high sequence  
XX variability such as HIV, HCV and Malaria  
XX  
XX Sequence 15 AA;  
SQ  
Query Match 6.4%; Score 15; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 150 TDGYVAPLTCSPQPE 164  
DB 1 TDGYVAPLTCSPQPE 15  
RESULT 14  
AAY98965  
ID AAY98965 standard; peptide; 15 AA.  
XX  
XX AAY98965;  
AC

XX 07-AUG-2000 (first entry)  
XX HLA class II binding antigen epitope peptide #154.  
XX Human leucocyte antigen; HLA class II; antigen epitope; pharmaceutical;  
XX immune response; chronic viral disease; cancer; autoimmune disease;  
XX rheumatoid arthritis; multiple sclerosis; myasthenia gravis; AIDS;  
XX allograft rejection; allergy; Lyme disease; hepatitis; prostate cancer;  
XX glomerulonephritis; food hypersensitivity; malaria.  
XX Unidentified.  
XX WO961916-A1.  
XX 02-DEC-1999.  
XX 28-MAY-1999; 99WO-US012066.  
XX 29-MAY-1998; 98US-0087192P.  
XX (EPIM-) EPIMMUNE INC.  
XX Sette A, Southwood S, Sidney J;  
XX WPI, 2000-097143/08.  
XX New compositions containing immunogenic peptide epitopes for various HLA  
XX class II DR molecules useful for inducing helper T cell response.  
XX Claim 1; Page 42; 60pp; English.  
XX The present invention relates to a new pharmaceutical composition  
XX comprising a unit dose form of a peptide, or analogue, comprising an  
XX epitope selected from those represented by peptides AAY98812-Y99339 which  
XX are derived from various antigens for various human leucocyte antigen  
XX class DR molecules, representative of the world wide population. The  
XX peptide/analogue binds to an HLA class II molecule at an IC-50 of less  
XX than or equal to 1,000 nM. The pharmaceutical focuses the immune response  
XX towards selected determinants and could therefore be used in cases of  
XX chronic viral diseases and cancer. Examples of diseases that can be  
XX treated using the peptide containing pharmaceutical include autoimmune  
XX diseases (rheumatoid arthritis, multiple sclerosis, and myasthenia  
XX gravis), allograft rejection, allergies, Lyme disease, hepatitis, post-  
XX streptococcal endocarditis or glomerulonephritis and food  
XX hypersensitivities. The peptide epitopes can be used to enhance immune  
XX responses against other immunogens administered with the peptides.  
XX Diseases which can be treated using immunogenic mixtures include prostate  
XX cancer, hepatitis B, hepatitis C, AIDS, renal carcinoma, cervical  
XX carcinoma, lymphoma, and condyloma acuminatum. The peptides may also be  
XX used to make monoclonal antibodies useful as potential diagnostic or  
XX therapeutic agents. The peptides may also be useful as diagnostic or  
XX reagents, for example, to determine the susceptibility of an individual  
XX to a treatment regimen. Also, the peptides may be used to predict which  
XX individuals will be at substantial risk of developing chronic infection.  
XX The selection of appropriate T and B cell epitopes should allow the  
XX development of epitope based vaccines particularly towards conserved  
XX epitopes of pathogens which are characterized by high sequence  
XX variability such as HIV, HCV and Malaria  
XX Sequence 15 AA:  
XX  
XX Query Match 6.4%; Score 15; DB 3; Length 15;  
XX Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX 2 FSRMARDPQRFVVIQ 16  
XX 1 FSRMARDPQRFVVIQ 15  
XX  
XX RESULT 15

AA98970  
ID AAY98970 standard; peptide; 15 AA.  
XX AAY98970;  
XX 07-AUG-2000 (first entry)  
XX HLA class II binding antigen epitope peptide #159.  
XX Human leucocyte antigen; HLA class II; antigen epitope; pharmaceutical;  
XX immune response; chronic viral disease; cancer; autoimmune disease;  
XX rheumatoid arthritis; multiple sclerosis; myasthenia gravis; AIDS;  
XX allograft rejection; allergy; Lyme disease; hepatitis; prostate cancer;  
XX glomerulonephritis; food hypersensitivity; malaria.  
XX Unidentified.  
XX WO961916-A1.  
XX 02-DEC-1999.  
XX 28-MAY-1999; 99WO-US012066.  
XX 29-MAY-1998; 98US-0087192P.  
XX (EPIM-) EPIMMUNE INC.  
XX Sette A, Southwood S, Sidney J;  
XX WPI, 2000-097143/08.  
XX New compositions containing immunogenic peptide epitopes for various HLA  
XX class II DR molecules useful for inducing helper T cell response.  
XX Claim 1; Page 42; 60pp; English.  
XX The present invention relates to a new pharmaceutical composition  
XX comprising a unit dose form of a peptide, or analogue, comprising an  
XX epitope selected from those represented by peptides AAY98812-Y99339 which  
XX are derived from various antigens for various human leucocyte antigen  
XX class DR molecules, representative of the world wide population. The  
XX peptide/analogue binds to an HLA class II molecule at an IC-50 of less  
XX than or equal to 1,000 nM. The pharmaceutical focuses the immune response  
XX towards selected determinants and could therefore be used in cases of  
XX chronic viral diseases and cancer. Examples of diseases that can be  
XX treated using the peptide containing pharmaceutical include autoimmune  
XX diseases (rheumatoid arthritis, multiple sclerosis, and myasthenia  
XX gravis), allograft rejection, allergies, Lyme disease, hepatitis, post-  
XX streptococcal endocarditis or glomerulonephritis and food  
XX hypersensitivities. The peptide epitopes can be used to enhance immune  
XX responses against other immunogens administered with the peptides.  
XX Diseases which can be treated using immunogenic mixtures include prostate  
XX cancer, hepatitis B, hepatitis C, AIDS, renal carcinoma, cervical  
XX carcinoma, lymphoma, and condyloma acuminatum. The peptides may also be  
XX used to make monoclonal antibodies useful as potential diagnostic or  
XX therapeutic agents. The peptides may also be useful as diagnostic or  
XX reagents, for example, to determine the susceptibility of an individual  
XX to a treatment regimen. Also, the peptides may be used to predict which  
XX individuals will be at substantial risk of developing chronic infection.  
XX The selection of appropriate T and B cell epitopes should allow the  
XX development of epitope based vaccines particularly towards conserved  
XX epitopes of pathogens which are characterized by high sequence  
XX variability such as HIV, HCV and Malaria  
XX Sequence 15 AA:  
XX  
XX Query Match 6.4%; Score 15; DB 3; Length 15;  
XX Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX 54 QGFPCDPAPQAGM 68  
XX  
XX RESULT 15

Db 1 OGFPCDPAPGAGCM 15

RESULT 16

AAV98973 standard; peptide; 15 AA.

AAV98973;

07-AUG-2000 (first entry)

HLA class II binding antigen epitope peptide #162.

Human leucocyte antigen; HLA class II; antigen epitope; pharmaceutical; immune response; chronic viral disease; cancer; autoimmune disease; rheumatoid arthritis; multiple sclerosis; myasthenia gravis; AIDS; allograft rejection; allergy; Lyme disease; hepatitis; prostate cancer; glomerulonephritis; food hypersensitivity; malaria.

Unidentified.

WO9961916-A1.

02-DEC-1999.

28-MAY-1999; 99WO-US012066.

29-MAY-1998; 98US-0087192P.

(EPIIM-) EPIIMUNE INC.

Sette A, Southwood S, Sidney J;

WPI: 2000-097143/08.

New compositions containing immunogenic peptide epitopes for various HLA class II DR molecules useful for inducing helper T cell response.

Claim 1; Page 42; 60pp; English.

The present invention relates to a new pharmaceutical composition comprising a unit dose form of a peptide, or analogue, comprising an epitope selected from those represented by peptides AAV98812-Y99339 which are derived from various antigens for various human leucocyte antigen class DR molecules, representative of the world wide population. The peptide/analogue binds to an HLA class II molecule at an IC-50 of less than or equal to 1,000 nM. The pharmaceutical can be used to induce a helper T cell response. The pharmaceutical focuses the immune response towards selected determinants and could therefore be used in cases of chronic viral diseases and cancer. Examples of diseases that can be treated using the peptide containing pharmaceutical include autoimmune diseases (rheumatoid arthritis, multiple sclerosis, and myasthenia gravis), allograft rejection, allergies, Lyme disease, hepatitis, post-streptococcal endocarditis or glomerulonephritis and food hypersensitivities. The peptide epitopes can be used to enhance immune responses against other immunogens administered with the peptides. Diseases against other immunogens administered with the peptides include cancer, hepatitis B, hepatitis C, AIDS, renal carcinoma, cervical carcinoma, lymphoma, and condyloma acuminatum. The peptides may also be used to make monoclonal antibodies useful as potential diagnostic or therapeutic agents. The peptides may also be useful as diagnostic reagents, for example, to determine the susceptibility of an individual to a treatment regimen. Also, the peptides may be used to predict which individuals will be at substantial risk of developing chronic infection. The selection of appropriate T and B cell epitopes should allow the development of epitope based vaccines particularly towards conserved epitopes of pathogens which are characterized by high sequence variability such as HIV, HCV and Malaria

Sequence 15 AA:

Query Match 6.4%; Score 15; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 135 LQRYSEDPVPLPSR 149

Db 1 LQRYSEDPVPLPSR 15

RESULT 17

AAV98975 standard; peptide; 15 AA.

AAV98975;

07-AUG-2000 (first entry)

HLA class II binding antigen epitope peptide #164.

Human leucocyte antigen; HLA class II; antigen epitope; pharmaceutical; immune response; chronic viral disease; cancer; autoimmune disease; rheumatoid arthritis; multiple sclerosis; myasthenia gravis; AIDS; allograft rejection; allergy; Lyme disease; hepatitis; prostate cancer; glomerulonephritis; food hypersensitivity; malaria.

Unidentified.

WO9961916-A1.

02-DEC-1999.

28-MAY-1999; 99WO-US012066.

29-MAY-1998; 98US-0087192P.

(EPIIM-) EPIIMUNE INC.

Sette A, Southwood S, Sidney J;

WPI: 2000-097143/08.

New compositions containing immunogenic peptide epitopes for various HLA class II DR molecules useful for inducing helper T cell response.

Claim 1; Page 42; 60pp; English.

The present invention relates to a new pharmaceutical composition comprising a unit dose form of a peptide, or analogue, comprising an epitope selected from those represented by peptides AAV98812-Y99339 which are derived from various antigens for various human leucocyte antigen class DR molecules, representative of the world wide population. The peptide/analogue binds to an HLA class II molecule at an IC-50 of less than or equal to 1,000 nM. The pharmaceutical can be used to induce a helper T cell response. The pharmaceutical focuses the immune response towards selected determinants and could therefore be used in cases of chronic viral diseases and cancer. Examples of diseases that can be treated using the peptide containing pharmaceutical include autoimmune diseases (rheumatoid arthritis, multiple sclerosis, and myasthenia gravis), allograft rejection, allergies, Lyme disease, hepatitis, post-streptococcal endocarditis or glomerulonephritis and food hypersensitivities. The peptide epitopes can be used to enhance immune responses against other immunogens administered with the peptides. Diseases against other immunogens administered with the peptides include cancer, hepatitis B, hepatitis C, AIDS, renal carcinoma, cervical carcinoma, lymphoma, and condyloma acuminatum. The peptides may also be used to make monoclonal antibodies useful as potential diagnostic or therapeutic agents. The peptides may also be useful as diagnostic reagents, for example, to determine the susceptibility of an individual to a treatment regimen. Also, the peptides may be used to predict which individuals will be at substantial risk of developing chronic infection. The selection of appropriate T and B cell epitopes should allow the development of epitope based vaccines particularly towards conserved epitopes of pathogens which are characterized by high sequence variability such as HIV, HCV and Malaria



SQ Sequence 15 AA;  
 Query Match 6.4%; Score 15; DB 3; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 203 KNGVWQVPAFGAV 217  
 |||||  
 1 KNGVWQVPAFGAV 15  
 Db  
 RESULT 18  
 AAY98967  
 ID AAY98967 standard; peptide; 15 AA.  
 AC AAY98967;  
 DT 07-AUG-2000 (first entry)  
 XX  
 XX HLA class II binding antigen epitope peptide #156.  
 DE  
 XX Human leucocyte antigen; HLA class II; antigen epitope; pharmaceutical;  
 KW immune response; chronic viral disease; cancer; autoimmune disease;  
 KW rheumatoid arthritis; multiple sclerosis; myasthenia gravis; AIDS;  
 KW allograft rejection; allergy; Lyme disease; hepatitis; prostate cancer;  
 KW glomerulonephritis; food hypersensitivity; malaria.  
 XX  
 OS Unidentified.  
 XX  
 XX MO961916-A1.  
 XX  
 XX 02-DEC-1999.  
 XX  
 XX 28-MAY-1999; 99WO-US012066.  
 XX  
 XX 29-MAY-1998; 98US-0087192P.  
 XX  
 PA (EPRM-) EPRIMUNE INC.  
 PI Sette A, Southwood S, Sidney J;  
 XX  
 XX WPI; 2000-097143/08.  
 DR  
 XX  
 PT New compositions containing immunogenic peptide epitopes for various HLA  
 PT class II DR molecules useful for inducing helper T cell response.  
 XX  
 XX  
 PS Claim 1; Page 42; 60pp; English.  
 CC The present invention relates to a new pharmaceutical composition  
 CC comprising a unit dose form of a peptide, or analogue, comprising an  
 CC epitope selected from those represented by peptides AAY98812-Y99339 which  
 CC are derived from various antigens for various human leucocyte antigen  
 CC class DR molecules, representative of the world wide population. The  
 CC peptide/analogue binds to an HLA class II molecule at an IC-50 of less  
 CC than or equal to 1,000 nM. The pharmaceutical can be used to induce a  
 CC helper T cell response. The pharmaceutical focuses the immune response  
 CC towards selected determinants and could therefore be used in cases of  
 CC chronic viral diseases and cancer. Examples of diseases that can be  
 CC treated using the peptide containing pharmaceutical include autoimmune  
 CC diseases (rheumatoid arthritis, multiple sclerosis, and myasthenia  
 CC gravis), allograft rejection, allergies, Lyme disease, hepatitis, post-  
 CC streptococcal endocarditis or glomerulonephritis and food  
 CC hypersensitivities. The peptide epitopes can be used to enhance immune  
 CC responses against other immunogens administered with the peptides.  
 CC Diseases which can be treated using immunogenic mixtures include prostate  
 CC cancer, hepatitis B, hepatitis C, AIDS, renal carcinoma, cervical  
 CC carcinoma, lymphoma, and condyloma acuminatum. The peptides may also be  
 CC used to make monoclonal antibodies useful as potential diagnostic or  
 CC therapeutic agents. The peptides may also be useful as diagnostic  
 CC reagents, for example, to determine the susceptibility of an individual  
 CC to a treatment regimen. Also, the peptides may be used to predict which  
 CC individuals will be at substantial risk of developing chronic infection.  
 CC The selection of appropriate T and B cell epitopes should allow the

CC development of epitope based vaccines particularly towards conserved  
 CC epitopes of pathogens which are characterized by high sequence  
 CC variability such as HIV, HCV and Malaria  
 CC  
 SQ Sequence 15 AA;  
 Query Match 6.4%; Score 15; DB 3; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 31 YRSLLEDDMDGLVD 45  
 |||||  
 1 YRSLLEDDMDGLVD 15  
 Db  
 RESULT 19  
 AAY98972  
 ID AAY98972 standard; peptide; 15 AA.  
 AC AAY98972;  
 DT 07-AUG-2000 (first entry)  
 XX  
 XX HLA class II binding antigen epitope peptide #161.  
 DE  
 XX Human leucocyte antigen; HLA class II; antigen epitope; pharmaceutical;  
 KW immune response; chronic viral disease; cancer; autoimmune disease;  
 KW rheumatoid arthritis; multiple sclerosis; myasthenia gravis; AIDS;  
 KW allograft rejection; allergy; Lyme disease; hepatitis; prostate cancer;  
 KW glomerulonephritis; food hypersensitivity; malaria.  
 XX  
 OS Unidentified.  
 XX  
 XX MO961916-A1.  
 XX  
 XX 02-DEC-1999.  
 XX  
 XX 28-MAY-1999; 99WO-US012066.  
 XX  
 XX 29-MAY-1998; 98US-0087192P.  
 XX  
 PA (EPRM-) EPRIMUNE INC.  
 PI Sette A, Southwood S, Sidney J;  
 XX  
 XX WPI; 2000-097143/08.  
 DR  
 XX  
 PT New compositions containing immunogenic peptide epitopes for various HLA  
 PT class II DR molecules useful for inducing helper T cell response.  
 XX  
 XX  
 PS Claim 1; Page 42; 60pp; English.  
 CC The present invention relates to a new pharmaceutical composition  
 CC comprising a unit dose form of a peptide, or analogue, comprising an  
 CC epitope selected from those represented by peptides AAY98812-Y99339 which  
 CC are derived from various antigens for various human leucocyte antigen  
 CC class DR molecules, representative of the world wide population. The  
 CC peptide/analogue binds to an HLA class II molecule at an IC-50 of less  
 CC than or equal to 1,000 nM. The pharmaceutical can be used to induce a  
 CC helper T cell response. The pharmaceutical focuses the immune response  
 CC towards selected determinants and could therefore be used in cases of  
 CC chronic viral diseases and cancer. Examples of diseases that can be  
 CC treated using the peptide containing pharmaceutical include autoimmune  
 CC diseases (rheumatoid arthritis, multiple sclerosis, and myasthenia  
 CC gravis), allograft rejection, allergies, Lyme disease, hepatitis, post-  
 CC streptococcal endocarditis or glomerulonephritis and food  
 CC hypersensitivities. The peptide epitopes can be used to enhance immune  
 CC responses against other immunogens administered with the peptides.  
 CC Diseases which can be treated using immunogenic mixtures include prostate  
 CC cancer, hepatitis B, hepatitis C, AIDS, renal carcinoma, cervical  
 CC carcinoma, lymphoma, and condyloma acuminatum. The peptides may also be  
 CC used to make monoclonal antibodies useful as potential diagnostic or  
 CC therapeutic agents. The peptides may also be useful as diagnostic

CC reagents, for example, to determine the susceptibility of an individual  
CC to a treatment regimen. Also, the peptides may be used to predict which  
CC individuals will be at substantial risk of developing chronic infection.  
CC The selection of appropriate T and B cell epitopes should allow the  
CC development of epitope based vaccines particularly towards conserved  
CC epitopes of pathogens which are characterized by high sequence  
CC variability such as HIV, HCV and Malaria  
XX  
SQ Sequence 15 AA;  
Query Match 6.4%; Score 15; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 109 SDVFDGDLGMGAAG 123  
1 SDVFDGDLGMGAAG 15  
DB 1 SDVFDGDLGMGAAG 15  
RESULT 20  
ID AAY98874 standard; peptide; 15 AA.  
XX AAY98874;  
AC AAY98874;  
XX AAY98874;  
DT 07-AUG-2000 (first entry)  
XX  
DE HLA class II binding antigen epitope peptide #63.  
XX Human leucocyte antigen; HLA class II; antigen epitope; pharmaceutical;  
KW immune response; chronic viral disease; cancer; autoimmune disease;  
KW rheumatoid arthritis; multiple sclerosis; myasthenia gravis; AIDS;  
KW allograft rejection; allergy; Lyme disease; hepatitis; prostate cancer;  
KW glomerulonephritis; food hypersensitivity; malaria.  
XX  
XX Unidentified.  
OS  
XX WO9961916-A1.  
PN  
XX 02-DEC-1999.  
PD  
XX 28-MAY-1999; 99WO-US012066.  
XX  
XX 29-MAY-1998; 98US-0087192P.  
XX  
XX (EPIM-) EPIMUNE INC.  
PA  
XX Sette A, Southwood S, Sidney J;  
PI  
XX WPI, 2000-097143/08.  
XX  
XX New compositions containing immunogenic peptide epitopes for various HLA  
PT class II DR molecules useful for inducing helper T cell response.  
XX  
XX Claim 1, Page 41; 60pp; English.  
PS  
XX The present invention relates to a new pharmaceutical composition  
CC comprising a unit dose form of a peptide, or analogue, comprising an  
CC epitope selected from those represented by peptides AAY98812-Y99339 which  
CC are derived from various antigens for various human leucocyte antigen  
CC class DR molecules, representative of the world wide population. The  
CC peptide/analogue binds to an HLA class II molecule at an IC-50 of less  
CC than or equal to 1,000 nM. The pharmaceutical can be used to induce a  
CC helper T cell response. The pharmaceutical focuses the immune response  
CC towards selected determinants and could therefore be used in cases of  
CC chronic viral diseases and cancer. Examples of diseases that can be  
CC treated using the peptide containing pharmaceutical include autoimmune  
CC diseases (rheumatoid arthritis, multiple sclerosis, and myasthenia  
CC gravis), allograft rejection, allergies, Lyme disease, hepatitis, post-  
CC streptococcal endocarditis or glomerulonephritis and food  
CC hypersensitivities. The peptide epitopes can be used to enhance immune  
CC responses against other immunogens administered with the peptides.  
CC Diseases which can be treated using immunogenic mixtures include prostate

CC cancer, hepatitis B, hepatitis C, AIDS, renal carcinoma, cervical  
CC carcinoma, lymphoma, and condyloma acuminatum. The peptides may also be  
CC used to make monoclonal antibodies useful as potential diagnostic or  
CC therapeutic agents. The peptides may also be useful as diagnostic  
CC reagents, for example, to determine the susceptibility of an individual  
CC to a treatment regimen. Also, the peptides may be used to predict which  
CC individuals will be at substantial risk of developing chronic infection.  
CC The selection of appropriate T and B cell epitopes should allow the  
CC development of epitope based vaccines particularly towards conserved  
CC epitopes of pathogens which are characterized by high sequence  
CC variability such as HIV, HCV and Malaria  
XX  
SQ Sequence 15 AA;  
Query Match 6.4%; Score 15; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 54 QGFPCDDPAPGAGM 68  
1 QGFPCDDPAPGAGM 15  
DB 1 QGFPCDDPAPGAGM 15  
RESULT 21  
ID AAY98971 standard; peptide; 15 AA.  
XX AAY98971;  
AC AAY98971;  
XX AAY98971;  
DT 07-AUG-2000 (first entry)  
XX  
DE HLA class II binding antigen epitope peptide #160.  
XX Human leucocyte antigen; HLA class II; antigen epitope; pharmaceutical;  
KW immune response; chronic viral disease; cancer; autoimmune disease;  
KW rheumatoid arthritis; multiple sclerosis; myasthenia gravis; AIDS;  
KW allograft rejection; allergy; Lyme disease; hepatitis; prostate cancer;  
KW glomerulonephritis; food hypersensitivity; malaria.  
XX  
XX Unidentified.  
OS  
XX WO9961916-A1.  
PN  
XX 02-DEC-1999.  
PD  
XX 28-MAY-1999; 99WO-US012066.  
XX  
XX 29-MAY-1998; 98US-0087192P.  
XX  
XX (EPIM-) EPIMUNE INC.  
PA  
XX Sette A, Southwood S, Sidney J;  
PI  
XX WPI, 2000-097143/08.  
XX  
XX New compositions containing immunogenic peptide epitopes for various HLA  
PT class II DR molecules useful for inducing helper T cell response.  
XX  
XX Claim 1, Page 42; 60pp; English.  
PS  
XX The present invention relates to a new pharmaceutical composition  
CC comprising a unit dose form of a peptide, or analogue, comprising an  
CC epitope selected from those represented by peptides AAY98812-Y99339 which  
CC are derived from various antigens for various human leucocyte antigen  
CC class DR molecules, representative of the world wide population. The  
CC peptide/analogue binds to an HLA class II molecule at an IC-50 of less  
CC than or equal to 1,000 nM. The pharmaceutical can be used to induce a  
CC helper T cell response. The pharmaceutical focuses the immune response  
CC towards selected determinants and could therefore be used in cases of  
CC chronic viral diseases and cancer. Examples of diseases that can be  
CC treated using the peptide containing pharmaceutical include autoimmune  
CC diseases (rheumatoid arthritis, multiple sclerosis, and myasthenia  
CC gravis), allograft rejection, allergies, Lyme disease, hepatitis, post-



CC peptide/analogue binds to an HLA class II molecule at an IC-50 of less  
CC than or equal to 1,000 nM. The pharmaceutical can be used to induce a  
CC helper T cell response. The pharmaceutical focuses the immune response  
CC towards selected determinants and could therefore be used in cases of  
CC chronic viral diseases and cancer. Examples of diseases that can be  
CC treated using the peptide containing pharmaceutical include autoimmune  
CC diseases (rheumatoid arthritis, multiple sclerosis, and myasthenia  
CC gravis), allograft rejection, allergies, Lyme disease, hepatitis, post-  
CC streptococcal endocarditis or glomerulonephritis and food  
CC hypersensitivities. The peptide epitopes can be used to enhance immune  
CC responses against other immunogens administered with the peptides.  
CC Diseases which can be treated using immunogenic mixtures include prostate  
CC cancer, hepatitis B, hepatitis C, AIDS, renal carcinoma, cervical  
CC carcinoma, lymphoma, and condyloma acuminatum. The peptides may also be  
CC used to make monoclonal antibodies useful as potential diagnostic or  
CC therapeutic agents. The peptides may also be useful as diagnostic  
CC reagents, for example, to determine the susceptibility of an individual  
CC to a treatment regimen. Also, the peptides may be used to predict which  
CC individuals will be at substantial risk of developing chronic infection.  
CC The selection of appropriate T and B cell epitopes should allow the  
CC development of epitope based vaccines particularly towards conserved  
CC epitopes of pathogens which are characterized by high sequence  
CC variability such as HIV, HCV and Malaria  
CC  
SQ Sequence 15 AA;

Query Match 6.4%; Score 15; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 143 TVPLPSETDGYVAPL 157  
|||  
1 TVPLPSETDGYVAPL 15

Db

RESULT 24  
AAG8728

ID AAG8728 standard; peptide; 15 AA.

XX AAG8728;

XX 11-SEP-2001 (first entry)

DE HER2/NEU DR 3a motif binding peptide exemplary sequence #12.

XX Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;  
XX immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;  
XX tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.

XX Homo sapiens.

OS Synthetic.

XX WO200141787-A1.

XX 14-JUN-2001.

XX 11-DEC-2000; 2000WO-US033591.

XX 10-DEC-1999; 99US-00458299.

XX (EPI-M-) EPI-MUNE INC.

XX Pike J, Sette A, Sidney J, Southwood S, Chesnut R, Cells E;  
XX Keogh E;

XX WPI; 2001-374995/39.

XX An isolated prepared HER2/neu epitope useful in a vaccine for inducing  
XX cellular immune responses for the prevention and treatment of cancer.

XX Disclosure; Page 174; 1999P; English.

XX The present invention describes isolated prepared HER2/neu epitopes (I).

CC Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is  
CC culture in vitro and binds to a complex of an epitope (I), bound to a  
CC human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)  
CC and a second epitope and the peptide is less than 50 contiguous amino  
CC acids that have 100% identity with a native peptide sequence of HER2/neu;  
CC (3) a vaccine composition (III) comprising (II) and a pharmaceutical  
CC excipient; (4) an isolated nucleic acid encoding a peptide comprising (I)  
CC ; and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and  
CC immunostimulant activities, and can be used in vaccines. (I), (II) and  
CC (III) are useful for inducing cellular immune responses for the  
CC prevention and treatment of cancer. (I) and (II) are useful for  
CC monitoring or evaluating an immune response to a tumour-associated  
CC antigen when incubated with a T lymphocyte sample from a patient and  
CC detecting the presence of bound T lymphocyte to (I) or (II). Epitope  
CC based vaccines mean that immunosuppressive epitopes that may be present  
CC in whole antigens may be avoided. Selected epitopes may be combined to  
CC enhance immunogenicity. The possible pathological side effects caused by  
CC infectious agents or whole protein antigen is eliminated. The vaccine  
CC provides the ability to direct and focus an immune response to multiple  
CC selected antigens from the same pathogen. Epitope-based anti-tumour  
CC vaccines provides the opportunity to combine epitopes derived from  
CC multiple tumour-associated molecules addressing the problem of tumour-  
CC tumour variability and reducing the likelihood of tumour escape due to  
CC antigen loss. AAG8726 to AAG89121 represent amino acid sequences used in  
CC the exemplification of the present invention  
CC  
SQ Sequence 15 AA;

Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 143 TVPLPSETDGYVAPL 157  
|||  
1 TVPLPSETDGYVAPL 15

Db

RESULT 25  
AAG89108

ID AAG89108 standard; peptide; 15 AA.

XX AAG89108;

XX 11-SEP-2001 (first entry)

DE HER2/neu DR3 binding peptide #43.

XX Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;  
XX immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;  
XX tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.

XX Homo sapiens.

OS Synthetic.

XX WO200141787-A1.

XX 14-JUN-2001.

XX 11-DEC-2000; 2000WO-US033591.

XX 10-DEC-1999; 99US-00458299.

XX (EPI-M-) EPI-MUNE INC.

XX Pike J, Sette A, Sidney J, Southwood S, Chesnut R, Cells E;  
XX Keogh E;

XX WPI; 2001-374995/39.

XX An isolated prepared HER2/neu epitope useful in a vaccine for inducing  
XX cellular immune responses for the prevention and treatment of cancer.

XX Example 5; Page 192; 1999P; English.

XX The present invention describes isolated prepared HER2/neu epitopes (I) .  
CC Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is  
CC culture in vitro and binds to a complex of an epitope (I) , bound to a  
CC human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)  
CC and a second epitope and the peptide is less than 50 contiguous amino  
CC acids that have 100% identity with a native peptide sequence of HER2/neu;  
CC (3) a vaccine composition (III) comprising (II) and a pharmaceutical  
CC excipient; (4) an isolated nucleic acid encoding a peptide comprising (I)  
CC ; and (5) an isolated nucleic acid encoding (II) . (I) has cytostatic and  
CC immunostimulant activities, and can be used in vaccines. (I) , (II) and  
CC (III) are useful for inducing cellular immune responses for the  
CC prevention and treatment of cancer. (I) and (II) are useful for  
CC monitoring or evaluating an immune response to a tumour-associated  
CC antigen when incubated with a T lymphocyte sample from a patient and  
CC detecting the presence of bound T lymphocyte to (I) or (II) . Epitope  
CC based vaccines mean that immunosuppressive epitopes that may be present  
CC in whole antigens may be avoided. Selected epitopes may be combined to  
CC enhance immunogenicity. The possible pathological side effects caused by  
CC infectious agents or whole protein antigen is eliminated. The vaccine  
CC provides the ability to direct and focus an immune response to multiple  
CC selected antigens from the same pathogen. Epitope-based anti-tumour  
CC vaccines provides the opportunity to combine epitopes derived from  
CC multiple tumour-associated molecules addressing the problem of tumour-  
CC tumour variability and reducing the likelihood of tumour escape due to  
CC antigen loss. AAG88266 to AAG89121 represent amino acid sequences used in  
CC the exemplification of the present invention  
XX  
SQ Sequence 15 AA;

Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 143 TVPLPSETDGYAPL 157  
Db 1 TVPLPSETDGYAPL 15

RESULT 26  
AAG88326  
ID AAG88326 standard; peptide; 15 AA.  
AC AAG88326;  
XX  
DT 11-SEP-2001 (first entry)  
XX  
DE HER2/NEU DR supermotif binding peptide exemplary sequence #19.  
XX  
KM Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;  
KM Immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;  
KM tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200141787-A1.  
XX  
PD 14-JUN-2001.  
XX  
PF 11-DEC-2000; 2000MO-US033591.  
XX  
PR 10-DEC-1999; 99US-00458299.  
XX  
PA (EPIM-) EPIMUNE INC.  
XX  
PI Pikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;  
PI Keogh E;  
XX  
XX WPI, 2001-374995/39.  
XX  
PT An isolated prepared HER2/neu epitope useful in a vaccine for inducing  
PT cellular immune responses for the prevention and treatment of cancer.

XX Disclosure; Page 166; 199pp; English.

XX The present invention describes isolated prepared HER2/neu epitopes (I) .  
XX Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is  
XX culture in vitro and binds to a complex of an epitope (I) , bound to a  
XX human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)  
XX and a second epitope and the peptide is less than 50 contiguous amino  
XX acids that have 100% identity with a native peptide sequence of HER2/neu;  
XX (3) a vaccine composition (III) comprising (II) and a pharmaceutical  
XX excipient; (4) an isolated nucleic acid encoding a peptide comprising (I)  
XX ; and (5) an isolated nucleic acid encoding (II) . (I) has cytostatic and  
XX immunostimulant activities, and can be used in vaccines. (I) , (II) and  
XX (III) are useful for inducing cellular immune responses for the  
XX prevention and treatment of cancer. (I) and (II) are useful for  
XX monitoring or evaluating an immune response to a tumour-associated  
XX antigen when incubated with a T lymphocyte sample from a patient and  
XX detecting the presence of bound T lymphocyte to (I) or (II) . Epitope  
XX based vaccines mean that immunosuppressive epitopes that may be present  
XX in whole antigens may be avoided. Selected epitopes may be combined to  
XX enhance immunogenicity. The possible pathological side effects caused by  
XX infectious agents or whole protein antigen is eliminated. The vaccine  
XX provides the ability to direct and focus an immune response to multiple  
XX selected antigens from the same pathogen. Epitope-based anti-tumour  
XX vaccines provides the opportunity to combine epitopes derived from  
XX multiple tumour-associated molecules addressing the problem of tumour-  
XX tumour variability and reducing the likelihood of tumour escape due to  
XX antigen loss. AAG88266 to AAG89121 represent amino acid sequences used in  
XX the exemplification of the present invention  
XX  
SQ Sequence 15 AA;

Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 DGDPLGMAAKGQSL 127  
Db 1 DGDPLGMAAKGQSL 15

RESULT 27  
AAG88362  
ID AAG88362 standard; peptide; 15 AA.  
AC AAG88362;  
XX  
DT 11-SEP-2001 (first entry)  
XX  
DE HER2/NEU DR supermotif binding peptide exemplary sequence #37.  
XX  
KM Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;  
KM Immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;  
KM tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200141787-A1.  
XX  
PD 14-JUN-2001.  
XX  
PF 11-DEC-2000; 2000MO-US033591.  
XX  
PR 10-DEC-1999; 99US-00458299.  
XX  
PA (EPIM-) EPIMUNE INC.  
XX  
PI Pikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;  
PI Keogh E;  
XX  
XX WPI, 2001-374995/39.  
XX  
DR

PT An isolated prepared HER2/neu epitope useful in a vaccine for inducing  
PT cellular immune responses for the prevention and treatment of cancer.  
XX  
PS Disclosure; Page 166; 199pp; English.

XX The present invention describes isolated prepared HER2/neu epitopes (I).  
CC Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is  
CC culture in vitro and binds to a complex of an epitope (I), bound to a  
CC human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)  
CC and a second epitope and the peptide is less than 50 contiguous amino  
CC acids that have 100% identity with a native peptide sequence of HER2/neu;  
CC (3) a vaccine composition (III) comprising (II) and a pharmaceutical  
CC excipient; (4) an isolated nucleic acid encoding a peptide comprising (I)  
CC and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and  
CC immunostimulant activities, and can be used in vaccines. (I), (II) and  
CC (III) are useful for inducing cellular immune responses for the  
CC prevention and treatment of cancer. (I) and (II) are useful for  
CC monitoring or evaluating an immune response to a tumour-associated  
CC antigen when incubated with a T lymphocyte sample from a patient and  
CC detecting the presence of bound T lymphocyte to (I) or (II). Epitope  
CC based vaccines mean that immunosuppressive epitopes that may be present  
CC in whole antigens may be avoided. Selected epitopes may be combined to  
CC enhance immunogenicity. The possible pathological side effects caused by  
CC infectious agents or whole protein antigen is eliminated. The vaccine  
CC provides the ability to direct and focus an immune response to multiple  
CC selected antigens from the same pathogen. Epitope-based anti-tumour  
CC vaccines provides the opportunity to combine epitopes derived from  
CC multiple tumour-associated molecules addressing the problem of tumour-  
CC tumour variability and reducing the likelihood of tumour escape due to  
CC antigen loss. AAG88266 to AAG89121 represent amino acid sequences used in  
CC the exemplification of the present invention

XX Sequence 15 AA;

Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 190 GATLERPPTLSFGKN 204  
1 GATLERPPTLSFGKN 15

RESULT 28

ID AAG89099 standard; peptide; 15 AA.

AC AAG89099;

DT 11-SEP-2001 (first entry)

DE HER2/neu DR3 binding peptide #34.

XX Human; HER2/neu; epitope; human leukocyte antigen, HLA; T cell;

KW immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;

KW tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.

XX Homo sapiens.

OS Synthetic.

PN WO200141787-A1.

PD 14-JUN-2001.

PF 11-DEC-2000; 2000WO-US033591.

PR 10-DEC-1999; 99US-00458299.

PA (EPIM-) EPIMUNE INC.

PI Files J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;

PI Keogh E;

XX

DR WPI; 2001-374995/39.

PT An isolated prepared HER2/neu epitope useful in a vaccine for inducing  
PT cellular immune responses for the prevention and treatment of cancer.  
XX  
PS Example 5; Page 192; 199pp; English.

XX The present invention describes isolated prepared HER2/neu epitopes (I).  
CC Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is  
CC culture in vitro and binds to a complex of an epitope (I), bound to a  
CC human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)  
CC and a second epitope and the peptide is less than 50 contiguous amino  
CC acids that have 100% identity with a native peptide sequence of HER2/neu;  
CC (3) a vaccine composition (III) comprising (II) and a pharmaceutical  
CC excipient; (4) an isolated nucleic acid encoding a peptide comprising (I)  
CC and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and  
CC immunostimulant activities, and can be used in vaccines. (I), (II) and  
CC (III) are useful for inducing cellular immune responses for the  
CC prevention and treatment of cancer. (I) and (II) are useful for  
CC monitoring or evaluating an immune response to a tumour-associated  
CC antigen when incubated with a T lymphocyte sample from a patient and  
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CC based vaccines mean that immunosuppressive epitopes that may be present  
CC in whole antigens may be avoided. Selected epitopes may be combined to  
CC enhance immunogenicity. The possible pathological side effects caused by  
CC infectious agents or whole protein antigen is eliminated. The vaccine  
CC provides the ability to direct and focus an immune response to multiple  
CC selected antigens from the same pathogen. Epitope-based anti-tumour  
CC vaccines provides the opportunity to combine epitopes derived from  
CC multiple tumour-associated molecules addressing the problem of tumour-  
CC tumour variability and reducing the likelihood of tumour escape due to  
CC antigen loss. AAG88266 to AAG89121 represent amino acid sequences used in  
CC the exemplification of the present invention

XX Sequence 15 AA;

Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FSRMADPQRFVVIQ 16  
1 FSRMADPQRFVVIQ 15

RESULT 29

ID AAG88294 standard; peptide; 15 AA.

AC AAG88294;

DT 11-SEP-2001 (first entry)

DE HER2/NEU DR supermotif binding peptide exemplary sequence #3.

XX Human; HER2/neu; epitope; human leukocyte antigen, HLA; T cell;

KW immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;

KW tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.

XX Homo sapiens.

OS Synthetic.

PN WO200141787-A1.

PD 14-JUN-2001.

PF 11-DEC-2000; 2000WO-US033591.

PR 10-DEC-1999; 99US-00458299.

PA (EPIM-) EPIMUNE INC.

PI Files J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;

PI

PI Keogh E;  
XX  
DR WPI; 2001-374995/39.  
XX  
PT An isolated prepared HER2/neu epitope useful in a vaccine for inducing  
XX cellular immune responses for the prevention and treatment of cancer.  
PS  
XX Disclosure; Page 166; 1999p; English.  
XX  
XX The present invention describes isolated prepared HER2/neu epitopes (I).  
XX Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is  
XX culture in vitro and binds to a complex of an epitope (I), bound to a  
XX human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)  
XX and a second epitope and the peptide is less than 50 contiguous amino  
XX acids that have 100% identity with a native peptide sequence of HER2/neu;  
XX (3) a vaccine composition (III) comprising (II) and a pharmaceutical  
XX excipient; (4) an isolated nucleic acid encoding a peptide comprising (I)  
XX; and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and  
XX immunostimulant activities, and can be used in vaccines. (I), (II) and  
XX (III) are useful for inducing cellular immune responses for the  
XX prevention and treatment of cancer. (I) and (II) are useful for  
XX monitoring or evaluating an immune response to a tumour-associated  
XX antigen when incubated with a T lymphocyte sample from a patient and  
XX detecting the presence of bound T lymphocyte to (I) or (II). Epitope  
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XX in whole antigens may be avoided. Selected epitopes may be combined to  
XX enhance immunogenicity. The possible pathological side effects caused by  
XX infectious agents or whole protein antigen is eliminated. The vaccine  
XX provides the ability to direct and focus an immune response to multiple  
XX selected antigens from the same pathogen. Epitope-based anti-tumour  
XX vaccines provides the opportunity to combine epitopes derived from  
XX multiple tumour-associated molecules addressing the problem of tumour-  
XX tumour variability and reducing the likelihood of tumour escape due to  
XX antigen loss. AAG88266 to AAG89121 represent amino acid sequences used in  
XX the exemplification of the present invention  
SQ Sequence 15 AA;  
Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 121 AKGLQSLPTHDPSPL 135  
DB 1 AKGLQSLPTHDPSPL 15  
RESULT 30  
AAG88474  
ID AAG88474 standard; peptide; 15 AA.  
XX  
AC AAG88474;  
XX  
DT 11-SBP-2001 (first entry)  
XX  
DE HER2/NEU DR supermotif binding peptide exemplary sequence #93.  
XX  
XX Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;  
XX immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;  
XX tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200141787-A1.  
XX  
PD 14-JUN-2001.  
XX  
PF 11-DEC-2000; 2000MO-US033591.  
XX  
PR 10-DEC-1999; 99US-00458299.  
XX  
PA (EPIM-) EPIMUNE INC.

XX  
PI Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;  
XX  
DR WPI; 2001-374995/39.  
XX  
PT An isolated prepared HER2/neu epitope useful in a vaccine for inducing  
XX cellular immune responses for the prevention and treatment of cancer.  
PS  
XX Disclosure; Page 168; 1999p; English.  
XX  
XX The present invention describes isolated prepared HER2/neu epitopes (I).  
XX Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is  
XX culture in vitro and binds to a complex of an epitope (I), bound to a  
XX human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)  
XX and a second epitope and the peptide is less than 50 contiguous amino  
XX acids that have 100% identity with a native peptide sequence of HER2/neu;  
XX (3) a vaccine composition (III) comprising (II) and a pharmaceutical  
XX excipient; (4) an isolated nucleic acid encoding a peptide comprising (I)  
XX; and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and  
XX immunostimulant activities, and can be used in vaccines. (I), (II) and  
XX (III) are useful for inducing cellular immune responses for the  
XX prevention and treatment of cancer. (I) and (II) are useful for  
XX monitoring or evaluating an immune response to a tumour-associated  
XX antigen when incubated with a T lymphocyte sample from a patient and  
XX detecting the presence of bound T lymphocyte to (I) or (II). Epitope  
XX based vaccines mean that immunosuppressive epitopes that may be present  
XX in whole antigens may be avoided. Selected epitopes may be combined to  
XX enhance immunogenicity. The possible pathological side effects caused by  
XX infectious agents or whole protein antigen is eliminated. The vaccine  
XX provides the ability to direct and focus an immune response to multiple  
XX selected antigens from the same pathogen. Epitope-based anti-tumour  
XX vaccines provides the opportunity to combine epitopes derived from  
XX multiple tumour-associated molecules addressing the problem of tumour-  
XX tumour variability and reducing the likelihood of tumour escape due to  
XX antigen loss. AAG88266 to AAG89121 represent amino acid sequences used in  
XX the exemplification of the present invention  
SQ Sequence 15 AA;  
Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 135 LQRYSDPTVPLPSE 149  
DB 1 LQRYSDPTVPLPSE 15  
RESULT 31  
AAG88720  
ID AAG88720 standard; peptide; 15 AA.  
XX  
AC AAG88720;  
XX  
DT 11-SBP-2001 (first entry)  
XX  
DE HER2/NEU DR 3a motif binding peptide exemplary sequence #28.  
XX  
XX Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;  
XX immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;  
XX tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200141787-A1.  
XX  
PD 14-JUN-2001.  
XX  
PF 11-DEC-2000; 2000MO-US033591.  
XX  
PR 10-DEC-1999; 99US-00458299.  
XX

XX (EPIM-) EPIMUNE INC.  
PA Files J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;  
PI Keogh E;  
XX WPI; 2001-374995/39.  
XX  
XX An isolated prepared HER2/neu epitope useful in a vaccine for inducing  
PT cellular immune responses for the prevention and treatment of cancer.  
XX  
XX Disclosure; Page 174; 1999p; English.  
XX  
XX The present invention describes isolated prepared HER2/neu epitopes (I).  
CC Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is  
CC culture in vitro and binds to a complex of an epitope (I), bound to a  
CC human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)  
CC and a second epitope and the peptide is less than 50 contiguous amino  
CC acids that have 100% identity with a native peptide sequence of HER2/neu;  
CC (3) a vaccine composition (III) comprising (II) and a pharmaceutical  
CC excipient; (4) an isolated nucleic acid encoding a peptide comprising (I)  
CC ; and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and  
CC immunostimulant activities, and can be used in vaccines. (I), (II) and  
CC (III) are useful for inducing cellular immune responses for the  
CC prevention and treatment of cancer. (I) and (II) are useful for  
CC monitoring or evaluating an immune response to a tumour-associated  
CC antigen when incubated with a T lymphocyte sample from a patient and  
CC detecting the presence of bound T lymphocyte to (I) or (II). Epitope  
CC based vaccines mean that immunosuppressive epitopes that may be present  
CC in whole antigens may be avoided. Selected epitopes may be combined to  
CC enhance immunogenicity. The possible pathological side effects caused by  
CC infectious agents or whole protein antigen is eliminated. The vaccine  
CC provides the ability to direct and focus an immune response to multiple  
CC selected antigens from the same pathogen. Epitope-based anti-tumour  
CC vaccines provides the opportunity to combine epitopes derived from  
CC multiple tumour-associated molecules addressing the problem of tumour-  
CC tumour variability and reducing the likelihood of tumour escape due to  
CC antigen loss. AAG88266 to AAG89121 represent amino acid sequences used in  
CC the exemplification of the present invention  
XX  
XX Sequence 15 AA:  
SQ  
Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 109 SDVPFGDLCMGAAKG 123  
DB 1 SDVPFGDLCMGAAKG 15  
RESULT 32  
AAG89046  
ID AAG89046 standard; peptide; 15 AA.  
XX  
XX AAG89046;  
XX  
XX 11-SEP-2001 (first entry)  
XX  
XX Her2/neu DR supertype primary binding peptide #40.  
XX  
XX Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;  
KW immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;  
KM tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.  
XX  
XX Homo sapiens.  
OS Synthetic.  
XX  
XX MO200141787-A1.  
XX  
XX 14-JUN-2001.  
XX  
XX 11-DEC-2000; 2000WO-US033591.  
XX  
XX

XX 10-DEC-1999; 99US-00458299.  
XX  
XX (EPIM-) EPIMUNE INC.  
XX  
XX Files J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;  
PI Keogh E;  
XX WPI; 2001-374995/39.  
XX  
XX An isolated prepared HER2/neu epitope useful in a vaccine for inducing  
PT cellular immune responses for the prevention and treatment of cancer.  
XX  
XX Example 5; Page 190; 1999p; English.  
XX  
XX The present invention describes isolated prepared HER2/neu epitopes (I).  
CC Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is  
CC culture in vitro and binds to a complex of an epitope (I), bound to a  
CC human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)  
CC and a second epitope and the peptide is less than 50 contiguous amino  
CC acids that have 100% identity with a native peptide sequence of HER2/neu;  
CC (3) a vaccine composition (III) comprising (II) and a pharmaceutical  
CC excipient; (4) an isolated nucleic acid encoding a peptide comprising (I)  
CC ; and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and  
CC immunostimulant activities, and can be used in vaccines. (I), (II) and  
CC (III) are useful for inducing cellular immune responses for the  
CC prevention and treatment of cancer. (I) and (II) are useful for  
CC monitoring or evaluating an immune response to a tumour-associated  
CC antigen when incubated with a T lymphocyte sample from a patient and  
CC detecting the presence of bound T lymphocyte to (I) or (II). Epitope  
CC based vaccines mean that immunosuppressive epitopes that may be present  
CC in whole antigens may be avoided. Selected epitopes may be combined to  
CC enhance immunogenicity. The possible pathological side effects caused by  
CC infectious agents or whole protein antigen is eliminated. The vaccine  
CC provides the ability to direct and focus an immune response to multiple  
CC selected antigens from the same pathogen. Epitope-based anti-tumour  
CC vaccines provides the opportunity to combine epitopes derived from  
CC multiple tumour-associated molecules addressing the problem of tumour-  
CC tumour variability and reducing the likelihood of tumour escape due to  
CC antigen loss. AAG88266 to AAG89121 represent amino acid sequences used in  
CC the exemplification of the present invention  
XX  
XX Sequence 15 AA:  
SQ  
Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 168 QPDVRRPPSPREGP 182  
DB 1 QPDVRRPPSPREGP 15  
RESULT 33  
AAG88360  
ID AAG88360 standard; peptide; 15 AA.  
XX  
XX AAG88360;  
XX  
XX 11-SEP-2001 (first entry)  
XX  
XX HER2/NEU DR supermotif binding peptide exemplary sequence #36.  
XX  
XX Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;  
KW immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;  
KM tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.  
XX  
XX Homo sapiens.  
OS Synthetic.  
XX  
XX MO200141787-A1.  
XX  
XX 14-JUN-2001.  
XX  
XX





XX WO200141787-A1.  
XX 14-JUN-2001.  
XX 11-DEC-2000; 2000WO-US033591.  
XX 10-DEC-1999; 99US-00458299.  
XX (EPIM-) EPIMUNE INC.  
XX Pikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E,  
XX Keogh E;  
XX WPI: 2001-374995/39.  
XX  
XX An isolated prepared HER2/neu epitope useful in a vaccine for inducing  
XX cellular immune responses for the prevention and treatment of cancer.  
XX  
XX Disclosure; Page 172; 199pp; English.

XX The present invention describes isolated prepared HER2/neu epitopes (I).  
XX Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is  
XX culture in vitro and binds to a complex of an epitope (I), bound to a  
XX human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)  
XX and a second epitope and the peptide is less than 50 contiguous amino  
XX acids that have 100% identity with a native peptide sequence of HER2/neu;  
XX (3) a vaccine composition (III) comprising (II) and a pharmaceutical  
XX excipient; (4) an isolated nucleic acid encoding a peptide comprising (I)  
XX ; and (5) an isolated nucleic acid encoding (II). (I) has cytosstatic and  
XX immunostimulant activities, and can be used in vaccines. (I), (II) and  
XX (III) are useful for inducing cellular immune responses for the  
XX prevention and treatment of cancer. (I) and (II) are useful for  
XX monitoring or evaluating an immune response to a tumour-associated  
XX antigen when incubated with a T lymphocyte sample from a patient and  
XX detecting the presence of bound T lymphocyte to (I) or (II). Epitope  
XX based vaccines mean that immunosuppressive epitopes that may be present  
XX in whole antigens may be avoided. Selected epitopes may be combined to  
XX enhance immunogenicity. The possible pathological side effects caused by  
XX infectious agents or whole protein antigen is eliminated. The vaccine  
XX provides the ability to direct and focus an immune response to multiple  
XX selected antigens from the same pathogen. Epitope-based anti-tumour  
XX vaccines provides the opportunity to combine epitopes derived from  
XX multiple tumour-associated molecules addressing the problem of tumour-  
XX tumour variability and reducing the likelihood of tumour escape due to  
XX antigen loss. AAG88266 to AAG89121 represent amino acid sequences used in  
XX the exemplification of the present invention  
XX  
XX Sequence 15 AA;  
XX

Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 RSLLEDDDDGDLVDA 46  
|||  
DB 1 RSLLEDDDDGDLVDA 15

RESULT 36  
AAG88514  
ID AAG88514 standard; peptide; 15 AA.

XX AAG88514;

XX 11-SEP-2001 (first entry)

XX HER2/NEU DR supermotif binding peptide exemplary sequence #113.

XX Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;  
XX Immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;  
XX tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.  
XX

OS Homo sapiens.  
OS Synthetic.  
XX WO200141787-A1.  
XX 14-JUN-2001.  
XX 11-DEC-2000; 2000WO-US033591.  
XX 10-DEC-1999; 99US-00458299.  
XX (EPIM-) EPIMUNE INC.  
XX Pikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E,  
XX Keogh E;  
XX WPI: 2001-374995/39.  
XX  
XX An isolated prepared HER2/neu epitope useful in a vaccine for inducing  
XX cellular immune responses for the prevention and treatment of cancer.  
XX  
XX Disclosure; Page 170; 199pp; English.

XX The present invention describes isolated prepared HER2/neu epitopes (I).  
XX Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is  
XX culture in vitro and binds to a complex of an epitope (I), bound to a  
XX human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)  
XX and a second epitope and the peptide is less than 50 contiguous amino  
XX acids that have 100% identity with a native peptide sequence of HER2/neu;  
XX (3) a vaccine composition (III) comprising (II) and a pharmaceutical  
XX excipient; (4) an isolated nucleic acid encoding a peptide comprising (I)  
XX ; and (5) an isolated nucleic acid encoding (II). (I) has cytosstatic and  
XX immunostimulant activities, and can be used in vaccines. (I), (II) and  
XX (III) are useful for inducing cellular immune responses for the  
XX prevention and treatment of cancer. (I) and (II) are useful for  
XX monitoring or evaluating an immune response to a tumour-associated  
XX antigen when incubated with a T lymphocyte sample from a patient and  
XX detecting the presence of bound T lymphocyte to (I) or (II). Epitope  
XX based vaccines mean that immunosuppressive epitopes that may be present  
XX in whole antigens may be avoided. Selected epitopes may be combined to  
XX enhance immunogenicity. The possible pathological side effects caused by  
XX infectious agents or whole protein antigen is eliminated. The vaccine  
XX provides the ability to direct and focus an immune response to multiple  
XX selected antigens from the same pathogen. Epitope-based anti-tumour  
XX vaccines provides the opportunity to combine epitopes derived from  
XX multiple tumour-associated molecules addressing the problem of tumour-  
XX tumour variability and reducing the likelihood of tumour escape due to  
XX antigen loss. AAG88266 to AAG89121 represent amino acid sequences used in  
XX the exemplification of the present invention  
XX  
XX Sequence 15 AA;  
XX

Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 NEDLGPAAPLDSTFY 31  
|||  
DB 1 NEDLGPAAPLDSTFY 15

RESULT 37  
AAG88540  
ID AAG88540 standard; peptide; 15 AA.

XX AAG88540;

XX 11-SEP-2001 (first entry)

XX HER2/NEU DR supermotif binding peptide exemplary sequence #126.

XX Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;  
XX Immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;  
XX

KM tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX WO200141787-A1.  
 XX 14-JUN-2001.  
 XX 11-DEC-2000; 2000WO-US033591.  
 XX 10-DEC-1999; 99US-00458299.  
 XX (EPI-M) EPI-MUNE INC.  
 XX Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Cells E;  
 PI Keogh E;  
 XX WPI; 2001-374995/39.  
 XX An isolated prepared HER2/neu epitope useful in a vaccine for inducing  
 PT cellular immune responses for the prevention and treatment of cancer.  
 XX Disclosure; Page 170; 1999p; English.  
 XX The present invention describes isolated prepared HER2/neu epitopes (I).  
 CC Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is  
 CC culture in vitro and binds to a complex of an epitope (I), bound to a  
 CC human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (1)  
 CC and a second epitope and the peptide is less than 50 contiguous amino  
 CC acids that have 100% identity with a native peptide sequence of HER2/neu;  
 CC (3) a vaccine composition (III) comprising (II) and a pharmaceutical  
 CC excipient; (4) an isolated nucleic acid encoding a peptide comprising (1)  
 CC ; and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and  
 CC immunostimulant activities, and can be used in vaccines. (I), (II) and  
 CC (III) are useful for inducing cellular immune responses for the  
 CC prevention and treatment of cancer. (I) and (II) are useful for  
 CC monitoring or evaluating an immune response to a tumour-associated  
 CC antigen when incubated with a T lymphocyte sample from a patient and  
 CC detecting the presence of bound T lymphocyte to (I) or (II). Epitope  
 CC based vaccines mean that immunosuppressive epitopes that may be present  
 CC in whole antigens may be avoided. Selected epitopes may be combined to  
 CC enhance immunogenicity. The possible pathological side effects caused by  
 CC infectious agents or whole protein antigen is eliminated. The vaccine  
 CC provides the ability to direct and focus an immune response to multiple  
 CC selected antigens from the same pathogen. Epitope-based anti-tumour  
 CC vaccines provides the opportunity to combine epitopes derived from  
 CC multiple tumour-associated molecules addressing the problem of tumour-  
 CC tumour variability and reducing the likelihood of tumour escape due to  
 CC antigen loss. AAG88266 to AAG89121 represent amino acid sequences used in  
 CC the exemplification of the present invention  
 CC XX  
 SQ Sequence 15 AA;  
 Query Match 6.4%; Score 15; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-06; Mismatches 0; Gaps 0;  
 Matches 15; Conservative 0; Indels 0;  
 QY 163 PERYNOPDVRRPPPS 177  
 Db 1 PERYNOPDVRRPPPS 15  
 RESULT 38  
 AAG88558  
 ID AAG88558 standard; peptide; 15 AA.  
 AC AAG88558;  
 XX 11-SEP-2001 (first entry)  
 DT HER2/NEU DR supermotif binding peptide exemplary sequence #135.  
 XX

KM Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;  
 XX immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;  
 KM tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX WO200141787-A1.  
 XX 14-JUN-2001.  
 XX 11-DEC-2000; 2000WO-US033591.  
 XX 10-DEC-1999; 99US-00458299.  
 XX (EPI-M) EPI-MUNE INC.  
 XX Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Cells E;  
 PI Keogh E;  
 XX WPI; 2001-374995/39.  
 XX An isolated prepared HER2/neu epitope useful in a vaccine for inducing  
 PT cellular immune responses for the prevention and treatment of cancer.  
 XX Disclosure; Page 170; 1999p; English.  
 XX The present invention describes isolated prepared HER2/neu epitopes (I).  
 CC Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is  
 CC culture in vitro and binds to a complex of an epitope (I), bound to a  
 CC human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (1)  
 CC and a second epitope and the peptide is less than 50 contiguous amino  
 CC acids that have 100% identity with a native peptide sequence of HER2/neu;  
 CC (3) a vaccine composition (III) comprising (II) and a pharmaceutical  
 CC excipient; (4) an isolated nucleic acid encoding a peptide comprising (1)  
 CC ; and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and  
 CC immunostimulant activities, and can be used in vaccines. (I), (II) and  
 CC (III) are useful for inducing cellular immune responses for the  
 CC prevention and treatment of cancer. (I) and (II) are useful for  
 CC monitoring or evaluating an immune response to a tumour-associated  
 CC antigen when incubated with a T lymphocyte sample from a patient and  
 CC detecting the presence of bound T lymphocyte to (I) or (II). Epitope  
 CC based vaccines mean that immunosuppressive epitopes that may be present  
 CC in whole antigens may be avoided. Selected epitopes may be combined to  
 CC enhance immunogenicity. The possible pathological side effects caused by  
 CC infectious agents or whole protein antigen is eliminated. The vaccine  
 CC provides the ability to direct and focus an immune response to multiple  
 CC selected antigens from the same pathogen. Epitope-based anti-tumour  
 CC vaccines provides the opportunity to combine epitopes derived from  
 CC multiple tumour-associated molecules addressing the problem of tumour-  
 CC tumour variability and reducing the likelihood of tumour escape due to  
 CC antigen loss. AAG88266 to AAG89121 represent amino acid sequences used in  
 CC the exemplification of the present invention  
 CC XX  
 SQ Sequence 15 AA;  
 Query Match 6.4%; Score 15; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-06; Mismatches 0; Gaps 0;  
 Matches 15; Conservative 0; Indels 0;  
 QY 54 QGFPCPDPAAGAGM 68  
 Db 1 QGFPCPDPAAGAGM 15  
 RESULT 39  
 AAG88672  
 ID AAG88672 standard; peptide; 15 AA.  
 AC AAG88672;  
 XX 11-SEP-2001 (first entry)  
 DT  
 XX

DE HER2/NEU DR 3a motif binding peptide exemplary sequence #4.  
XX  
XX Human, HER2/neu; epitope; human leukocyte antigen; HLA: T cell;  
KW immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;  
KW tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.  
XX  
OS Homo sapiens.  
XX Synthetic.  
XX WO200141787-A1.  
XX  
XX 14-JUN-2001.  
XX  
XX 11-DEC-2000; 2000MO-US033591.  
XX  
XX 10-DEC-1999; 99US-00458299.  
XX  
XX (EPIM-) EPIMUNE INC.  
XX  
XX Pikes J, Sette A, Sidney J, Southwood S, Chesnut R, Cells E;  
XX Keogh E;  
XX WPI; 2001-374995/39.  
XX  
XX  
XX An isolated prepared HER2/neu epitope useful in a vaccine for inducing  
XX cellular immune responses for the prevention and treatment of cancer.  
XX  
XX Disclosure; Page 174, 199pp; English.  
XX  
XX  
XX The present invention describes isolated prepared HER2/neu epitopes (I).  
XX Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is  
XX culture in vitro and binds to a complex of an epitope (I), bound to a  
XX human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)  
XX and a second epitope and the peptide is less than 50 contiguous amino  
XX acids that have 100% identity with a native peptide sequence of HER2/neu;  
XX (3) a vaccine composition (III) comprising (II) and a pharmaceutical  
XX excipient; (4) an isolated nucleic acid encoding a peptide comprising (I)  
XX ; and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and  
XX immunostimulant activities, and can be used in vaccines. (I), (II) and  
XX (III) are useful for inducing cellular immune responses for the  
XX prevention and treatment of cancer. (I) and (II) are useful for  
XX monitoring or evaluating an immune response to a tumour-associated  
XX antigen when incubated with a T lymphocyte sample form a patient and  
XX detecting the presence of bound T lymphocyte to (I) or (II). Epitope  
XX based vaccines mean that immunosuppressive epitopes that may be present  
XX in whole antigens may be avoided. Selected epitopes may be combined to  
XX enhance immunogenicity. The possible pathological side effects caused by  
XX infectious agents or whole protein antigen is eliminated. The vaccine  
XX provides the ability to direct and focus an immune response to multiple  
XX selected antigens from the same pathogen. Epitope-based anti-tumour  
XX vaccines provides the opportunity to combine epitopes derived from  
XX multiple tumour-associated molecules addressing the problem of tumour-  
XX tumour variability and reducing the likelihood of tumour escape due to  
XX antigen loss. AAG88266 to AAG89121 represent amino acid sequences used in  
XX the exemplification of the present invention  
XX  
SQ Sequence 15 AA:  
Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 84 DLTGLPESEEPAPR 98  
DB 1 DLTGLPESEEPAPR 15  
RESULT 40  
AAG88684  
ID AAG88684 standard; peptide; 15 AA.  
XX  
XX AAG88684;  
XX ,XX

DT 11-SEP-2001 (first entry)  
XX  
XX  
XX HER2/NEU DR 3a motif binding peptide exemplary sequence #10.  
XX  
XX Human, HER2/neu; epitope; human leukocyte antigen; HLA: T cell;  
KW immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;  
KW tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.  
XX  
XX Homo sapiens.  
XX Synthetic.  
XX WO200141787-A1.  
XX  
XX 14-JUN-2001.  
XX  
XX 11-DEC-2000; 2000MO-US033591.  
XX  
XX 10-DEC-1999; 99US-00458299.  
XX  
XX (EPIM-) EPIMUNE INC.  
XX  
XX Pikes J, Sette A, Sidney J, Southwood S, Chesnut R, Cells E;  
XX Keogh E;  
XX WPI; 2001-374995/39.  
XX  
XX  
XX An isolated prepared HER2/neu epitope useful in a vaccine for inducing  
XX cellular immune responses for the prevention and treatment of cancer.  
XX  
XX Disclosure; Page 174, 199pp; English.  
XX  
XX  
XX The present invention describes isolated prepared HER2/neu epitopes (I).  
XX Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is  
XX culture in vitro and binds to a complex of an epitope (I), bound to a  
XX human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)  
XX and a second epitope and the peptide is less than 50 contiguous amino  
XX acids that have 100% identity with a native peptide sequence of HER2/neu;  
XX (3) a vaccine composition (III) comprising (II) and a pharmaceutical  
XX excipient; (4) an isolated nucleic acid encoding a peptide comprising (I)  
XX ; and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and  
XX immunostimulant activities, and can be used in vaccines. (I), (II) and  
XX (III) are useful for inducing cellular immune responses for the  
XX prevention and treatment of cancer. (I) and (II) are useful for  
XX monitoring or evaluating an immune response to a tumour-associated  
XX antigen when incubated with a T lymphocyte sample form a patient and  
XX detecting the presence of bound T lymphocyte to (I) or (II). Epitope  
XX based vaccines mean that immunosuppressive epitopes that may be present  
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XX enhance immunogenicity. The possible pathological side effects caused by  
XX infectious agents or whole protein antigen is eliminated. The vaccine  
XX provides the ability to direct and focus an immune response to multiple  
XX selected antigens from the same pathogen. Epitope-based anti-tumour  
XX vaccines provides the opportunity to combine epitopes derived from  
XX multiple tumour-associated molecules addressing the problem of tumour-  
XX tumour variability and reducing the likelihood of tumour escape due to  
XX antigen loss. AAG88266 to AAG89121 represent amino acid sequences used in  
XX the exemplification of the present invention  
XX  
SQ Sequence 15 AA:  
Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 12 FVIONEDLGPASPL 26  
DB 1 FVIONEDLGPASPL 15  
RESULT 41  
AAG88566  
ID AAG88566 standard; peptide; 15 AA.  
XX  
XX AAG88566;  
XX ,XX

AC AAG88566;  
XX  
DT 11-SEP-2001 (first entry)  
XX  
DE HER2/NEU DR supermotif binding peptide exemplary sequence #139.  
XX  
KM Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;  
XX immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;  
KM tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.  
XX  
OS Homo sapiens.  
XX Synthetic.  
XX MO200141787-A1.  
XX  
PD 14-JUN-2001.  
XX  
PF 11-DEC-2000; 2000MO-US033591.  
XX  
PR 10-DEC-1999; 99US-00458299.  
XX  
PA (EPIM-) EPIMMUNE INC.  
XX  
PI Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;  
PI Keogh E;  
XX WPI; 2001-374995/39.  
XX  
PT An isolated prepared HER2/neu epitope useful in a vaccine for inducing  
PT cellular immune responses for the prevention and treatment of cancer.  
XX  
PS Disclosure; Page 170; 1999p; English.  
XX  
XX The present invention describes isolated prepared HER2/neu epitopes (I).  
XX Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is  
XX culture in vitro and binds to a complex of an epitope (I), bound to a  
XX human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)  
XX and a second epitope and the peptide is less than 50 contiguous amino  
XX acids that have 100% identity with a native peptide sequence of HER2/neu;  
XX (3) a vaccine composition (III) comprising (II) and a pharmaceutical  
XX excipient; (4) an isolated nucleic acid encoding a peptide comprising (I)  
XX; and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and  
XX immunostimulant activities, and can be used in vaccines. (I), (II) and  
XX (III) are useful for inducing cellular immune responses for the  
XX prevention and treatment of cancer. (I) and (II) are useful for  
XX monitoring or evaluating an immune response to a tumour-associated  
XX antigen when incubated with a T lymphocyte sample from a patient and  
XX detecting the presence of bound T lymphocyte to (I) or (II). Epitope  
XX based vaccines mean that immunosuppressive epitopes that may be present  
XX in whole antigens may be avoided. Selected epitopes may be combined to  
XX enhance immunogenicity. The possible pathological side effects caused by  
XX infectious agents or whole protein antigen is eliminated. The vaccine  
XX provides the ability to direct and focus an immune response to multiple  
XX selected antigens from the same pathogen. Epitope-based anti-tumour  
XX vaccines provides the opportunity to combine epitopes derived from  
XX multiple tumour-associated molecules addressing the problem of tumour-  
XX tumour variability and reducing the likelihood of tumour escape due to  
XX antigen loss. AAG88266 to AAG89121 represent amino acid sequences used in  
XX the exemplification of the present invention  
XX  
SQ Sequence 15 AA;  
XX  
Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ID AAG88682 standard; peptide; 15 AA.  
XX  
AC AAG88682;  
XX  
DT 11-SEP-2001 (first entry)  
XX  
DE HER2/NEU DR 3a motif binding peptide exemplary sequence #9.  
XX  
KM Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;  
XX immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;  
KM tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.  
XX  
OS Homo sapiens.  
XX Synthetic.  
XX MO200141787-A1.  
XX  
PD 14-JUN-2001.  
XX  
PF 11-DEC-2000; 2000MO-US033591.  
XX  
PR 10-DEC-1999; 99US-00458299.  
XX  
PA (EPIM-) EPIMMUNE INC.  
XX  
PI Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;  
PI Keogh E;  
XX WPI; 2001-374995/39.  
XX  
PT An isolated prepared HER2/neu epitope useful in a vaccine for inducing  
PT cellular immune responses for the prevention and treatment of cancer.  
XX  
PS Disclosure; Page 174; 1999p; English.  
XX  
XX The present invention describes isolated prepared HER2/neu epitopes (I).  
XX Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is  
XX culture in vitro and binds to a complex of an epitope (I), bound to a  
XX human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)  
XX and a second epitope and the peptide is less than 50 contiguous amino  
XX acids that have 100% identity with a native peptide sequence of HER2/neu;  
XX (3) a vaccine composition (III) comprising (II) and a pharmaceutical  
XX excipient; (4) an isolated nucleic acid encoding a peptide comprising (I)  
XX; and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and  
XX immunostimulant activities, and can be used in vaccines. (I), (II) and  
XX (III) are useful for inducing cellular immune responses for the  
XX prevention and treatment of cancer. (I) and (II) are useful for  
XX monitoring or evaluating an immune response to a tumour-associated  
XX antigen when incubated with a T lymphocyte sample from a patient and  
XX detecting the presence of bound T lymphocyte to (I) or (II). Epitope  
XX based vaccines mean that immunosuppressive epitopes that may be present  
XX in whole antigens may be avoided. Selected epitopes may be combined to  
XX enhance immunogenicity. The possible pathological side effects caused by  
XX infectious agents or whole protein antigen is eliminated. The vaccine  
XX provides the ability to direct and focus an immune response to multiple  
XX selected antigens from the same pathogen. Epitope-based anti-tumour  
XX vaccines provides the opportunity to combine epitopes derived from  
XX multiple tumour-associated molecules addressing the problem of tumour-  
XX tumour variability and reducing the likelihood of tumour escape due to  
XX antigen loss. AAG88266 to AAG89121 represent amino acid sequences used in  
XX the exemplification of the present invention  
XX  
SQ Sequence 15 AA;  
XX  
Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 43  
AAG89336  
ID AAG89336 standard; peptide; 15 AA.  
AC AAG89336;  
XX  
XX  
DT 11-SEP-2001 (first entry)  
XX  
XX  
DE HER2/NEU DR supermotif binding peptide exemplary sequence #24.  
XX  
XX  
KM Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;  
KW immune response; vaccine; cancer; cytostatic; immunostimulant;  
XX tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.  
OS Homo sapiens.  
OS Synthetic.  
XX  
XX  
PN WO200141787-A1.  
XX  
XX  
PD 14-JUN-2001.  
XX  
XX  
PF 11-DEC-2000; 2000WO-US033591.  
XX  
XX  
PR 10-DEC-1999; 99US-00458299.  
XX  
XX  
PA (EPIM-) EPIMUNE INC.  
XX  
PI Pikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;  
PI Keogh E;  
XX  
XX  
DR WPI; 2001-374995/39.  
XX  
XX  
PT An isolated prepared HER2/neu epitope useful in a vaccine for inducing  
PT cellular immune responses for the prevention and treatment of cancer.  
XX  
XX  
PS Disclosure; Page 166; 1999p; English.  
XX  
XX  
CC The present invention describes isolated prepared HER2/neu epitopes (I).  
CC Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is  
CC culture in vitro and binds to a complex of an epitope (I) bound to a  
CC human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)  
CC and a second epitope and the peptide is less than 50 contiguous amino  
CC acids that have 100% identity with a native peptide sequence of HER2/neu;  
CC (3) a vaccine composition (III) comprising (II) and a pharmaceutical  
CC excipient; (4) an isolated nucleic acid encoding a peptide comprising (I)  
CC; and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and  
CC immunostimulant activities, and can be used in vaccines. (I), (II) and  
CC (III) are useful for inducing cellular immune responses for the  
CC prevention and treatment of cancer. (I) and (II) are useful for  
CC monitoring or evaluating an immune response to a tumour-associated  
CC antigen when incubated with a T lymphocyte sample form a patient and  
CC detecting the presence of bound T lymphocyte to (I) or (II). Epitope  
CC based vaccines mean that immunosuppressive epitopes that may be present  
CC in whole antigens may be avoided. Selected epitopes may be combined to  
CC enhance immunogenicity. The possible pathological side effects caused by  
CC infectious agents or whole protein antigen is eliminated. The vaccine  
CC provides the ability to direct and focus an immune response to multiple  
CC selected antigens from the same pathogen. Epitope-based anti-tumour  
CC vaccines provides the opportunity to combine epitopes derived from  
CC multiple tumour-associated molecules addressing the problem of tumour-  
CC tumour variability and reducing the likelihood of tumour escape due to  
CC antigen loss. AAG89266 to AAG89121 represent amino acid sequences used in  
CC the exemplification of the present invention  
XX  
XX  
SQ Sequence 15 AA;  
XX  
XX  
Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX  
QY 27 DSTFYSLLBDDMG 41  
1 DSTFYSLLBDDMG 15  
DB

RESULT 44  
AAG9045  
ID AAG9045 standard; peptide; 15 AA.  
AC AAG9045;  
XX  
XX  
DT 11-SEP-2001 (first entry)  
XX  
XX  
DE Her2/neu DR supertype primary binding peptide #39.  
XX  
XX  
KM Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;  
KW immune response; vaccine; cancer; cytostatic; immunostimulant;  
XX tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.  
OS Homo sapiens.  
OS Synthetic.  
XX  
XX  
PN WO200141787-A1.  
XX  
XX  
PD 14-JUN-2001.  
XX  
XX  
PF 11-DEC-2000; 2000WO-US033591.  
XX  
XX  
PR 10-DEC-1999; 99US-00458299.  
XX  
XX  
PA (EPIM-) EPIMUNE INC.  
XX  
PI Pikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;  
PI Keogh E;  
XX  
XX  
DR WPI; 2001-374995/39.  
XX  
XX  
PT An isolated prepared HER2/neu epitope useful in a vaccine for inducing  
PT cellular immune responses for the prevention and treatment of cancer.  
XX  
XX  
PS Example 5; Page 190; 1999p; English.  
XX  
XX  
CC The present invention describes isolated prepared HER2/neu epitopes (I).  
CC Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is  
CC culture in vitro and binds to a complex of an epitope (I) bound to a  
CC human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)  
CC and a second epitope and the peptide is less than 50 contiguous amino  
CC acids that have 100% identity with a native peptide sequence of HER2/neu;  
CC (3) a vaccine composition (III) comprising (II) and a pharmaceutical  
CC excipient; (4) an isolated nucleic acid encoding a peptide comprising (I)  
CC; and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and  
CC immunostimulant activities, and can be used in vaccines. (I), (II) and  
CC (III) are useful for inducing cellular immune responses for the  
CC prevention and treatment of cancer. (I) and (II) are useful for  
CC monitoring or evaluating an immune response to a tumour-associated  
CC antigen when incubated with a T lymphocyte sample form a patient and  
CC detecting the presence of bound T lymphocyte to (I) or (II). Epitope  
CC based vaccines mean that immunosuppressive epitopes that may be present  
CC in whole antigens may be avoided. Selected epitopes may be combined to  
CC enhance immunogenicity. The possible pathological side effects caused by  
CC infectious agents or whole protein antigen is eliminated. The vaccine  
CC provides the ability to direct and focus an immune response to multiple  
CC selected antigens from the same pathogen. Epitope-based anti-tumour  
CC vaccines provides the opportunity to combine epitopes derived from  
CC multiple tumour-associated molecules addressing the problem of tumour-  
CC tumour variability and reducing the likelihood of tumour escape due to  
CC antigen loss. AAG89266 to AAG89121 represent amino acid sequences used in  
CC the exemplification of the present invention  
XX  
XX  
SQ Sequence 15 AA;  
XX  
XX  
Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX  
QY 150 TDGYVAVPLTCSPOPE 164

Db 1 TGGYVAPLTCSPQPE 15

## RESULT 45

AA689109 standard; peptide; 15 AA.

AA689109;

11-SEP-2001 (first entry)

HER2/neu DR3 binding peptide #44.

Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;  
immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;  
tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.

Homo sapiens.  
Synthetic.

WO200141787-A1.

14-JUN-2001.

11-DEC-2000; 2000MO-US033591.

10-DEC-1999; 99US-00458299.

(EPIM-) EPIMMUNE INC.

Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;  
Keogh E;

WPI; 2001-374995/39.

An isolated prepared HER2/neu epitope useful in a vaccine for inducing  
cellular immune responses for the prevention and treatment of cancer.

Example 5; Page 192; 1999P; English.

The present invention describes isolated prepared HER2/neu epitopes (I).  
Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is  
culture in vitro and binds to a complex of an epitope (I) bound to a  
human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (1)  
and a second epitope and the peptide is less than 50 contiguous amino  
acids that have 100% identity with a native peptide sequence of HER2/neu;  
(3) a vaccine composition (III) comprising (II) and a pharmaceutical  
excipient; (4) an isolated nucleic acid encoding a peptide comprising (I)  
; and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and  
immunostimulant activities, and can be used in vaccines. (I), (II) and  
(III) are useful for inducing cellular immune responses for the  
prevention and treatment of cancer. (I) and (II) are useful for  
monitoring or evaluating an immune response to a tumour-associated  
antigen when incubated with a T lymphocyte sample from a patient and  
detecting the presence of bound T lymphocyte to (I) or (II). Epitope  
based vaccines mean that immunosuppressive epitopes that may be present  
in whole antigens may be avoided. Selected epitopes may be combined to  
enhance immunogenicity. The possible pathological side effects caused by  
infectious agents or whole protein antigen is eliminated. The vaccine  
provides the ability to direct and focus an immune response to multiple  
selected antigens from the same pathogen. Epitope-based anti-tumour  
vaccines provides the opportunity to combine epitopes derived from  
multiple tumour-associated molecules addressing the problem of tumour-  
tumour variability and reducing the likelihood of tumour escape due to  
antigen loss. AA689109 to AA689121 represent amino acid sequences used in  
the exemplification of the present invention

Sequence 15 AA;

Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 203 KNGVVDVPAFGAV 217  
Db 1 KNGVVDVPAFGAV 15

## RESULT 46

AA689100 standard; peptide; 15 AA.

AA689100;

11-SEP-2001 (first entry)

HER2/neu DR3 binding peptide #35.

Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;  
immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;  
tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.

Homo sapiens.  
Synthetic.

WO200141787-A1.

14-JUN-2001.

11-DEC-2000; 2000MO-US033591.

10-DEC-1999; 99US-00458299.

(EPIM-) EPIMMUNE INC.

Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;  
Keogh E;

WPI; 2001-374995/39.

An isolated prepared HER2/neu epitope useful in a vaccine for inducing  
cellular immune responses for the prevention and treatment of cancer.

Example 5; Page 192; 1999P; English.

The present invention describes isolated prepared HER2/neu epitopes (I).  
Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is  
culture in vitro and binds to a complex of an epitope (I) bound to a  
human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (1)  
and a second epitope and the peptide is less than 50 contiguous amino  
acids that have 100% identity with a native peptide sequence of HER2/neu;  
(3) a vaccine composition (III) comprising (II) and a pharmaceutical  
excipient; (4) an isolated nucleic acid encoding a peptide comprising (I)  
; and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and  
immunostimulant activities, and can be used in vaccines. (I), (II) and  
(III) are useful for inducing cellular immune responses for the  
prevention and treatment of cancer. (I) and (II) are useful for  
monitoring or evaluating an immune response to a tumour-associated  
antigen when incubated with a T lymphocyte sample from a patient and  
detecting the presence of bound T lymphocyte to (I) or (II). Epitope  
based vaccines mean that immunosuppressive epitopes that may be present  
in whole antigens may be avoided. Selected epitopes may be combined to  
enhance immunogenicity. The possible pathological side effects caused by  
infectious agents or whole protein antigen is eliminated. The vaccine  
provides the ability to direct and focus an immune response to multiple  
selected antigens from the same pathogen. Epitope-based anti-tumour  
vaccines provides the opportunity to combine epitopes derived from  
multiple tumour-associated molecules addressing the problem of tumour-  
tumour variability and reducing the likelihood of tumour escape due to  
antigen loss. AA689100 to AA689121 represent amino acid sequences used in  
the exemplification of the present invention

Sequence 15 AA;

Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 FVVIONEDLGPASPL 26  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 FVVIONEDLGPASPL 15

## RESULT 47

AA689101 standard; peptide; 15 AA.

AA689101;

11-SEP-2001 (first entry)

HER2/neu DR3 binding peptide #36.

Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;  
immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;  
tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.

Homo sapiens.  
Synthetic.

MO200141787-A1.

14-JUN-2001.

11-DEC-2000; 2000WO-US033591.

10-DEC-1999; 99US-00458299.

(EPI-M-) EPIIMUNE INC.

Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;  
Keogh E;

WPI; 2001-374995/39.

An isolated prepared HER2/neu epitope useful in a vaccine for inducing  
cellular immune responses for the prevention and treatment of cancer.

Example 5; Page 192; 199pp; English.

The present invention describes isolated prepared HER2/neu epitopes (I).  
Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is  
culture in vitro and binds to a complex of an epitope (I), bound to a  
human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)  
and a second epitope and the peptide is less than 50 contiguous amino  
acids that have 100% identity with a native peptide sequence of HER2/neu;  
(3) a vaccine composition (III) comprising (II) and a pharmaceutical  
excipient; (4) an isolated nucleic acid encoding a peptide comprising (I)  
; and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and  
immunostimulant activities, and can be used in vaccines. (I), (II) and  
(III) are useful for inducing cellular immune responses for the  
prevention and treatment of cancer. (I) and (II) are useful for  
monitoring or evaluating an immune response to a tumour-associated  
antigen when incubated with a T lymphocyte sample from a patient and  
detecting the presence of bound T lymphocyte to (I) or (II). Epitope  
based vaccines mean that immunosuppressive epitopes that may be present  
in whole antigens may be avoided. Selected epitopes may be combined to  
enhance immunogenicity. The possible pathological side effects caused by  
infectious agents or whole protein antigen is eliminated. The vaccine  
provides the ability to direct and focus an immune response to multiple  
selected antigens from the same pathogen. Epitope-based anti-tumour  
vaccines provides the opportunity to combine epitopes derived from  
multiple tumour-associated molecules addressing the problem of tumour-  
tumour variability and reducing the likelihood of tumour escape due to  
antigen loss. AA688266 to AA689121 represent amino acid sequences used in  
the exemplification of the present invention

Sequence 15 AA;

Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 31 YRSLLDDDDMGDLVD 45  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 YRSLLDDDDMGDLVD 15

## RESULT 48

AA689105 standard; peptide; 15 AA.

AA689105;

11-SEP-2001 (first entry)

HER2/neu DR3 binding peptide #40.

Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;  
immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;  
tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.

Homo sapiens.  
Synthetic.

MO200141787-A1.

14-JUN-2001.

11-DEC-2000; 2000WO-US033591.

10-DEC-1999; 99US-00458299.

(EPI-M-) EPIIMUNE INC.

Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;  
Keogh E;

WPI; 2001-374995/39.

An isolated prepared HER2/neu epitope useful in a vaccine for inducing  
cellular immune responses for the prevention and treatment of cancer.

Example 5; Page 192; 199pp; English.

The present invention describes isolated prepared HER2/neu epitopes (I).  
Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is  
culture in vitro and binds to a complex of an epitope (I), bound to a  
human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)  
and a second epitope and the peptide is less than 50 contiguous amino  
acids that have 100% identity with a native peptide sequence of HER2/neu;  
(3) a vaccine composition (III) comprising (II) and a pharmaceutical  
excipient; (4) an isolated nucleic acid encoding a peptide comprising (I)  
; and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and  
immunostimulant activities, and can be used in vaccines. (I), (II) and  
(III) are useful for inducing cellular immune responses for the  
prevention and treatment of cancer. (I) and (II) are useful for  
monitoring or evaluating an immune response to a tumour-associated  
antigen when incubated with a T lymphocyte sample from a patient and  
detecting the presence of bound T lymphocyte to (I) or (II). Epitope  
based vaccines mean that immunosuppressive epitopes that may be present  
in whole antigens may be avoided. Selected epitopes may be combined to  
enhance immunogenicity. The possible pathological side effects caused by  
infectious agents or whole protein antigen is eliminated. The vaccine  
provides the ability to direct and focus an immune response to multiple  
selected antigens from the same pathogen. Epitope-based anti-tumour  
vaccines provides the opportunity to combine epitopes derived from  
multiple tumour-associated molecules addressing the problem of tumour-  
tumour variability and reducing the likelihood of tumour escape due to  
antigen loss. AA688266 to AA689121 represent amino acid sequences used in  
the exemplification of the present invention



XX Sequence 15 AA; Score 15; DB 4; Length 15;  
 Query Match 6.4%; Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 84 DLTGLPEPSEERAPR 98  
 DB 1 DLTGLPEPSEERAPR 15

RESULT 49  
 AAG88346  
 ID AAG88346 standard; peptide; 15 AA.  
 AC AAG88346;  
 XX  
 DT 11-SEP-2001 (first entry)  
 XX  
 DE HER2/NEU DR supermotif binding peptide exemplary sequence #29.  
 XX  
 KM Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;  
 KM immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;  
 KM tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.  
 OS Homo sapiens.  
 OS Synthetic.  
 PN WO200141787-A1.  
 XX  
 PD 14-JUN-2001.  
 XX  
 PF 11-DEC-2000; 2000MO-US033591.  
 XX  
 PR 10-DEC-1999; 99US-00458299.  
 XX  
 PA (EPIM-) EPIMMUNE INC.  
 PI Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;  
 PI Keogh E;  
 XX  
 WPI; 2001-374995/39.  
 XX  
 PT An isolated prepared HER2/neu epitope useful in a vaccine for inducing  
 PT cellular immune responses for the prevention and treatment of cancer.  
 XX  
 PS Disclosure; Page 166; 199pp; English.

The present invention describes isolated prepared HER2/neu epitopes (I).  
 CC Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is  
 CC culture in vitro and binds to a complex of an epitope (I), bound to a  
 CC human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (1)  
 CC and a second epitope and the peptide is less than 50 contiguous amino  
 CC acids that have 100% identity with a native peptide sequence of HER2/neu;  
 CC (3) a vaccine composition (III) comprising (II) and a pharmaceutical  
 CC excipient; (4) an isolated nucleic acid encoding a peptide comprising (I)  
 CC ; and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and  
 CC immunostimulant activities, and can be used in vaccines. (I), (II) and  
 CC (III) are useful for inducing cellular immune responses for the  
 CC prevention and treatment of cancer. (I) and (II) are useful for  
 CC monitoring or evaluating an immune response to a tumour-associated  
 CC antigen when incubated with a T lymphocyte sample from a patient and  
 CC detecting the presence of bound T lymphocyte to (I) or (II). Epitope  
 CC based vaccines mean that immunosuppressive epitopes that may be present  
 CC in whole antigens may be avoided. Selected epitopes may be combined to  
 CC enhance immunogenicity. The possible pathological side effects caused by  
 CC infectious agents or whole protein antigen is eliminated. The vaccine  
 CC provides the ability to direct and focus an immune response to multiple  
 CC selected antigens from the same pathogen. Epitope-based anti-tumour  
 CC vaccines provides the opportunity to combine epitopes derived from  
 CC multiple tumour-associated molecules addressing the problem of tumour-  
 CC tumour variability and reducing the likelihood of tumour escape due to

CC antigen loss. AAG88266 to AAG89121 represent amino acid sequences used in  
 CC the exemplification of the present invention  
 CC  
 XX Sequence 15 AA; Score 15; DB 4; Length 15;  
 Query Match 6.4%; Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 180 EGPLPAPRPAGATLE 194  
 DB 1 EGPLPAPRPAGATLE 15

RESULT 50  
 AAG89104  
 ID AAG89104 standard; peptide; 15 AA.  
 AC AAG89104;  
 XX  
 DT 11-SEP-2001 (first entry)  
 XX  
 DE HER2/NEU DR3 binding peptide #39.  
 XX  
 KM Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;  
 KM immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;  
 KM tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.  
 OS Homo sapiens.  
 OS Synthetic.  
 PN WO200141787-A1.  
 XX  
 PD 14-JUN-2001.  
 XX  
 PF 11-DEC-2000; 2000MO-US033591.  
 XX  
 PR 10-DEC-1999; 99US-00458299.  
 XX  
 PA (EPIM-) EPIMMUNE INC.  
 PI Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;  
 PI Keogh E;  
 XX  
 WPI; 2001-374995/39.  
 XX  
 PT An isolated prepared HER2/neu epitope useful in a vaccine for inducing  
 PT cellular immune responses for the prevention and treatment of cancer.  
 XX  
 PS Example 5; Page 192; 199pp; English.

The present invention describes isolated prepared HER2/neu epitopes (I).  
 CC Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is  
 CC culture in vitro and binds to a complex of an epitope (I), bound to a  
 CC human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (1)  
 CC and a second epitope and the peptide is less than 50 contiguous amino  
 CC acids that have 100% identity with a native peptide sequence of HER2/neu;  
 CC (3) a vaccine composition (III) comprising (II) and a pharmaceutical  
 CC excipient; (4) an isolated nucleic acid encoding a peptide comprising (I)  
 CC ; and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and  
 CC immunostimulant activities, and can be used in vaccines. (I), (II) and  
 CC (III) are useful for inducing cellular immune responses for the  
 CC prevention and treatment of cancer. (I) and (II) are useful for  
 CC monitoring or evaluating an immune response to a tumour-associated  
 CC antigen when incubated with a T lymphocyte sample from a patient and  
 CC detecting the presence of bound T lymphocyte to (I) or (II). Epitope  
 CC based vaccines mean that immunosuppressive epitopes that may be present  
 CC in whole antigens may be avoided. Selected epitopes may be combined to  
 CC enhance immunogenicity. The possible pathological side effects caused by  
 CC infectious agents or whole protein antigen is eliminated. The vaccine  
 CC provides the ability to direct and focus an immune response to multiple  
 CC selected antigens from the same pathogen. Epitope-based anti-tumour  
 CC vaccines provides the opportunity to combine epitopes derived from

multiple tumour-associated molecules addressing the problem of tumour-  
antigen variability and reducing the likelihood of tumour escape due to  
antigen loss. AAG88265 to AAG89121 represent amino acid sequences used  
in the exemplification of the present invention

**SQ** Sequence 15 AA;

Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| QY | 54 | QGFPCPDPAFGAGM | 68 |
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| Db | 1  | QGFPCPDPAFGAGM | 15 |

Search completed: January 18, 2006, 20:47:41  
Job time : 81 secs